

CGGTTCCGAG	GTGTCTGCCC	TGCTGGGTCG	TATCCCCCTCT	GCCGTCGGTT	400
ACCAGCCCAC	CCTCGCCGTC	GACATGGGTG	GCATGCAGGA	GCGTATCACC	450
ACCACCAAGA	AGGGCTCTAT	CACCTCCG			478

5

2) INFORMATION FOR SEQ ID NO: 892

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 481 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Penicillium marneffe*
(B) STRAIN: ATCC 58950
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

GTCTTTATCC	AGGAGTTGAT	TGTACGTCTT	TACCTTTCTG	CCTGACTGTT	50
TACGACAACT	AACGAAAGCG	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	100
25 TACTCTGTCT	TCACTGGTGT	CGGTGAACGT	ACTCGTGAGG	GTAACGATTT	150
GTACCACGAA	ATGCAGGAAA	CTGGTGTCAT	TCAGCTCGAG	GGTGAATCCA	200
AGGTCGCCCT	CGTGTTCCGT	CAGATGAACG	AGCCCCCCGG	TGCCCCGTGCC	250
CGTGTCGCTC	TTACTGGTTT	GACCATTGCC	GAGTACTTCC	GTGACGAGGA	300
AGGTCAGGAC	GTGCTTCTCT	TCATTGACAA	CATTTTCCGT	TTCACTCAGG	350
30 CCGGTTCTGA	GGTGTCTGCC	CTTCTGGGTC	GTATCCCCTC	TGCCGTCCGT	400
TACCAGCCCA	CCCTTGCCGT	CGACATGGGT	ATCATGCAGG	AGCGTATTAC	450
CACCACCACC	AAGGGTTCCA	TCACCTCCGT	C		481

35

2) INFORMATION FOR SEQ ID NO: 893

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 1208 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 45 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: ATCC 14285
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
CGTCGGCCCC	GGTACCCTCG	GTCGCATCAT	GAACGTCACC	GGTGACCCGA	100
TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCCGTCC	CATCCACGCT	150
55 GAGGCTCCCG	AGTTCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCGT	GGTGGTAAGA	250
TTGGTCTGTT	TGGCGGTGCC	GGTGTGGCA	AGACCGTGTT	CATCCAGGAG	300
CTCATCAACA	ACATCGCCAA	GGCCCACGGT	GGTTACTCCG	TCTTCACCGG	350
TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
60 AGACCTCTGT	CATTCAGCTT	GACGGTGACT	CCAAGGTCGC	CCTGGTGTTC	450

	GGTCAGATGA	ACGAGCCCCC	TGGTGCTCGT	GCCCGTGTCTG	CCTTGACCGG	500
	TTTGACTGTC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCCTTGTCG	TACAGTTCCA	AATCGAAGAA	TTACTAACTT	600
	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
5	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATTC	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCGCTGACG	800
	ATCTGACGGA	TCCCCGCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
	ACTGTGCTGT	CCCGAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCTGA	900
10	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGC	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGACGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCCTGAGCC	1100
	AGCCGTTTAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150
15	GATCTGAAGG	ACACTATCGC	TTCGTTCAAG	GCTATCCTGA	GCGGTGAGGG	1200
	TGACAGCC					1208

20 2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

35	TTCAGGAACT	TATTGTAAGC	CGCCCTCTTT	ATGCATTGAG	GGTGAATAAG	50
	AAGGCTGACA	GGTAATAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	100
	CGTGTTCACT	GGTGTCCGGT	AGCGTACCCG	TGAAGGAAAC	GATCTGTACC	150
	ATGAAATGCA	GGAAACCCGC	GTCATCCAGC	TTGATGGCGA	GTCTAAGGTC	200
40	GCCCTTGTTG	TCGGTCAGAT	GAACGAGCCC	CCTGGAGCCC	GTGCCCCTGT	250
	CGCTCTTACT	GGTCTTACCG	TTGCCGAATA	CTTCCGTGAC	GAGGAGGGCC	300
	AAGATGGTAT	GCCTTTTAC	TCTTCTTATT	CTTCGGGTCG	GACTACAGAA	350
	CTAACCCTGCT	CCAGTGCTTC	TCTTCATTGA	TAACATTTTC	CGTTTCACAC	400
	AAGCCGGTTC	TGAGGTGTCT	GCCTTGCTTG	GACGTATTCC	CTCTGCCGTC	450
45	GGTTACCAGC	CCACTCTCGC	CGTCGACATG	GGTGGTATGC	AGGAACGTAT	500
	CACAACCACC	AACAAGGGTT	CCATTACTTC	CGTG		534

50 2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

5	CAAGGCTCAC	GGTGGTTACT	CCGTCTTCAC	TGGTGTCTGGT	GAGCGTACCC	50
	GTGAGGGTAA	CGATCTGTAC	CACGAAATGC	AGGAGACCTC	GGTCATTTCAG	100
	CTCGAGGGCG	AGTCTAAGGT	GGCCCTGGTC	TTTGGTCAGA	TGAACGAGCC	150
	CCCGGGTGCT	CGTGCCCGTG	TCGCTCTTAC	TGGTCTTACC	GTCGCCGAGT	200
10	ACTTCCGTGA	CCAGGAGGGT	CAGGATGGTT	AGTTCTCGTC	CACTCATGCC	250
	GAAACATGTG	CGTGTTCGGA	GGCTAATCAA	CGTGCCAGTG	CTGCTTTTCA	300
	TCGACAACAT	TTTCCGATTG	ACCCAGGCCG	GTTCCGAGGT	GTCTGCCCTG	350
	CTGGGTCGTA	TCCCCTCTGC	CGTCGGTTAC	CAGCCCACCC	TCGCCGTCGA	400
15	CATGGGTGGC	ATGCAGGAGC	GTATCACCAC	CACCAAGAAG	GGCTCTAT	448

2) INFORMATION FOR SEQ ID NO: 896

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

35	ATTCAGGAGC	TGATTGTAAG	TTGCCAATCC	ATGAACTGGA	GATTTGGTGT	50
	GACCCATAGA	ACTAACAAAT	TATTTAGAAC	AACATCGCCA	AGGCTCACGG	100
	TGGTTACTCC	GTCTTCTGTG	GTGTCGGTGA	GCGTACTCGT	GAGGGTAACG	150
	ATCTGTACCA	CGAAATGCAG	GAGACTGGTG	TCATCCAGCT	CGAGGGTGAC	200
	TCCAAGGTCG	CTCTGGTCTT	CGGTGAGATG	AACGAGCCCC	CGGGTGCCCCG	250
	TGCCCCGTGTC	GCCCTTACCG	GTCTGACCAT	TGCCGAGTAC	TTCCGTGACG	300
40	AGGAGGGTCA	GGACGTGCTG	CTCTTTCATTG	ACAACATTTT	CCGTTTTCACC	350
	CAGGCCGGTT	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATCC	CCTCTGCCGT	400
	CGGTTACCAG	CCCACTCTGG	CCGTCGACAT	GGGTGGTATG	CAGGAGCGTA	450
45	TTACCACCAC	CACCAAGGGT	TCCATTACCT	CCG		483

2) INFORMATION FOR SEQ ID NO: 897

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
5	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
10	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTY	CAACAAGCCC	600
15	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCCGC	CGTGTGAGAG	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
20	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCC			1124

2) INFORMATION FOR SEQ ID NO: 898

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Penicillium marneffei*
 (D) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

45	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCTCTGG	TACTGGTGAA	TTGAGGCTG	GTATCTCCAA	200
	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTCACC	CTCGGTGTCC	250
50	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	ACACTTGCAA	GTGGTCTCAG	300
	GGTGAGTACT	CGTACCTGCG	TTTGGCCTTG	AATATCTTAC	TAATGCACCA	350
	TAGATCGTTA	CAACGAAATT	GTCAAGGAGA	CTTCCAACCT	CATCAAGAAG	400
	GTCGGATACA	ACCCTAAGAA	CGTTCCTTTC	GTTCCTATCT	CCGGTTTCAA	450
	CGGTGACAAC	ATGCTTGAGC	CCTCCCCCAA	CTGCCCCTGG	TACAAGGGTT	500
55	GGGAGAAGGA	GACCAAGGCC	GGTAAGGTCA	CTGGTAAGAC	CCTCCTCGAG	550
	GCCATCGACG	CCATTGAGCC	CCCTACCCGT	CCCGCCAACA	AGGTTAGTCC	600
	CTCCTCGACT	ACTCAAACCC	TCCTCATAAG	TTCATGATTA	CGACTCGTTC	650
	ACAGCCCCTC	CGTCTTCCCC	TCCAGGATGT	CTACAAGATC	GGTGGTATTG	700
	GAACGGTTCC	CGTCGGTCGT	GTTGAGACTG	GTACCATCGT	TCCTGGTATG	750
60	GTTGTACACT	TGTAAGTCAC	TCTCCTCGCT	TATCCTACCT	GAAATCATCA	800

	TGTGCTAACT	TGACACTCAG	CGCTCCCGCC	AACGTCACCA	CTGAAGTCAA	850
	GAGTGTGAA	ATGCACCACC	AGCAGCTCAC	TGCCGGTCAG	CCCGGTGACA	900
	ACGTTGGTTT	CAACGTGAAG	AACGTCTCCG	TCAAGGAAAT	CCGTCGTGGT	950
	AACGTTGCTG	GTGACAGCAA	GAACGACCCC	CCTGCCGGTG	CTGCCTCCTT	1000
5	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	GGTGCTGGTT	1050
	ACGCCCCAGT	CCTCGATTGC	CACACTGCCC	ACATTGCTTG	CAAGTTCGCT	1100
	GAGCTCCTCG	AGAAGATTGA	CCGTCGTACC	GGAAAGTCTG	TTGAGGACCA	1150
	CCCCAAGTTC	ATCAAGTCCG	GTGACGCTGC	CATCGTCAAG	ATGATTCCTT	1200
	CCAAGCCCAT	GTGTGTTGAG	GCTTTCACCG	AGTACCCTCC	TCTCGGTCGT	1250
10	TTCGCCGTTT	GCGAGTAAGT	TTTATCTCCG	TTGTCTATTT	TCCATCCTTC	1300
	CCTTCTCCTC	CGTCTTCCAT	ATATATTTTT	TCAGTTATAT	GTGACTAACC	1350
	ACAAATCACG	GGA				1363

15

2) INFORMATION FOR SEQ ID NO: 899

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1147 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Piedraia hortai*

(B) STRAIN: ATCC 24292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

	CAAGCTGAAA	GCCGAGCGTG	AGCGTGGTAT	CACTATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGCAT	100
	TATCTCACTC	CTCACAGAAG	CACGCTCCTA	ACATCACACA	GACGCTCCCG	150
35	GTCACCGTGA	TTTCATCAAG	AACATGATCA	CTGGTACCCTC	CCAGGCCGAC	200
	TGCGCTATCC	TCATTATCGC	TGCCGGTACT	GGTGAGTTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCC	TACACCCTCG	300
	GTGTGCGTCA	GCTCATCGTC	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCTGAGGCCC	GTTACCAGGA	GATCATCAAG	GAGACCTCCA	ACTTCATCAA	400
40	GAAGGTCGGC	TACAACCCCA	AGACCGTCGC	TTTCGTCCCC	ATCTCTGGCT	450
	TCAACGGCGA	CAACATGCTT	GCCCCCTCCA	CCAAC TGCCC	CTGGTACAAG	500
	GGATGGGAGC	GTGAGGTCAA	GGGCAACAAG	CAGACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGGCATTG	AGCCCCCAAA	GCGTCCTTCC	GACAAGCCCC	600
	TCCGTCTTCC	TCTCCAGGAT	GTTTACAAGA	TCGGTGGTAT	CGGAACTGTT	650
45	CCTGTCGGCC	GTATCGAGAC	TGGTGTCTCTC	AAGCCCCGGTA	TGGTCGTTAC	700
	CTTCGCTCCC	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	CACTGAGGGT	CTTCCCGGTG	ACAACGTCGG	TTTCAACGTG	800
	AAGAACGTTT	CCGTCAAGGA	CATCCGCCGT	GGTAACGTTG	CCAGTGACTC	850
	CAAGAACGAC	CCCGCTCTGG	GTGCCGCTTC	TTTCGACGCC	CAGGTCATCG	900
50	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	GGTCCTCGAT	950
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
	CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
55	GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCG	TCCGTGA	1147

2) INFORMATION FOR SEQ ID NO: 900

(i) SEQUENCE CHARACTERISTICS:

505

- (A) LENGTH: 1150 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
10 (B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

```
15 CTCAAGGCCG AGCGTGAGCG TGGTATCACC ATCGACATTG CCCTCTGGAA      50
   GTTCGAGACT CCCAAGTACT ATGTCACCGT CATTGGTACG TCGACTCGCG      100
   CGAGACTGGT CGCAATTTCC ACGTCGCTAA CGTGCTTGAA CAGACGCTCC      150
   CGGCCACCGT GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG      200
   ACTGCGCTAT CCTCATTATC GCTGCCGCGA CTGGTGAGTT CGAGGCTGGT      250
   ATCTCCAAGG ATGGCCAGAC CCGTGAGCAC GCTCTGCTCG CCTACACCCT      300
20 GGTCTGAGGC CCGTTTCCAG GAGATCATCA AGGAGACCTC CAACTTCATC      350
   GGTCTGAGGC CCGTTTCCAG GAGATCATCA AGGAGACCTC CAACTTCATC      400
   AAGAAGGTCG GCTACAACCC CAAGACCGTC GCTTTCGTCC CCATCTCTGG      450
   TTTCCACGGC GACAACATGC TTTCCCCCTC CACCAACTGC CCCTGGTACA      500
   AGGGCTGGGA GAAGGAGACC AAGGCTGGCA AGTCCACCGG CAAGACCCTC      550
25 CTTGAGGCCA TCGACTCCAT CGAGCCCCCC AAGCGCCCCA GCGACAAGCC      600
   CCTCCGCTT CCCCTTCAGG ATGTGTACAA GATCGGCGGT ATCGGCACAG      650
   TCCCTGTCGG CCGTATCGAG ACTGGTGTCA TCAAGCCCGG CATGGTCGTG      700
   ACCTTCGCTC CTTCCAACGT CACCACCGAA GTCAAGTCCG TTGAGATGCA      750
   CCACGAGCAG CTCTCCGAGG GTGTCCCCGG TGACAACGTC GGCTTCAACG      800
30 TCAAGAACGT CTCCGTCAAG GAGATCCGTC GTGGCAACGT CGCCGGTGAC      850
   TCCAAGAACG ACCCCCCCTCT GGGTGCCGCT TCTTTCGATG CCCAGGTCAT      900
   CGTCCTCAAC CACCCCGGCC AGGTCGGTGC TGGCTACGCC CCCGTCCTCG      950
   ACTGCCACAC CGCCACATT GCCTGCAAGT TCGCCGAGAT CAAGGAGAAG      1000
   ATCGACCGCC GTACCGGCAA GTCTGTGCGAG TCCGCCCCCA AGTTCATCAA      1050
35 GTCTGGCGAC TCTGCCATCG TCAAGATGAT TCCCTCCAAG CCCATGTGCG      1100
   TTGAGGCTTT CACCGACTAC CCTCCTCTGG GCCGCTTCGC CGTCCGTGAC      1150
```

40 2) INFORMATION FOR SEQ ID NO: 901

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
(B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

```
55 TACCACTAAG TGGTCCGAGA CCCGATTCAA TGAAATTATC AAGGAAGTCA      50
   CCAATTTTCA TAAGAAGGTC GGATATAACC CCAAGACTGT TCCTTTCGTT      100
   CCCATTTCTG GTTTCGAGGG TGACAACATG ATCGAGCCCT CTGCCAACTG      150
   CCCATGGTAC AAGGGCTGGT CCAAGGAGAC TGCTCAGGGC AAGTACTCTG      200
60 GCAAGACCCT TCTTGAGGCC ATCGACGCCA TTGAGCCCCC CACCCGTCCT      250
```

	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GA CTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
5	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
	GCCCAGGTCA	TCGTCCCTCAA	CCACCCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACC GGAA	AGTCTGTTGA	GAACAACCCC	700
10	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	G					751

15 2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

30	CGTGAGCGCG	GTATCACCAT	CGATATTGCT	CTGTGGAAGT	TCGAGACCCC	50
	CAAGTACTAC	GTCACCGTCA	TTGACGCCCC	CGGTCATCGC	GATTTCATCA	100
	AGAACATGAT	CACTGGTACC	TCGCAGGCCG	ACTGCGCCAT	TCTCATCATT	150
	GCCGCTGGTA	CTGGTGAGTT	CGAGGCTGGT	ATCTCCAAGG	ATGGCCAGAC	200
35	TCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	GGGTGTGCGG	CAGCTGATCG	250
	TCGCCATCAA	CAAGATGGAC	ACGGCCAAGT	GGGCTGAGGC	TCGTTACCAG	300
	GAGATCATCA	AGGAGACCTC	CAACTTCATC	AAGAAGGTCG	GCTACAACCC	350
	CAAGACTGTT	GCCTTCGTCC	CCATCTCGGG	CTTCCACGGC	GACAACATGC	400
	TTACTCCCTC	GACCAACTGC	CCCTGGTACA	AGGGCTGGGA	GAAGGAGGGC	450
40	AAGAGCGGCA	AGGTTACCGG	TAAGACTCTG	CTGGACGCCA	TTGACGCCGT	500
	CGAGCCCCCC	AAGCGCCCCA	CGGACAAGCC	CCTGCGTCTG	CCCCTCCAGG	550
	ATGTCTACAA	GATCGGCGGT	ATCGGCACTG	TCCCTGTCGG	CCGTATCGAG	600
	ACTGGTGTTCC	TGAAGCCCGG	CATGGTCGTC	ACCTTTGCCC	CGTCCAACGT	650
	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	CCACGAGCAG	CTTGTTGAGG	700
45	GTGTTCCCGG	CGACAACGTC	GGCTTCAACG	TCAAGAACGT	CTCCGTCAAG	750
	GAGATCCGTC	GTGGCAACGT	TGCCGGTGAC	TCCAAGAACG	ACCCCCCCTC	800
	GGGCGCCGCC	ACCTTCAACG	CCCAGGTCAT	TGTCCTGAAC	CACCCCGGCC	850
	AGGTCGGCAA	CGGCTACGCC	CCGGTTCTGG	ACTGCCACAC	CGCCACATT	900
	GCCTGCAAGT	TCACCGAGAT	CCTTGAGAAG	ATCGACCGCC	GTACCGGCAA	950
50	GTCGGTTGAG	AACAACCCCA	AGTTCATCAA	GTCGGGTGAC	GCCGCCATTG	1000
	TCAAGCTGAC	GCCCTCGAAG	CCCATGTGCG	TTGAGGCCTT	CACTGACTAC	1050
	CCCCCT					1056

55

2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1366 bases
 60 (B) TYPE: Nucleic acid

507

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 58950

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

CAAGGCTGAG CGTGAGCGTG GTATCACCAT CGATATTGCT CTCTGGAAGT 50
 TCCAGACTGC CAAGTACGAG GTTACCGTCA TTGACGCCCC CGGTACCCGT 100
 GATTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCCG ATTGCGCTAT 150
 15 TCTCATCATT GCCTCTGGTA CTGGTGAATT CGAGGCTGGT ATCTCCAAGG 200
 ATGGCCAGAC TCGTGAGCAC GCTCTTTTGG CTTTCACCCCT CGGTGTCCGT 250
 CAGCTCATTG TTGCCCTCAA CAAGATGGAC ACTTGCAAGT GGTCTCAGGG 300
 TGAGTACTCG TACCTGCGTT TGGCCTTGAA TATCTTACTA ATGCACCATA 350
 GATCGTTACA ACGAAATTGT CAAGGAGACT TCCAACCTCA TCAAGAAGGT 400
 20 CGGATACAAC CCTAAGAACG TTCCTTTCGT TCCTATCTCC GGTTTCAACG 450
 GTGACAACAT GCTTGAGCCC TCCCCCAACT GCCCCTGGTA CAAGGGTTGG 500
 GAGAAGGAGA CCAAGGCCGG TAAGGTCACT GGTAAGACCC TCCTCGAGGC 550
 CATCGACGCC ATTGAGCCCC CTACCCGTCC CGCCAACAAG GTTAGTCCCT 600
 CCTCGACTAC TCAAACCCTC CTCATAAGTT CAGATTACTG ACTCGTTCAC 650
 25 AGCCCCCTCCG TCTTCCCCTC CAGGATGTCT ACAAGATCGG TGGTATTGGA 700
 ACGGTTCCCG TCGGTCGTGT TGAGACTGGT ACCATCGTTC CTGGTATGGT 750
 TGTCACCTTG TAAGTCACTC TCCTCGCTTA TCCTACCTGA AATCATCATG 800
 TGCTAACTTG ACACTCAGCG CTCCC GCCAA CGTCACCACT GAAGTCAAGA 850
 GTGTTGAAAT GCACCACCAG CAGCTCACTG CCGGTCAGCC CGGTGACAAC 900
 30 GTTGTTTCA ACGTGAAGAA CGTCTCCGTC AAGGAAATCC GTCGTGGTAA 950
 CGTTGCTGGT GACAGCAAGA ACGACCCCCC TGCCGGTGCT GCCTCCTTCA 1000
 ACGCCCAGGT CATCGTCCTC AACCACCCCG GTCAGGTCGG TGCTGGTTAC 1050
 GCCCCAGTCC TCGATTGCCA CACTGCCCCA ATTGCTTGCA AGTTCGCTGA 1100
 GCTCCTCGAG AAGATTGACC GTCGTACCGG AAAGTCTGTT GAGGACCACC 1150
 35 CCAAGTTCAT CAAGTCCGGT GACGCTGCCA TCGTCAAGAT GATTCCTTCC 1200
 AAGCCCATGT GTGTTGAGGC TTTCACCGAG TACCCTCCTC TCGGTCGTTT 1250
 CGCCGTTCCG GAGTAAGTTT TATCTCCGTT GTCTATTTTC CATCCTTCCC 1300
 TTCTCTCCG TCTTCCATAT ATATTTTTTC AGTTATATGT GACTAACCAC 1350
 AAATCACGGG AATAGC 1366
 40

2) INFORMATION FOR SEQ ID NO: 904

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

55 (B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

CTATTATCGT TGTTGCCGCT TCCGACGGTC AAATGCCCCA GACTCGTGAG 50
 60 CATCTGCTGC TCGCCCGCCA GGTCGGTGTC CAGAAGATCG TTGTCTTCGT 100

	CAACAAGGTC	GATGCTGTTG	AGGACAAGGA	GATGTTGGAG	CTCGTCGAGA	150
	TGGAGATGCG	CGAATTGCTC	AGCAGCTACG	GCTTCGAGGG	CGACGAGACT	200
	CCCATCATCA	TGGGATCTGC	CCTCTGCGCC	ATTGAGGGCC	GCGAACCTGA	250
	GATTGGTGTC	AACCGAATTG	ATGAGCTGCT	CGAGGCCGTT	GATACTTGGA	300
5	TCCCCACCCC	TCAGCGTGAG	ACCGACAAGC	CTTTCCTCAT	GGCCGTCGAG	350
	GATGTCTTCT	CCATTGCTGG	TCGTGGCACT	GTCGTCTCTG	GCCGTGTCGA	400
	GCGAGGTATC	CTGAAGCGCG	ATGCTGAAGT	TGAGCTCGTC	GGCAAGGGCA	450
	CCGCCCCCAT	CAAGACCAAG	GTTACCGATA	TCGAGACCTT	CAAGAAGTCC	500
	TGCGAGGAGT	CTCGCGCTGG	TGACAACTCC	GGTCTCCTTC	TTCGTGGTGT	550
10	CAAGCGTGAT	GAAGTCCGCC	GTGGTATGGT	CGTTTCCGTC	CCTGGACAGG	600
	TCAAGGCGCA	CAAGAA GTTC	CTTGTCTCCA	TGTACGTGTT	GAGCAAGGAG	650
	GAAGGTGGTC	GTCACACTGG	CTTCGGTGAG	AACTACAGGC	CGCAAATGTT	700
	CATCCGCACT	GCCGACGAGT	CGTGTGCCCT	GTA CTGGCCA	GAAGGCACCG	750
	AGGACGCCCA	TGACAAGCTT	GTTATGCCCG	GTGACAACGT	CGAGATGGTT	800
15	TGCGAGCTCC	ATGCACCACA	CGTCTTGGAG	CCTGGTCAAC	G	841

2) INFORMATION FOR SEQ ID NO: 905

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Aspergillus niger*
- (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

35	CGGTGCTATC	ATTGTCGTCG	CCGCCTCCGA	CGGTCAGATG	TACGTTAACC	50
	TTAAAAGAAT	AACTCTCCTT	CAGTATATAT	GCTTACACTG	GCGATCAACA	100
	GGCCCCAGAC	TCGTGAGCAC	TTGCTGCTTG	CTCGTCAGGT	CGGTGTCCAG	150
	AAGATCGTTG	TCTTCGTCAA	CAAGGTCGAT	GCTATCGATG	ACCCCGAGAT	200
	GCTGGAGCTC	GTTGAGCTGG	AAATGCGCGA	GCTTCTCAGC	ACCTACGGAT	250
40	TCGAGGGTGA	GGAGACCCCC	ATCGTCTTCG	GCTCTGCTCT	CTGCGCCATT	300
	GAGGACCGCC	GCCCCGACAT	CGGTACCGAG	CGTATCGACG	CTCTCCTCGA	350
	GGCCGTTGAC	ACCTGGATCC	CCACTCCCCA	CGGTGACCTT	GACAAGCCTT	400
	TCTTGATGTC	CATTGAGGAA	GTTTCTCTCCA	TCCCCGGTCG	TGGTACCGTC	450
	GCCCTCCGCC	GTGTCGAGCG	TGGTCTCCTG	AAGCGTGATA	GCGAGGTTGA	500
45	GATCATCGGT	ACCACCAACG	AGGTCATCAA	GACCAAGGTT	ACCGACATTG	550
	AGACCTTCAA	GAAGTCCTGC	TCCGAGTCCC	GCGCCGGTGA	CAACTCCGGT	600
	CTCCTGCTCC	GTGGTGTCGG	CCGTGAGGAT	CTCCGCCGTG	GTATGGTCAT	650
	TGCCGCTCCT	GGCAGCGCCA	AGGCCAACAG	CAAGTTCATG	GTCTCCATGT	700
	ACGTCCTGAC	CGAGGCTGAR	GGTGGTCGCC	GTACCGGTTT	CGGTGTCCAG	750
50	TACCGTCCCC	AGCTGTTCAT	CCGCACTGCC	GGTAAGTAAA	ATTGCATTCT	800
	ATTCCGCTAC	TAGGGAACCA	TCTCTAATTC	TATTTGCTAC	AGATGAGGCT	850
	GCTGAGTTCA	GCTTCCCCGA	CGGAGACCAG	TCCCCGCCGT	TCATGCCCGG	900
	TGACAACGTC	GAGATGATCG	TCAAGACCCA	CCGCCCCGTC	GCCGCCGAGG	950
55	CCGGTCAGCG	CTTCAAC				967

2) INFORMATION FOR SEQ ID NO: 906

60

(i) SEQUENCE CHARACTERISTICS:

509

(A) LENGTH: 852 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bipolaris hawaiiensis*
(B) STRAIN: ATCC 26067

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

15 TGGTGCTATT ATTGTTGTTG CCGCTTCCGA CGGTCAAATG CCCAGACTC 50
GTGAGCATCT GCTGCTCGCC CGTCAGGTCG GTGTTTCAGAA GATCGTTGTC 100
TTCGTTAACA AGGTCGACGC TGTCGAGGAC AAGGAGATGT TGGAGCTTGT 150
CGAGATGGAG ATGCGCGAAC TGCTCAGCAG CTATGGCTTC GAGGGCGACG 200
AGACCCCTAT CATCATGGGT TCTGCTCTCT GCGCCATTGA AGGCCGTCAA 250
CCCGACATTG GTGTGCAACG AATTGACGAG CTGCTCGAGG CTGTTGATAC 300
20 TTGGATTCCC ACCCTCAGC GTGAGACCGA AAAGCCTTTC CTCATGGCCG 350
TCGAGGATGT CTTCTCCATT GCTGGTCGTG GTACCGTCGT CTCTGGCCGT 400
GTCGAACGAG GTATCCTGAA GCGCGATGCT GAAGTTGAGC TTGTGGGCAA 450
GGGCAGCGCA CCCATCAAGA CCAAGGTTAC CGATATCGAG ACCTTCAAGA 500
AGTCTTGCGA GGAGTCCCGC GCTGGTGACA ACTCCGGTCT CCTTCTTCGT 550
25 GGTGTTAAGC GTGATGAAGT CCGCCGTGGT ATGGTCGTTT CCGTCCCTGG 600
ACAGGTTAAG GCGCACAAGA AGTTCCTTGT CTCCATGTAT GTGCTGAGCA 650
AGGAGGAAGG TGGCCGACAC ACTGGCTTCG GTGAGAACTA CAGGCCGCAA 700
ATGTTTCATCC GCACTGCCGA CGAGTCGTGT GCCCTGTACT GGCCAGAAGG 750
CACCGAGGAT GCCCACGACA AGCTTGTCAT GCCCGGTGAC AACGTCGAGA 800
30 TGGTTTGCGA GCTCCATGCA CCACACGTCT TGGAGACTGG TCAGCGCTTC 850
AA 852

35 2) INFORMATION FOR SEQ ID NO: 907

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 966 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus flavus*
(B) STRAIN: ATCC 26947

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907

50

GGTGCTATTG TTGTCGTTGC TGCTTCGGAT GGTCATGATG TATGGACAGG 50
CCCTTTGCTA CTGAATGGTT TCAAGATCTC GCGCTTACAC GTATTATAAT 100
AGGCCCCAGA CCCGGGAGCA CTTGCTGCTT GCCCGTCAGG TCGGTGTCCA 150
GAAGATCGTC GTTTTTGTCA ACAAGATTGA TGCCGTTGAG GACCCTGAGA 200
55 TGTGTGAGCT TGTCGAGTTG GAAATGCGCG AGCTCCTTAG CAGCTACGGC 250
TTCGAGGGCG AAGAGACTCC CATCATCTTC GGTTCGTGCTC TGTGTGCTTT 300
GGAGGACCGT CGCCCCGACA TTGGTGCCGA GCGTATCGAC GAGCTCATGA 350
AGGCCGTTGA CACCTGGATC CCTACCCCTC AGCGTGATCT TGACAAGCCT 400
TTCCTCATGT CTGTGAGGA AGTCTTCTCC ATCGCCGGTC GTGGTACCGT 450
60 TGCCTCCGGC CGTGTCGAAC GTGGTATCCT GAAGAAGGAC AGCGAAGTCG 500

510

	AGATCATCGG	AGGTAGCTTC	GATGCTACCA	AGACCAAGGT	CACCGACATT	550
	GAGACCTTCA	AGAAGTCTTG	TGACGAGTCC	CGCGCTGGTG	ACAACTCTGG	600
	CTTGCTTCTC	CGTGGTATCC	GTCGTGAAGA	CGTCCGCCGC	GGAATGATCA	650
	TTGCTGCTCC	TGGCAGCACC	AAGGCCACG	ACCAGTTCTT	GGTGTCCATG	700
5	TACGTTCTCA	CTGAGGCTGA	GGGTGGTCGT	CGTACTGGCT	TCGGCTCCAA	750
	CTACCGCCCC	CAGGTGTTTCG	TTCGCACTGC	TGGTAAGTCA	AGCCTTTTGC	800
	TCACTTAACG	GTATTGATTA	AGTTCTAACT	GTTGTATCCT	AGATGAGGCT	850
	GCTGACCTCA	GCTTCCCCGA	CGGTGATGAG	TCCCGGAGGG	TGATGCCTGG	900
	TGACAACGTC	GAGATGGTCC	TCAAGACTCA	CCGCCCCATT	GCTGCTGAGG	950
10	CTGGCCAGCG	CTTCAA				966

2) INFORMATION FOR SEQ ID NO: 908

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Alternaria alternata*
- (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

30	GGTGCTATCA	TCGTCGTTGC	TGCTTCCGAT	GGTCAGATGC	CCCAGACCCG	50
	TGAGCACTTG	CTGCTCGCCC	GTCAGGTCGG	TGTTCAAGAAG	ATCGTTGTCT	100
	TCGTCAACAA	GGTCGATGCT	GTCGAAGACC	CGGAGATGTT	GGAACTCGTC	150
	GAGATGGAGA	TGCGTGAGTT	ACTCACCAGC	TACGGCTTCG	AGGGCGACGA	200
	GACACCCATC	ATCATGGGTT	CCGCTCTATG	CGCCATCGAG	GGCCGCCAGC	250
35	CCGAGATCGG	TGTTACCAAG	GTCGACGAGC	TAATGGACGC	TGTCGACTCA	300
	TGGATCCCCA	CCCCTCAGCG	TGAGACCGAG	AAGCCTTTCC	TCATGGCTGT	350
	TGAGGATGTC	TTCTCGATTG	CTGGACGTGG	TACCGTCGTT	TCGGGCCGTG	400
	TCGAGCGCGG	TATCTTGAAG	CGTGACGCTG	AAGTCGAGCT	TGTCGGCAAG	450
	GGCACCGCGC	CAATCAAGAC	CAAGGTCACT	GATATTGAGA	CCTTCAAGAA	500
40	GTCGTGCGAG	GAGTCGCGCG	CGGGTGATAA	CTCCGGTCTT	CTCCTCCGTG	550
	GTGTCAAGCG	TGATGACGTT	CGCCGCGGTA	TGGTTGTTTC	CGTTCCCGBA	600
	CAAGTCAAGG	CTCACAAGAA	GTTCTCTGTC	TCCATGTACG	TTCTAAGCAA	650
	AGAGGAGGGT	GGTCGTCACA	CCGGCTTCGG	CGAGAACTAC	AGGCCGCAAA	700
	TGTTTCATCG	AACTGCCGAT	GAATCCTGCG	CACTTCACTT	CCCAGAGGGT	750
45	ACCGAGGATG	CGCACGACAA	GCTAGTTATG	CCCGGTGACA	ACGTCGAGAT	800
	GGTCTGCGAA	CTCCACCAGC	CCCACGTTCT	AGAGACCGGT	CAGCG	845

50 2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

5
 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
 AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
 CACTTGCTCC TCGCCCGTCA GGTCCGGTGT CAAAAGATCG TCGTCTTCGT 150
 CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
 10 TGGAAATGCG TGAACCTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
 GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
 TCCCCACCCC CCAGCGTGAC CTTGACAAGC CTTTCTTGAT GTCCGTTGAG 400
 GAAGTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
 15 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
 AGAACCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
 TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
 CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
 20 GAAGGTGGTC GTCGTAAGG ATTTCGCGCC AACTACCGTC CTCAAGCTTT 750
 CATCCGTAAT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850
 CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
 ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931
 25

2) INFORMATION FOR SEQ ID NO: 910

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 40 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

45 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
 AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
 CACTTGCTCC TCGCCCGTCA GGTCCGGTGT CAAAAGATCG TCGTCTTCGT 150
 CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
 TGGAAATGCG TGAACCTTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
 50 GATTGGCGAA CAGAAGATTG ACGAGCTCAT GAACGCCGTT GATACCTGGA 350
 TCCCCACCCC CCAGCGTGAC CTTGACAAGC CTTTCTTGAT GTCCGTTGAG 400
 GAAGTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
 AGAACCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
 55 TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
 CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
 GAAGGTGGTC GTCGTAAGG ATTTCGCGCC AACTACCGTC CTCAAGCTTT 750
 CATCCGTAAT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
 60 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850

CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

5

2) INFORMATION FOR SEQ ID NO: 911

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC

20

20

2) INFORMATION FOR SEQ ID NO: 912

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

GACGGCGKCA TGCCGCARAC

20

35

2) INFORMATION FOR SEQ ID NO: 913

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

50 GACGGYSYCA TGCKCAGAC

20

55

2) INFORMATION FOR SEQ ID NO: 914

- (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

513

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

5

GAARAGCTGC GGRCGRTAGT G

21

10 2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single,

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915

AAACGCCTGA GGRCGGTAGT T

21

25

2) INFORMATION FOR SEQ ID NO: 916

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

GCCGAGCTGG CCGGCTTCAG

20

40

2) INFORMATION FOR SEQ ID NO: 917

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

TCGTGCTACC CGTYGCCGCC AT

22

55

2) INFORMATION FOR SEQ ID NO: 918

(i) SEQUENCE CHARACTERISTICS:

60

514

(A) LENGTH: 1391 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(E) ACCESSION NUMBER: J01672

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

	AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTTGCCACT	GCCCGCGGTG	50
15	AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
	GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
	AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
	TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
	GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
20	ATTTGGTAAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
	TGGAAACCAT	CTCTACCGGT	TCGCTTTCAC	TGGATATCGC	GCTTGGGGCA	400
	GGTGGTCTGC	CGATGGGCGG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
	CGGTAAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
	GTAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
25	GCACGTAAAC	TGGGCGTCGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
	CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
	CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
	GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
	GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
30	CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAAATTGG	TGTGATGTTT	850
	GGTAACCCGG	AAACCACTAC	CGGTGGTAAC	GCGCTGAAAT	TCTACGCCTC	900
	TGTTCTGCTC	GACATCCGTC	GTATCGGCGC	GGTGAAAGAG	GGCGAAAACG	950
	TGGTGGGTAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
	CCGTTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
35	CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
	CAGGCGCGTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
	AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
	GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGAACTCA	ACGCCGGATT	1250
	TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTAA	1300
40	TCGTCTTGTT	TGATACACAA	GGGTCGCATC	TGCGGCCCTT	TTGCTTTTTT	1350
	AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

45 2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCCIGART CITMIGGIAA RAC

23

60

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

15

2) INFORMATION FOR SEQ ID NO: 921

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

TIYRTIGAYG CIGARCAIGC

20

30

2) INFORMATION FOR SEQ ID NO: 922

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

45 TARAAYTTIA RIGCIYKICC ICC

23

2) INFORMATION FOR SEQ ID NO: 923

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

60

5 2) INFORMATION FOR SEQ ID NO: 924

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

20

2) INFORMATION FOR SEQ ID NO: 925

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

35

2) INFORMATION FOR SEQ ID NO: 926

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

50

2) INFORMATION FOR SEQ ID NO: 927

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

5 ACGCGGAGAA GGTGCGCTT

19

2) INFORMATION FOR SEQ ID NO: 928

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

20

GGTCGTTCTT CGAGTCACCG CA

22

25 2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides fragilis*

(B) STRAIN: ATCC 25285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

40

TTCAGCATGC	CATTTCAAAA	CAGGCCGAAG	CCGATATCGT	GATTATCGCT	50
GCTTGTGGGG	AGCGTGCAA	TGAAGTTGTG	GAAATCTTTA	CCGAATTTCC	100
GGAATTGGTG	GACCCGCACA	CGGGACGTAA	GCTGATGGAG	CGTACCATTA	150
TTATCGCAAA	TACATCGAAC	ATGCCGGTAG	CAGCGCGTGA	AGCTTCTGTG	200
45 TATACGGCCA	TGACGATTGC	CGAATACTAT	CGTGCCATGG	GATTGAAAGT	250
CCTGCTGATG	GCAGACTCCA	CTTCCC GTTG	GGCGCAGGCA	TTGCGTGAGA	300
TGTCGAACCG	TATGGAGGAG	TTGCCCGGAC	CGGATGCATT	CCC GATGGAC	350
CTGTCTCTAA	TCATTTCTAA	CTTCTATGGC	CGTGCAGGCT	ACGTGAAACT	400
50 GAATAACGGC	GAGAGCGGTT	CTATTACCTT	TATCGGTACA	GTATCACC	448

50

2) INFORMATION FOR SEQ ID NO: 930

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides distasonis*
(B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

```
10 GCTATCTCTA AACAAAGCGGA AGCGGATATC GTGATTATCG CCGCCTGCGG 50
    TGAGCGTGCG AATGAGGTTC TAGAGGTATT TACGGAGTTC CCGGAATTGG 100
    TAGACCCGCA TACGGGACGT AAATTGATGG AACGTACGAT CATTATCGCC 150
    AATACATCCA ACATGCCGGT AGCCGCTCGT GAGGCATCCG TATATACGGC 200
    GATGACCATC GCCGAGTATT ATCGCAGCAT GGGTTTGAAG GTTCTGTTGA 250
    TGGCCGACTC TACTTCCCGC TGGGCACAGG CTTTGCGTGA GATGTCCAAC 300
15 CGTTTGGAGG AGTTGCCGGG ACCGGATGCT TTCCCGATGG ACTTGTCCGC 350
    TATCGTGGCG AACTTCTACG CTCGTGCGGG ATTCGTTTCA TTGAATAACA 400
    ACGCTACAGG CTCCGTCCTT TTCATCGGTA CCGTATCG 438
```

20

2) INFORMATION FOR SEQ ID NO: 931

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 453 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
(B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

```
40 CCTCCAGCAC GCTATCTCTA AGCAGGCGGA GGCTGATATC GTCATTATGG 50
    CAGCCTGCGG TGAGCGTGCT AATGAGGTGG TGGAGATCTT TGCCGAGTTC 100
    CCTGAGCTCG AAGACCCACA CACGGGACGC AAGCTGATGG AGCGTACGAT 150
    CATCATCGCT AACACGAGTA ACATGCCAGT GGCTGCTCGT GAGGCTTCGG 200
    TCTACACCGC TATGACCATC GCTGAGTACT ACCGCTCGAT GGGTCTCAAA 250
    GTACTCCTAA TGGCTGACTC GACCTCTCGC TGGGCACAGG CACTGCGTGA 300
    GATGTCTAAC CGTCTAGAGG AGCTGCCTGG ACCAGATGCA TTCCCGATGG 350
    ACTTGTCCGC TATCGTGGCA AACTTCTACG CTCGTGCCGG CTTCGTCTAT 400
45 CTCAACAACG GTGAGACAGG TTCTGTAACC TTCATCGGTA CCGTCTCTCC 450
    AGC 453
```

50 2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

5 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC 50
 GTGAACATAT CTTACTTTCA CGTCAAGTTG GTGTTCATA CATCGTTGTA 100
 TTCATGAACA AATGTGACAT GGTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA ATTCTGTGATC TATTAAGTGA ATATGAATTC CCTGGCGATG 200
 10 ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA AGGTGAAGCT 250
 GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
 TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCTATGATG CCAGTTGAGG 350
 ATGTATTCTC AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA 400
 CGTGGACAAG TTAAAGTTGG TGACGAAGTA GAAGTTATCG GTATCGAAGA 450
 15 AGAAAGCAAA AAAGTAGTAG TAACTGGAGT AGAAATGTTC CGTAAATTAC 500
 TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT ACGTGGTGT 550
 GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
 TACTCCACAC ACTAAGTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT 700
 20 TTCCGTACTA CTGACGTAAC TGGTATTGTT ACACTTCCAG AAGGTACTGA 750
 AATGGTAAYG CCTGGTGATA ACATTGAGCT TGCAGTTGAA CTAATTGCAC 800
 CAATCGCTAT CGAAGACGGT ACTAAATTCT CTATC 835

25

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

40

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

55

2) INFORMATION FOR SEQ ID NO: 935

(i) SEQUENCE CHARACTERISTICS:

60

520

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

10 GGIAARWSIC ARYTITGYCA YAC

23

2) INFORMATION FOR SEQ ID NO: 936

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936

25

TCISIIYTCIG GIARRCAIGG

20

2) INFORMATION FOR SEQ ID NO: 937

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937

40

ATACIGARG YITTYGGIGA RTT

23

2) INFORMATION FOR SEQ ID NO: 938

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938

55

CYIGTIGYIS WIGCRTGIGC

20

60

2) INFORMATION FOR SEQ ID NO: 939

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1203 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: D10023

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

ATGTCTCAAG TTCAAGAACA ACATATATCA GAGTCACAGC TTCAGTACGG 50
GAACGGTTCG TTGATGTCCA CTGTACCAGC AGACCTTTCA CAGTCAGTCG 100
TTGATGGAAA CGGCAACGGT AGCAGCGAAG ATATTGAGGC CACCAACGGC 150
20 TCCGGCGATG GTGGCGGATT GCAGGAGCAA GCGGAAGCGC AAGGTGAAAT 200
GGAGGATGAA GCATACGATG AAGCTGCCTT AGGTTTCGTTT GTGCCAATAG 250
AAAAACTGCA AGTGAACGGG ATTACTATGG CGGATGTGAA AAAACTAAGG 300
GAGAGTGGGC TTCACACTGC TGAAGCGGTA GCATATGCTC CCAGAAAGGA 350
TTTATTGGAA ATCAAAGGTA TATCGGAAGC TAAGGCAGAT AAGTTGCTAA 400
25 ACGAAGCGGC AAGGCTAGTG CCTATGGGAT TTGTCACGGC TGCTGATTTT 450
CATATGAGAA GATCGGAGCT GATTTGTTTG ACAACGGGTT CTAAGAATTT 500
GGACACTCTT TTGGGTGGTG GTGTGGAAAC TGGTTCCTATT ACTGAGCTTT 550
TCGGTGAATT CAGGACAGGT AAGTCCCAGC TATGTCACAC TTTGGCCGTG 600
ACATGCCAAA TTCCATTGGA TATTGGTGGC GGTGAAGGTA AGTGTTTGTA 650
30 TATCGATACC GAAGGTACTT TCAGGCCGGT AAGATTGGTA FCCATAGCTC 700
AGCGGTTCGG ATTAGACCCG GATGATGCTT TGAACAACGT TCGGTATGCA 750
AGAGCCTATA ACGCCGATCA TCAGTTAAGA CTTCTGGATG CTGCTGCCCCA 800
AATGATGAGC GAGTCTCGGT TTTCCTTGAT TGTGGTCGAT TCTGTTATGG 850
CTCTATACCG TACGGATTTT TCTGGTCGTG GTGAACTAAG CGCAAGGCAA 900
35 ATGCATTTAG CCAAATTTAT GCGTGCTTTG CAAAGGCTGG CCGACCAATT 950
TGGTGTGCA GTCGTCGTTA CTAACCAAGT GGTCGCCCAA GTTGATGGTG 1000
GTATGGCTTT TAATCCAGAT CCAAAGAAGC CTATCGGTGG TAATATTATG 1050
GCACATTCTT CCACCACGCG ATTAGGTTTC AAAAAGGGTA AGGGATGTCA 1100
AAGATTATGC AAAGTTGTTG ACTCACCTTG CTTACCAGAG GCTGAATGTG 1150
40 TGTTGCGGAT CTATGAAGAT GGTGTTGGTG ACCCCAGAGA AGAAGACGAG 1200
TAG 1203

45 2) INFORMATION FOR SEQ ID NO: 940

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1800 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(B) STRAIN: GRF88
(C) ACCESSION NUMBER: M87549

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
5	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTGCC	250
	TCTAGGGATT	AATTAATTCG	TAAGGAAAAA	TAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
	CAAGTATATT	TTAACTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCTT	400
10	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCTT	550
	TTATATTTGC	TGTAGTCTGT	TATGCCAATC	AGGAAAGCAT	TTGAACAAAT	600
	ATGTCTGTTA	CAGGAAGTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650
15	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAACCTT	CTGCTGTAGA	GGTCTTTTCC	CCCTTTCTTT	TACTAACTAA	800
	TATTTTGGA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGA	AAAATTAAAG	900
20	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGTCTCATAC	TTTGTGTGTT	1100
	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
25	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
	CAAACCTCAG	AGTAGACTAC	TGCGGTAGAG	GTGAACTAAG	CGAAAGACAG	1400
30	CAAAAGCTAA	ATCAACATCT	TTTCAAATTG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
35	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTTAATGAA	GATGACATTG	CTCCTTTATT	AACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

2) INFORMATION FOR SEQ ID NO: 941

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus humicolus*
 (B) STRAIN: ATCC 38294

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941

	CGTCCTTATC	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCC	CACGGTGGTT	50
	TCTCCGTCTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGACCTG	100
	TACCACGAGA	TGCGTGAGAC	TGGTGTTCATC	AACCTCGAGG	GCGACTCCAA	150
20	GGTCGCTCTC	GTCTTCGGCC	AGATGAACGA	GCCCCCGGA	GCCCGTGCCC	200
	GTGTGCGCCT	TACCGGCCTC	ACCATCGCCG	AGTACTTCCG	TGACGAGGAG	250
	GGTCAGGACG	TGCTTCTCTT	CATCGACAAC	ATTTTCCGTT	TCACCCAGGC	300
	CGGTTCCGAG	GTGTCTGCCC	TTCTCGGTCG	TATCCCCTCG	GCCGTCGGTT	350
	ACCAGCCAC	CCTCGCTACC	GACATGGGTT	CCATGCAGGA	GCGTATCACC	400
25	ACCACCAAGA	AGGGTTCGAT	TACCTCCGTC			430

2) INFORMATION FOR SEQ ID NO: 942

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942

45	CGTGTACGAT	GCTCTTGAGG	TGCAAAATGG	TAATGAGCGT	CTGGTGCTGG	50
	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TGCGTACCAT	CGCAATGGGT	100
	TCCTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAAGACC	TCGAACACCC	150
	GATCGAAGTC	CCGGTAGGTA	AAGCGACTCT	GGGCCGTATC	ATGAACGTAC	200
	TGGGTGAACC	GGTCGACATG	AAAGGCGAGA	TCCGTGAAGA	AGAGCGTTGG	250
50	GCGATTACAC	GCGCAGCACC	TTCCTACGAA	GAGCTGTCAA	ACTCTCAGGA	300
	ACTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	CCGTTCGCTA	350
	AGGGCGGTAA	AGTTGGTCTG	TTCGGTGGTG	CGGGTGTAGG	TAAAACCGTA	400
	AACATGATGG	AGCTCATTCG	TAACATCGCG	ATCGAGCACT	CCGGTTACTC	450
	TGTGTTTGCG	GGCGTAGGTG	AACGTACTCG	TGAGGGGAAC	GACTTCTACC	500
55	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	GGTGTATGGC	550
	CAGATGAACG	AGCCGCCGGG	AAACCGTCTG	CGCGTAGCTC	TGACCGGTCT	600
	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTT	CTGCTGTTCC	650
	TTGACAACAT	CTATCGTTAC	ACCCTGGCCG	GTACGGAAGT	ATCCGCACATG	700
	CTGGGCCGTA	TGCCTTCAGC	GGTAGGTTAT	CAGCCGACCC	TGGCGGAAGA	750
60	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAAACC	GGTT	794

2) INFORMATION FOR SEQ ID NO: 943

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943

20	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTACGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATTGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
25	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAAGTCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGTG	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
30	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
35	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACTGGTTCTA	TCAC				814

40 2) INFORMATION FOR SEQ ID NO: 944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 11775

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944

55

	GTGTACGATG	CTCTTGAGGT	GCAAATGGT	AATGAGCGTC	TGGTGCTGGA	50
	AGTTCAGCAG	CAGCTCGGCG	GCGGTATCGT	GCGTACCATC	GCAATGGGTT	100
	CCTCCGACGG	TCTGCGTCGC	GGTCTGGATG	TAAAAGACCT	CGAACACCCG	150
	ATCGAAGTCC	CGGTAGGTAA	AGCGACTCTG	GGCCGTATCA	TGAACGTACT	200
60	GGGTGAACCG	GTCGACATGA	AAGGCGAGAT	CGGTGAAGAA	GAGCGTTGGG	250

	CGATTCACCG	CGCAGCACCT	TCCTACGAAG	AGCTGTCAAA	CTCTCAGGAA	300
	CTGCTGGAAA	CCGGTATCAA	AGTTATCGAC	CTGATGTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTAA	400
	ACATGATGGA	GCTTATTCGT	AACATCGCGA	TCGAGCACTC	CGGTTACTCT	450
5	GTGTTTTCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
	CGAAATGACC	GACTCCAACG	TTATCGACAA	AGTATCCCTG	GTGTATGGCC	550
	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	CGTGACGTTT	TGCTGTTCGT	650
	TGACAACATC	TATCGTTACA	CCCTGGCCGG	TACGGAAGTA	TCCGCACTGC	700
10	TGGGCCGTAT	GCCTTCAGCG	GTAGGTTATC	AGCCGACCCT	GGCGGAAGAG	750
	ATGGGCGTTC	TGCAGGAACG	TATCACCTCC	ACCAAAACCG	GTTCTATC	798

15 2) INFORMATION FOR SEQ ID NO: 945

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 812 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945

30	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
35	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTA	GGAAGTCTG	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTTCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAACATGA	TGGAGCTTAT	TCGTAACATC	GCGATCGAGC	450
40	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CTTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTATTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACCGA	700
45	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

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2) INFORMATION FOR SEQ ID NO: 946

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

55 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946

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GCGACGCTAT CCCGCATGTT TACGATGCCC TGAAATTGGA CGAGAACGGT      50
CTGACTCTGG AAGTTCAACA ACTTCTGGGT GACGGCGTTG TCCGTACTAT      100
TGCAATGGGT AGTTCAGACG GCCTGAAACG CGGCATGTCT GTAAGCAATA      150
10 CTGGTGCGCC AATCACTGTG CCGGTAGGTA AAGGTACTTT GGGTCGTATT      200
GTCGACGTAT TGGGTACGCC TGTTGATGAA GCAGGTCCGA TCGATACCGA      250
CAAGAGCCGT GCCATTCAAC AAACCTGCTCC GAAATTCGAC GAGTTGTCTG      300
CAACTACCGA ATTGTTGGAA ACCGGTATTA AAGTGATCGA CTTGCTGTGT      350
CCGTTTGCTA AAGGCGGTAA AGTAGGTCTG TTCGGTGGTG CCGGTGTAGG      400
15 CAAAACCGTG AACATGATGG AATTGATCAA CAACATCGCC AAAGCGCACA      450
GCGGTCTGTC CGTGTTCGCA GGTGTGGGCG AGCGTACCCG TGAAGGTAAC      500
GACTTCTACC ACGAGATGAA AGATTCCAAC GTATTGGATA AAGTGGCAAT      550
GGTTTACGGT CAGATGAACG AACCTCCGGG CAACCGTTTG CGCGTCGCAT      600
TGACCGGTTT GACCATGGCG GAATACTTCC GTGACGAAAA AGACGAAAAAC      650
20 GGTAAAGGTC GCGACGTATT GTTCTTCGTT GACAACATCT ACCGTTACAC      700
TCTGGCCGGT ACCGAAGTAT CTGCACTGTT GGGCCGTATG CCTTCTGCAG      750
TGGGTTACCA ACCGACATTG GCTGAAGAAA TGGGTCGTTT GCAAGAGCGT      800
ATTACCTCTA CCCAAACCGG TTCCATTACT TC                        832

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25

2) INFORMATION FOR SEQ ID NO: 947

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947

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TCCGCGCGAT GCCATTCCGC ATGTTTACGA CGCCCTGAAA TTGGATGCAA      50
ACGGCCTGAC TTTGGAAGTA CAACAGCTTC TGGGCGACGG CGTGGTTCGT      100
45 ACTATTGCAA TGGGTAGTTC GGACGGTCTG AAACGCGGCA TGAAGTAAAG      150
CAATACAGAT GCGCCGATTA CTGTGCCGGT AGGTAAAGGT ACTTTGGGAC      200
GTATTGTCGA TGTGTTGGGT ACACCTGTTG ATGAAGCAGG TCCGATTGAT      250
ACCGACAAAC ACCGTGCTAT CCATCAGACA GCTCCGAAAT TCGATGAGTT      300
GTCTGCTACT ACCGAGCTGC TGGAAACAGG CATTAAAGTG ATTGACTTGC      350
50 TGTGTCCGTT TGCCAAAGGC GGTAAAGTAG GTCTGTTCGG TGGTGCCGGT      400
GTAGGCAAAA CCGTCAACAT GATGGAATTG ATTAACAACA TCGCCAAAGC      450
GCATAGTGGT TTGTCCGTGT TCGCCGGTGT GGGGGAACGT ACCCGTGAAG      500
GTAACGACTT CTACCACGAG ATGAAAGATT CCAACGTATT GGACAAAGTG      550
GCGATGGTTT ACGGTCAGAT GAACGAACCT CCGGGTAACC GTCTGCGTGT      600
55 AGCCTTGACC GGTTTGACGA TGGCCGAATA CTTCCGTGAT GAAAAAGACG      650
AAAGCGGCAA AGGTCGCGAC GTATTGTTCT TCGTGGACAA CATTACCGT      700
TACACTCTGG CCGGTACAGA AGTATCCGCA TTGCTCGGTC GTATGCCTTC      750
AGCAGTAGGT TACCAACCGA CATTGGCTGA AGAAATGGGT CGTCTGCAAG      800
AGCGTATTAC CCTCTACTCA AACAGGCTCC ATTACTTCTA      840

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2) INFORMATION FOR SEQ ID NO: 948

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 15 (B) STRAIN: ATCC 903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948

	GCAGCTGGCG	ACAAGCTACC	TGAGATCAAT	AATGCACTTG	TAGTCTATAA	50
20	AAATGACGAA	AAAAAATCAA	AAATCGTCCT	TGAAGTAGCT	CTTGAGCTTG	100
	GTGATGGAGT	GGTTCGGACC	ATCGCTATGG	AATCAACGGA	TGGGTTGACT	150
	CGTGGCATGG	AAGTGCTAGA	TACTGGCCGT	CCAATTTCTG	TGCCAGTCGG	200
	CAAAGAAACA	CTTGGTCGCG	TCTTTAACGT	TTTGGGAGAT	ACCATTGACT	250
	TGGATGCTCC	TTTTGCGGAT	GATGCAGAGC	GCCAGCCAAT	CCATAAGAAA	300
25	GCTCCAACCT	TTGATGAGTT	GTCTACTTCT	TCAGAGATCT	TAGAGACAGG	350
	TATCAAGGTT	ATCGACCTGT	TAGCCCCTTA	TCTGAAAGGT	GGTAAAGTTG	400
	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAGA	CCGTCTTGAT	TCAAGAATTG	450
	ATCCACAACA	TTGCCCAAGA	ACACGGTGGT	ATTTCTGTAT	TTACTGGCGT	500
	TGGGGAACGT	ACCCGTGAAG	GGAATGACCT	TTATTGGGAA	ATGAAAGAGT	550
30	CTGGTGTTAT	CGAGAAAACA	GCCATGGTCT	TCGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCGC	GTATGCGGGT	TGCTTTGACT	GGTTTGACGA	TTGCAGAATA	650
	CTTCCGTGAT	GTGGAAGGTC	AAGATGTCTT	GCTCTTCATT	GACAACTCT	700
	TCCGTTTCAC	GCAGGCAGGT	TCTGAAGTTT	CTGCCCTTTT	GGGTCGGATG	750
	CCGTCAGCCG	TTGGTTACCA	ACCAACACTT	GCGACAGAAA	TGGGGCAATT	800
35	GCAAGAGCGT	ATCACATCGA	CTAAGAAGGG	TTCTGTAACC	TCT	843

2) INFORMATION FOR SEQ ID NO: 949

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949

55	GCAGCAGGGG	AAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GAGATGGTAT	GGTCCGTACT	ATCGCCATGG	AATCAACAGA	TGGTTTACT	150
	CGTGGAAATG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAATGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GATGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAAC	TTGATGA	ATTGTCT	TACCTCT	TCTGAA	ATCC	TTGAA	ACAGG	350
	GATTAAG	GTTATCG	ACCTTC	TTGCC	CCCTTA	CCTTAA	AGGT	GGTAAG	400
	GACTTTT	TCGGTGG	TGCCGA	GTTGGT	AAAA	CCGTCT	TAAT	CCAAGA	450
	ATTCACA	ACA	TTGCC	CAAGA	ACACGG	TGGT	ATTTCA	GAT	500
5	TGGGGA	ACGT	ACTCGT	GAGG	GTAATG	ACCT	TTACTG	GGAA	550
	CAGGTG	TTAT	CGAGAA	ACA	GCCATG	GTAT	TTGGTC	CAGAT	600
	CCAGGAG	CAC	GTATGC	GTGT	TGCCCT	AACT	GGTTTG	ACAA	650
	CTTCCG	TGAT	GTGGA	AGGCC	AAGACG	TGCT	TCTCTT	TATC	700
	TCCGTTT	CAC	TCAGG	CTGGT	TCAGAA	GTAT	CTGCC	CTTTT	750
10	CCATCAG	CCG	TTGGTT	ACCA	ACCAAC	ACTT	GCTACG	GAA	800
	GCAAGAG	CGT	ATTACAT	CAA	CTAAAA	AGGG	TTCTGT	AACC	841
							T		

15 2) INFORMATION FOR SEQ ID NO: 950,

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950

30	GCTACCTGAG	ATCAATAATG	CACTTG	TAGT	CTATAAAAAT	GACGAAAATA	50
	AATCAAAAAT	CGTCCTTGAA	G	TAGCTCTTG	AGCTTGGTGA	TGGAGTGGTT	100
	CGGACCATCG	CTATGGAATC	AACGGATGGG	TTGACTCGTG	GCATGGAAGT		150
	GCTAGATACT	GGTCGTCCAA	TTTCTGTGCC	AGTCGGCAA	GAAACACTTG		200
35	GTCGCGTCTT	TAACGTTTTG	GGAGATACCA	TTGACTTGGA	TGCTCCTTTT		250
	GCGGATGATG	CAGAGCGCCA	GCCAATCCAT	AAGAAAGCTC	CAACCTTTGA		300
	TGAGTTGTCT	ACTTCATCAG	AGATCTTAGA	GACAGGTATC	AAGGTTATCG		350
	ACCTGTTAGC	ACCTTATCTG	AAAGGTGGTA	AAGTCGGACT	CTTCGGTGGT		400
	GCCGGAGTTG	GTAAGACCGT	CCTGATTGAG	GAATTGATCC	ACAACATTGC		450
40	CCAAGAGCAT	GGTGGTATTT	CCGTGTTTAC	CGGTGTTGGG	GAACGTACCC		500
	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AGGAGTCTGG	CGTTATCGAG		550
	AAAACAGCCA	TGGTCTTCGG	TCAGATGAAT	GAGCCACCAG	GAGCGCGTAT		600
	GCGGGTTGCT	TTGACTGGTT	TGACGATTGC	AGAGTACTTC	CGTGATGTAG		650
	AAGGTCAAGA	TGTCTTGCTC	TTCATTGACA	ACATCTTCCG	TTTCACGCAG		700
45	GCAGGTTCTG	AAGTCTCTGC	CCTTTTGGGT	CGGATGCCAT	CAGCCGTTGG		750
	TTACCAACCA	AACTTGCGA	CTGAAATGGG	ACAACTCCAA	GAGCGTATTA		800
	CATCGACTAA	GAAAGGTTCT	GTAACCT				827

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2) INFORMATION FOR SEQ ID NO: 951

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951

	GCAGCAGGGG	AAACACTTCC	TGAGATTAAT	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTGG	100
	GTGATGGTAT	GGTCCGTACG	ATCGCCATGG	AATCAACAGA	TGGTTTGA	150
10	CGTGGAATGG	AAGTTTTGGA	CACAGGCCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACTATTGACT	250
	TGGATGCTCC	TTTCGCTGAA	GACGCTGAGC	GTCAGCCAAT	TCATAAGAAA	300
	GCTCCAACCT	TTGATGAATT	GTCTACCTCA	TCTGAAATCT	TGGAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCCCTTA	CCTTAAAGGT	GGGAAAGTTG	400
15	GACTCTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTGAT	CCAAGAGTTG	450
	ATTCACAACA	TTGCCCAAGA	ACATGGTGGT	ATTTCAGTAT	TTACCGGTGT	500
	TGGAGAACGT	ACCCGTGAGG	GGAACGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCA	600
	CCTGGAGCAC	GTATGCGTGT	TGCTCTTACT	GGTTTGACAA	TCGCCGAATA	650
20	CTTCCGTGAT	GTAGAAGGCC	AAGATGTGCT	TCTCTTTATC	GACAATATCT	700
	TCCGTTTCAC	TCAAGCTGGT	TCAGAAAGTAT	CTGCCCTTTT	GGGTCGGATG	750
	CCTTCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CTAAGAAGGG	TTCTGTAACC	TCTA	844

25

2) INFORMATION FOR SEQ ID NO: 952

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952

	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
45	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGA	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	250
	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300
	GCTCCAACCT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
50	GATCAAGGTT	ATTGACCTTC	TTGCCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTCAGTAT	TTACTGGTGT	500
	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
55	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG			830

60

2) INFORMATION FOR SEQ ID NO: 953

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 15 (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953

	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
20	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTA	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCTT	300
25	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
	TTGCCCAAGA	GCACGGTGGT	ATTTCACTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
30	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
35	ATCACATCAA	CTAAGAAGGG	TTC			823

2) INFORMATION FOR SEQ ID NO: 954

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
	GAGATGGTAT	GGTTCGTA	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAAC	TTGATGAG	GTCTACCT	TCTGAAAT	CC	350
	GATCAAGG	TTTGACCT	TTGCCCTT	CCTTAAAG	GGTAAAG	400
	GACTTTTC	GGTGCCGG	GTTGGTAA	CTGTCTTA	CCAAGAAT	450
	ATTCACAACA	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTGCTGGTGT	500
5	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
10	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA	844

15 2) INFORMATION FOR SEQ ID NO: 955

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955

30	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
35	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCTT	300
	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCTT	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
40	TTGCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
45	TCAGGCTGGT	TCAGAAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA		834

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2) INFORMATION FOR SEQ ID NO: 956

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microti*
 (B) STRAIN: Persing-1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956

	TTGTATATCA	CAGGCACTCA	GCAAATATTC	CGATACTGAC	GTAATTATAT	50
	ACGTGGGTTG	TGGTGAACGT	GGGAATGAAA	TGGCTGAGAT	TCTATGCGAA	100
	TTCCCTGAAC	TATCTACTGT	AGTTAATGAT	GAAAAGGTGG	CCATTATGGA	150
10	ACGTACATGC	TTAGTTGCCA	ATACTTCTAA	TATGCCAGTG	GCCGCTAGAG	200
	AAGCTAGTAT	ATACACTGGT	ATTACAATTG	CTGAATATTT	CCGTGATATG	250
	GGTTACAAC	GCACTCTTAT	GGCCGATTCC	ACTAGCCGAT	GGGCAGAGGC	300
	TCTAAGGGAA	ATTTCTGGTA	GATTGGCTGA	AATGCCTGCA	GATTCTGGCT	350
	ATCCGGCCTA	TTTATCGTCA	AGGTTGTCAG	CTTTTATGA	ACGTGCAGGT	400
15	GGGATAACTG	TCTAATTAAT	TTAGGCTTGA	TTAAGTGCTT	AGGTTACCA	450
	ACACGAACCG	GATCTATTAC	GGTTGTAGGA	GCAGTTTCTC	CACCA	495

20 2) INFORMATION FOR SEQ ID NO: 957

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Entamoeba histolytica*
 (B) STRAIN: HM1-1MSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957

35	AGTTATTTCA	CAAGCATTA	GTAAATATAG	TAATTCAGAT	GTTATTATTT	50
	ATGTAGGATG	TGGTGAACGA	GGAAATGAAA	TGGCAGAAGT	TCTTCGAGAT	100
	TTTCAGCTC	TTTCTATTAA	AGTAGGAGAT	AAAGAAGAAT	CTATTATGAC	150
	AAGAACAGCA	CTTGTTGCTA	ATACATCTAA	TATGCCTGTT	GCAGCACGTG	200
40	AAGCATCAAT	TTATACTGGA	ATTACATTAT	CAGAATATTA	TAGAGATATG	250
	GGATATAATG	TTGCTATGAT	GGCAGATTCA	ACATCAAGAT	GGGCTGAAGC	300
	ACTTAGAGAA	ATTTCAGGAC	GTCTTGACGA	AATGCCAGCT	GATTCTGGAT	350
	ATCCAGCATA	TCTTGACGCA	CGTTTAGCAT	CATTTTATGA	ACGTGCAGGT	400
	ATGGTTGAAT	GTTTAGGATC	ACCAAAAAGA	ATAGGGTCAG	TTTCTATTGT	450
45	AGGAGCTGTT	TCACCACCT				469

2) INFORMATION FOR SEQ ID NO: 958

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*

(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958

```

5  TACAACACCA ACTTGCTAAA TGGGCAGATG CAGAAGTAGT TGTTTATGTT      50
   GGTGTGGGG AACGTGGAAA TGAAATGACC GATGTACTTA TGGAATTCCC      100
   AGAAATTATT GACCCTAAGA CAGGACAATC TTTAATGAAG AGAACAGTTC      150
   TTATAGCTAA TACTTCTAAT ATGCCAGTTG CTGCTCGTGA GGCTTCAATC      200
   TATACTGGTA TAACTATTGC AGAATATTTT AGAGATATGG GATATTCACT      250
10 GGCACCTATG GCAGATTCAA CAAGTCGTTG GGCAGAAGCA CTTCGTGAAA      300
   TGTCAGGACG TTTGGAAGAA ATGCCAGGTG ATGAAGGATA TCCAGCATAT      350
   CTATCAAGTA GAATAGCAGA GTTTTATGAA AGAGCAGGGC TTGTTGAATG      400
   TCTAGGTAAT GGAGAAGAAG GAGCATTAACTGTAATTGGA GCAGTATCTC      450
   CA                                                    452
15

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2) INFORMATION FOR SEQ ID NO: 959

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 469 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Leishmania aethiopica
30  (B) STRAIN: ATCC 50119

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959

```

35  TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGGTCATCT      50
   ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG      100
   TTCCCGACCC TGACGACCGT GATCAATGGT CGCGAGGAGT CGATCATGAA      150
   GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG      200
   AGGCCTCTAT TTACACCGGC ATCACCTGG CCGAGTACTA CCGTGATATG      250
   GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC      300
40  GCTTCGTGAG ATTTCTGGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT      350
   ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC      400
   CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT      450
   CGGTGCCGTG TCTCCGCCG                                                    469
45

```

2) INFORMATION FOR SEQ ID NO: 960

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50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 469 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
55  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Leishmania tropica
60  (B) STRAIN: ATCC 30815

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960

5 TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TCGGTCATCT 50
 ATGTCGGCTG CGGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG 100
 10 TTCCCGACCC TGACGACCGT GATCGATGGT CGCGAGGAGT CGATCATGAA 150
 GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG 200
 AGGCCTCTAT TTACACCGGC ATCACCCTGG CCGAGTACTA CCGTGATATG 250
 GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC 300
 GCTTCGTGAG ATTTCCGGGTC GTTTGGCGGA GATGCCGGCC GATGGTGGCT 350
 15 ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC 400
 CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT 450
 CCGTGCCGTG TCTCCGCCG 469

15

2) INFORMATION FOR SEQ ID NO: 961

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961

35 TGTCATCAGT CAGGCCCTCT CCAAGTACTC CAACTCGGAC TGTGTCATCT 50
 ATGTCGGCTG CGGTGAACGC GGTAACGAGA TGGCCGAGGT GCTCATGGAG 100
 TTCCCGACCC TGACGACTGT GATCGATGGT CGCGAAGAGT CCATCATGAA 150
 GCGCACCTGC CTCGTGGCGA ACACCTCGAA CATGCCCGTC GCAGCCCGTG 200
 AGGCCTCTAT TTATACCGGC ATCACCCTTG CTGAGTACTA CCGTGATATG 250
 GGCAAGCACA TTGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC 300
 GCTGCGTGAG ATTTCCGGGTC GATTGGCGGA GATGCCGGCT GATGGTGGCT 350
 ACCCTGCCTA CCTCAGCGCC CGCCTCGCCT CCTTCTACGA GCGCGCCGGT 400
 40 CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATCGT 450
 CCGTGCACTG TCTCCACCG 469

45 2) INFORMATION FOR SEQ ID NO: 962

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962

	TGTCATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAT	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACCGT	GATCGATGGC	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACCTCGAA	CATGCCAGTC	GCAGCCCGTG	200
5	AGGCCTCTAT	TTACACCGGC	ATCACCTTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCTGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCCGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
10	CGGTGCCGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 963

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963

30	TGTGATCAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCGGAC	TGCGTCATCT	50
	ACGTCGGCTG	TGGTGAGCGC	GGGAACGAGA	TGGCCGAGGT	GCTCATGGAT	100
	TTCCCGACTT	TGACGACTGT	GATCGATGGT	CGCGAGGAGT	CCATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACCTCCAA	CATGCCAGTT	GCAGCCCGTG	200
	AGGCTTCTAT	CTATACCGGC	ATCACACTGG	CTGAGTACTA	TCGTGATATG	250
35	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GTTGCGTGAG	ATTTCCGGTC	GGCTGGCGGA	GATGCCGGCC	GATGGTGGTT	350
	ACCCCGCCTA	CCTCAGTGCC	CGTCTCGCCT	CCTTCTACGA	GCGCGCTGGC	400
	CTCGTGACCT	GTATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACAATTGT	450
	TGGTGCGGTG	TCTCCACCG				469

40

2) INFORMATION FOR SEQ ID NO: 964

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964

60	GGTCATTAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCTGAC	TGCGTCATCT	50
	ACGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100

TCCCCGACCC TGACGACCAT GATCGATGGT CGGGAGGAGT CGATCATGAA 150
 GCGCACCTGC CTCGTGGCGA ACACCTCGAA CATGCCCGTC GCAGCCCGTG 200
 AGGCCTCTAT CTACACCGGC ATCACCTCG CCGAGTACTA CCGTGATATG 250
 GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCTGAGGC 300
 5 GCTTCGTGAG ATTTTCGGGTC GTCTGGCGGA GATGCCGGCC GATGGTGGCT 350
 ACCCCGCCTA CCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC 400
 CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATCGT 450
 CGGTGCCGTG TCTCCGCCG 469

10

2) INFORMATION FOR SEQ ID NO: 965

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965

TGTAATTAGT CAGGCCCTCT CCAAGTACTC CAACTCCGAC TGCATCATCT 50
 ATGTCGGCTG CCGCGAGCGC GGTAATGAGA TGGCCGAGGT GCTCATGGAG 100
 30 TCCCCGACCC TGACGACCGT GATCGATGGT CCGGAGGAGT CGATCATGAA 150
 GCGCACCTGC CTCGTGGCGA ACACTTCGAA CATGCCAGTC GCAGCCCGTG 200
 AGGCCTCTAT TTACACCGGC ATCACCTTGG CCGAGTACTA CCGTGATATG 250
 GGCAAGCATA TCGCCATGAT GGCCGACTCG ACGTCTCGCT GGGCCGAGGC 300
 GCTTCGTGAG ATTTTCGGGTC GTTTGGCGGA GATGCCGGCC GATGGTGGCT 350
 35 ACCCTGCCTA TCTCAGCGCT CGTCTCGCCT CCTTCTACGA GCGCGCCGGC 400
 CTCGTACCT GCATCGGCGG GCCGAAGCGC CAGGGCTCCG TCACGATTGT 450
 CGGTGCCGTG TCTCCGCCG 469

40

2) INFORMATION FOR SEQ ID NO: 966

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966

CACCAGTTCG CCAAGTGGGC AGATGCTCAG ATAGTTGTAT ACGTTGGTTG 50
 TGGAGAACGT GGTAACGAGA TGACAGACGT TCTAAATGAA TTCCAGAAC 100
 TGATTGACCC TCATACAGGC GAATCTCTAA TGAAGAGAAC AGTTCTTATA 150
 60 GCTAATACGT CAAATATGCC AGTTGCAGCC AGAGAGGCAA GTATATATAC 200

	AGGTATTACA	ATAGCTGAAT	ATTTTAGAGA	CATGGGATAT	TCAGTAGCGG	250
	TAATGGCCGA	CTCTACATCA	AGATGGGCAG	AGGCCCTAAG	AGAGATGTCA	300
	GGTCGTCTAG	AAGAAATGCC	TGGTGATGAA	GGTTATCCAG	CCTATCTAGG	350
	TTCTAGAGCT	GCAGAGTTCT	ATGAAAGAGC	AGGTAAGGTA	ATATGTAAGG	400
5	GTAGCGATAA	TAGAGAGGGA	GCCCTTACAA	TAATAGGTGC	CGTGTCACC	449

2) INFORMATION FOR SEQ ID NO: 967

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Bordetella pertussis*
- (B) STRAIN: ATCC 9797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967

25	CTGGTGGTGT	CGGCCGCAGA	CGGCCCCGATG	CCGCAGACGC	GCGAGCACAT	50
	TTTGCTGTCTG	CGCCAGGTTG	GCGTGCCGTA	CATCATCGTG	TTCCTGAACA	100
	AGGCGGACAT	GGTTGATGAC	GCGGAGCTGC	TCGAGCTGGT	GAAGATGGAA	150
	GTCCGCGAAC	TGCTGAGCAA	GTACGATTTC	CCGGGCGATG	ACACGCCGAT	200
	CGTGAAGGGT	TCGGCCAAGC	TGGCGCTGGA	AGGCGACAAG	GGCGAACTGG	250
30	GCGAGCAGGC	GATTCTGTCTG	CTGGCGCAAG	CGCTGGACAC	GTACATTCCG	300
	ACGCCGGAGC	GCGCGGTCGA	CGGTGCGTTC	CTGATGCCCG	TGGAAGACGT	350
	GTTCTCGATC	TCGGGCCGTG	GCACGGTGGT	GACTGGCCGT	ATCGAGCGCG	400
	GCGTGGTGAA	GGTTGGCGAG	GAAATCGAAA	TCGTGGGCAT	CAAGCCGACG	450
	GTGAAGACGA	CCTGCACGGG	CGTGGAGATG	TTCCGCAAGC	TGCTGGACCA	500
35	GGGCCAGGCG	GGCGACAACG	TGGGTATCTT	GCTGCGCGGC	ACCAAGCGTG	550
	AAGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGTTT	GATCAACCCG	600
	CACACGGACT	TCACGGCCGA	GGTGATACAT	CTGTCCAAGG	AAGAGGGTGG	650
	CCGTCACACG	CCGTTCTTCA	ACGGCTATCG	TCCGCAGTTC	TACTTCCGCA	700
	CGACGGACGT	GACCGGCACG	ATCGACCTGC	CGGCGGACAA	GGAAATGGTG	750
40	CTGCCGGGCG	ACAACGTGTC	GATGACCGTC	AAGCTGCTGG	CCCCGATCGC	800
	CATGGAAGAA	GGTCTGCGTT	TCGCCA			826

45 2) INFORMATION FOR SEQ ID NO: 968

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55

- (A) ORGANISM: *Bordetella pertussis*
- (B) STRAIN: BD180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968

60

	CGATCCTGGT	GGTGTGCGCC	GCAGACGGCC	CGATGCCGCA	GACGCGCGAG	50
	CACATTTTGC	TGTCGCGCCA	GGTTGGCGTG	CCGTACATCA	TCGTGTTTCCT	100
	GAACAAGGCG	GACATGGTTG	ATGACGCGGA	GCTGCTCGAG	CTGGTGGAGA	150
	TGGAAGTCCG	CGAACTGCTG	AGCAAGTACG	ATTTCCC GGG	CGATGACACG	200
5	CCGATCGTGA	AGGGTTCGGC	CAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
	ACTGGGCGAG	CAGGCGATTC	TGTCGCTGGC	GCAAGCGCTG	GACACGTACA	300
	TTCCGACGCC	GGAGCGCGCG	GTCGACGGTG	CGTTCCTGAT	GCCGGTGGAA	350
	GACGTGTTCT	CGATCTCGGG	CCGTGGCACG	GTGGTGACTG	GCCGTATCGA	400
	GCGCGGCGTG	GTGAAGGTTG	GCGAGGAAAT	CGAAATCGTG	GGCATCAAGC	450
10	CGACGGTGAA	GACGACCTGC	ACGGGCGTGG	AGATGTTCCG	CAAGCTGCTG	500
	GACCAGGGCC	AGGCGGGCGA	CAACGTGGGT	ATCTTGCTGC	GCGGCACCAA	550
	GCGTGAAGAC	GTCGAGCGTG	GCCAGGTGCT	GGCCAAGCCG	GGTTCGATCA	600
	ACCCGCACAC	GGACTTCACG	GCCGAGGTGT	ACATTCTGTC	CAAGGAAGAG	650
	GGTGGCCGTC	ACACGCCGTT	CTTCAACGGC	TATCGTCCGC	AGTTCTACTT	700
15	CCGCACGACG	GACGTGACCG	GCACGATCGA	CCTGCCGGCG	GACAAGGAAA	750
	TGGTGCTGCC	GGGCGACAAC	GTGTCGATGA	CCGTCAAGCT	GCTGGCCCCG	800
	ATCGCCATGG	AAGAAGG				817

20

2) INFORMATION FOR SEQ ID NO: 969

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969

	CCTATGCCAC	AAACTCGTGA	ACACATTCTT	TTATCACGTA	ACGTTGGTGT	50
	GCCATACATC	GTTGTTTTCT	TAAACAAAGT	TGATATGGTT	GACGACGAAG	100
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	AACTGAATAT	150
40	GACTTCCCAG	GAGACGATGT	TCCTGTAATC	GCTGGTTCCTG	CATTAAAAGC	200
	TTTAGAAGGC	GACCCTGCTT	ACGAAGAAAA	AATCTTAGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACATCCCA	ACTCCAGAAC	GTGACAACGA	CAAACCATTC	300
	ATGATGCCAG	TTGAAGACGT	GTTCTCAATT	ACTGGTCGTG	GTACTGTTGC	350
	TACAGGTCGT	GTTGAACGTG	GACAAGTTCG	TGTTGGTGAC	GAAGTTGAAA	400
45	TCGTTGGTAT	CGCTGACGAA	ACTTCTAAAA	CAACAGTTAC	TGGTGTTGAA	450
	ATGTTCCGTA	AATTATTAGA	TTACGCTGAA	GCTGGAGACA	ACATCGGTGC	500
	ATTATTACGT	GGTGTGGCTC	GTGAAGACAT	CCAACGTGGT	CAAGTATTAG	550
	CTAAACCAGG	TTCAATCACT	CCACATACAA	AATTCACTGC	TGAAGTGTAC	600
50	GTTTTAACTA	AAGAAGAAGG	TGGACGTCAT	ACTCCAT		637

2) INFORMATION FOR SEQ ID NO: 970

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

5 (B) STRAIN: ATCC 49997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970

	TATGCCTCAA	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	50
10	CATACATCGT	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	150
	CTTCCCAGGC	GACGATGTTT	CTGTAATCGC	TGGTTCCTGT	TTGAAAGCTC	200
	TTGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	250
	GTTGACGAAT	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTTCAT	300
15	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGAAAC	TGCTAAAACA	ACTGTAACTG	GTGTTGAAAT	450
	GTTCCGTAA	TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	500
	TGCTACGTGG	GGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTAGCT	550
20	AAAGCTGGTA	CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	600
	TTTAACAAAA	GAAGAAGGTG	GACGTCACAC	TCCA		634

25 2) INFORMATION FOR SEQ ID NO: 971

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971

40	GGACCAATGC	CACAAACTCG	TGAGCACATC	CTTCTTTCAC	GTCAGGTTGG	50
	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	AGTTGACTTG	GTTGACGACG	100
	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	TCCGTGACCT	ATTGTCAGAA	150
	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	ATCCAAGGTT	CAGCACTTAA	200
45	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	CATCGTTATG	GAATTGATGA	250
	ACACAGTTGA	TGAGTATATC	CCAGAACCAG	AACGTGACAC	TGACAAACCA	300
	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	ATCACTGGAC	GTGGTACAGT	350
	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	TAAAGTCAAC	GACGAAATCG	400
	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	AAGCAGTTGT	TACTGGTGTG	450
50	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	500
	TGTCCTTCTT	CGTGGTGTTC	AACGTGATGA	AATCGAACGT	GGACAAGTTA	550
	TCGCTAAACC	AGGTTCAATC	AACCCACACA	CTAAATTCAA	AGGTGAAGTC	600
	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	CACACTCCAT	TCTTCAACAA	650
	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	TGACGTTACA	GGTTCAATCG	700
55	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	CTGGTGATAA	CGTGACAATC	750
	GACGTTGAGT	TGATTCACCC	AATCGCCGTA	GAACAAG		787

60 2) INFORMATION FOR SEQ ID NO: 972

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972

15 TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA GCACATCCTG 50
 CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC TGAACAAATG 100
 CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA ATGGAAGTTC 150
 GTGAAC TTCT GTCTCAGTAC GACTTCCCGG GCGACGACAC TCCGATCGTT 200
 20 CGTG GTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT GGGAAGCGAA 250
 AATCCTGGAA CTGGCTGGCT TCCTGGATTC TTACATTCCG GAACCAGAGC 300
 GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT ATTCTCCATC 350
 TCCGGTCGTG GTACCGTTGT TACCGTCTGT GTAGAACGCG GTATCATCAA 400
 AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT CAGAAGTCTA 450
 25 CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA AGGCCGTGCT 500
 GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG AAGAAATCGA 550
 ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG CACACCAAGT 600
 TCGAATCTGA AGTGACATT CTGTCCAAAG ATGAAGGCGG CCGTCATACT 650
 CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA CTACTGACGT 700
 30 GACTGGTACC ATCGAACTGC CGGAAGGCGT AGAGATGGTA ATGCCGGGCG 750
 ACAACATCAA AATGGTTGTT ACCCTGATCC ACCCGATCGC GATGGACGAC 800
 GGT 803

35

2) INFORMATION FOR SEQ ID NO: 973

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973

ACTGACGGCC CGATGCCGCA GACTCGTGAG CACATCCTGC TGGGTCGTCA 50
 GG TAGGCGTT CCGTACATCA TCGTGTTCTT GAACAAATGC GACATGGTTG 100
 ATGACGAAGA GCTGCTGGAA CTGGTTGAAA TGGAAGTTTC TGAAC TTCTG 150
 55 TCTCAGTACG ACTTCCCGGG CGACGACACT CCGATCGTTC GTGGTTCTGC 200
 TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG GGAAGCGAAA ATCCTGGAAC 250
 TGGCTGGCTT CCTGGATTCC TACATTCCCG AACCAGAGCG TGCRATTGAC 300
 AAGCCGTTCC TGCTGCCGAT CGAAGACGTA TTCTCCATCT CCGGTCGTGG 350
 TACCGTTGTT ACCGTCGTG TAGAACGCGG TATCATCAA GTTGGTGAAG 400
 60 AAGTTGAAAT CGTTGGTATC AAAGAGACTC AGAAGTCTAC CTGTACTGGC 450

GTTGAAATGT TCCGCAAAC TCTGGACGAA GGCCGTGCTG GTGAGAACGT 500
 AGGTGTTCTG CTGCGTGGTA TCAAACGTGA AGAAATCGAA CGTGGTCAGG 550
 TACTGGCTAA GCCGGGCACC ATCAAGCCGC ACACCAAGTT CGAATCTGAA 600
 GTGTACATTC TGTCCAAAGA TGAAGGCGGC CGTCATACTC CGTTCTTCAA 650
 5 AGGCTACCGT CCGCAGTTCT ACTTCCGTAC TACTGACGTG ACTGGTACCA 700
 TTGAAGTACC GGAAGGCGTA GAGATGGTAA TGCCGGGCGA CAACATCAAA 750
 ATGGTTGTTA CC 762

10

2) INFORMATION FOR SEQ ID NO: 974

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 804 bases
 - 15 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Escherichia coli*
 - (B) STRAIN: ATCC 11775

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974

CCTGGTAGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA 50
 TCCTGCTGGG TCGTCAGGTA GCGGTTCCGT ACATCATCGT GTTCCTGAAC 100
 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACTGG TTGAAATGGA 150
 30 AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACTCCGA 200
 TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250
 GCGAAAATCC TGGAAGTGGC TGGCTTCCTG GATTCCTACA TTCCGGAACC 300
 AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
 CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA ACGCGGTATC 400
 35 ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
 GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
 GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GCGGTATCAA ACGTGAAGAA 550
 ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
 CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGTCGTC 650
 40 ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
 GACGTGACTG GTACCATCGA ACTGCCGGAA GGCCTAGAGA TGGTAATGCC 750
 GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
 ACGA 804

45

2) INFORMATION FOR SEQ ID NO: 975

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 804 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 55 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Escherichia coli*
 - (B) STRAIN: ATCC 25922

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975

```

5   GCGATCCTGG TAGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA      50
    GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC      100
    TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTTGAA      150
    ATGGAAGTTC GTGAACTTCT GTCTCAGTAC GACTTCCCGG GCGACGACAC      200
    TCCGATCGTT CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GACGCAGAGT      250
    GGGAAAGCGAA AATCCTGGAA CTGGCTGGCT TCCTGGATTG YTACATTCCG      300
    GAACCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCGA TCGAAGACGT      350
10  ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAACGCG      400
    GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGAGACT      450
    CAGAAGTCTA CCTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      500
    AGGCCGTGCT GGTGAGAACG TAGGTGTTCT GCTGCGTGGT ATCAAACGTG      550
    AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCAC CATCAAGCCG      600
15  CACACCAAGT TCGAATCTGA AGTGATACAT CTGTCCAAAG ATGAAGGCGG      650
    TCGTCATACT CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA      700
    CTACTGACGT GACTGGTACC ATCGAAGTGC CGGAAGGTGT AGAGATGGTA      750
    ATGCCGGGCG ACAACATCAA AATGTTGTT ACCCTGATCC ACCCGATCGC      800
    GATG                                                                804
20

```

2) INFORMATION FOR SEQ ID NO: 976

```

25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 825 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
30
    (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Mycobacterium avium
          (B) STRAIN: Mavi-1
35

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976

```

40  GGCGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCGATGC CGCAGACCCG      50
    TGAGCACGTG CTGCTCGCCC GTCAGGTCGG TGTGCCCTAC ATCCTGGTCG      100
    CCCTGAACAA GGCCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC      150
    GAGATGGAGG TCCGCGAGCT GCTGGCCGCC CAGGAGTTCG ACGAGGACGC      200
    CCCGGTGGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGC GACGCCAAGT      250
    GGGTCGAGTC CGTCGAGCAG CTGATGGAGG CCGTCGACGA GTCGATCCCG      300
45  GACCCGGTCC GCGAGACGGA GAAGCCGTTT CTGATGCCGG TGGAGGACGT      350
    CTTACCATC ACCGGGCGTG GCACCGTGGT CACCGGTCGT GTCGAGCGCG      400
    GTGTGATCAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CCGCCCGACC      450
    AGCACCAAGA CCACGGTCAC CGGTGTGGAR ATGTTCCGCA AGCTGCTCGA      500
    CCAGGGCCAG GCCGGTGACA ACGTCGGTCT GCTGCTGCGT GGTATCAAGC      550
50  GTGAGGACGT CGAGCGCGGC CAGGTCGTGA CCAAGCCCGG CACCACCACG      600
    CCGCACACCG AGTTCGAGGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG      650
    CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG TTCTACTTCC      700
    GCACCACCGA CGTGACCGGT GTGGTGACGC TGCCGGAGGG CACCGAGATG      750
    GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGCTGA TCCAGCCCGT      800
55  CGCCATGGAC GACGGTSTGC GGTTC                                                                825

```

2) INFORMATION FOR SEQ ID NO: 977

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977

```

15  TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
    ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG      100
    AACAAAGTTG ACTTGGTGTA CGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
    GGAAATCCGT GACCTATTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
    CAGTTATCCA AGGTTTACGA CTTAAAGCTC TTGAAGGTGA CTCTAAATAC      250
20  GAAGACATCG TTATGGAATT GATGAACACA GTTGATGAGT ATATCCCAGA      300
    ACCAGAACGT GACACTGACA AACCATTGCT TCTTCCAGTC GAGGACGTAT      350
    TCTCAATCAC TGGACGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
    ATCGTTAAAG TCAACGACGA AATCGAAATT GTTGGTATCA AAGAAGAAAC      450
    TCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAACTTGACG      500
25  AAGGTCTTGC TGGAGATAAC GTAGGTGTCC TTCTTCGTGG TGTTCACGT      550
    GATGAAATCG AACGTGGACA AGTTATCGCT AAACCAGGTT CAATCAACCC      600
    ACACACTAAA TTCAAAGGTG AAGTCTACAT CCTTACTAAA GAAGAAGGTG      650
    GACGTCACAC TCCATTCTTC AACAACTACC GTCCACAATT CTACTTCCGT      700
    ACTACTGACG TTACAGGTTC AATCGAACTT CCAGCAGGTA CTGAAATGGT      750
30  AATGCCTGGT GATAACGTGA CAATCGACGT TGAGTTGATT CACCCAATCG      800
    CCGTAGAACA AGGTACTACA                                820
  
```

35 2) INFORMATION FOR SEQ ID NO: 978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
 (B) STRAIN: M-Gor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978

```

50  GGCGCGATCC TGGTGGTCGC CGCCACCGAT GGCCCGATGC CGCAGACCCG      50
    TGAGCACGTG CTGCTCGCCC GTCAGGTGGG CGTGCCCTAC ATCCTGGTGG      100
    CGCTGAACAA GTCCGACGCG GTCGACGACG AGGAGCTGCT CGAGCTCGTC      150
    GAGCTGGAGG TCCGCGAGTT GCTGGCCGCC CAGGACTTCG ACGAGGAAGC      200
55  TCCGGTGGTC CGGGTCTCGG CGCTGAAGGC GCTCGAGGGC GACGCCACCT      250
    GGGTGAAGTC GGTAGAGGAC TTGATGGACG CGGTCGACGA GTCGATTCCG      300
    GACCCGGTCC GCGACACCGA CAAGCCGTTT CTGATGCCCG TCGAGGACGT      350
    CTTACCATC ACCGGTCGTG GCACCGTCGT CACCGGCCGT GTGGAGCGCG      400
    GCGTGGTGAA CGTGAACGAG GAAGTCGAGA TCGTCGGCAT CAAGCCGACC      450
60  AGCACCAAGA CCACGGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500
  
```


	CCAGGGTCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTGTCAAGC	550
	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTCA	TCAAGCCCGG	CACCACCACT	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAACATA	CCGTCCGCAG	TTCTACTTCC	700
5	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAAATG	750
	GTGATGCCCG	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCGT	800
	CGCCATGGAC	GACGGTCTGC	GG			822

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2) INFORMATION FOR SEQ ID NO: 979

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979

	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
30	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTGAGC	ACTTAAAGCT	CTTGAAGGTG	ACTCTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TATATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAGGACGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
35	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGGTTGAA	TGTTCCGTAA	ACAACCTGAC	500
	GAAGGTCTTG	CTGGAGATAA	CGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTCTACA	TCCTTACTAA	AGAAGAAGGT	650
40	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	A			821

45

2) INFORMATION FOR SEQ ID NO: 980

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: ATCC 25177

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980

```

GGTGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCGATGC CCCAGACCCG      50
CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC ATCCTGGTAG      100
5  CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC      150
GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTTC ACGAGGACGC      200
CCCGGTTGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT      250
GGGTTGCCCT TGTCGAGGAA CTGATGAACG CGGTCGACGA GTCGATTCCG      300
GACCCGGTCC GCGAGACCGA CAAGCCGTTT CTGATGCCGG TCGAGGACGT      350
10 CTTACCAATT ACCGGCCGCG GAACCGTGGT CACCGGACGT GTGGAGCGCG      400
GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG      450
ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500
CCAGGGCCAG GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GGCGTCAAGC      550
GCGAGGACGT CGAGCGTGCG CAGGTGTGCA CCAAGCCCGG CACCACCACG      600
15 CCGCACACCG AGTTCGAAGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG      650
CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG TTCTACTTCC      700
GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG      750
GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT      800
CGCCATGGAC GAAGGTNTGC GTTTCGCG      828
20

```

2) INFORMATION FOR SEQ ID NO: 981

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 144

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981

```

CGGCCGTATC TTAGTAGTAT CTGCTGCAGA TGGCCCAATG CCACAAACTC      50
40 GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA      100
TTCTTAAACA AAGCTGACAT GGTGACGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTATCTGA ATACGACTTC CCTGGTGACG      200
ATGTACCAGT TATCGTTGGT TCTGCATTAA AAGCTTTAGA AGGCGACCCA      250
GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCTGTAG ATGACTACAT      300
45 CCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG      350
ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCAACAGG CCGTGTTGAA      400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATCACTGA      450
AGAAAGCAAG AAAACAACAG TTACAGGTGT AGAAATGTTT CGTAAATTAT      500
TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTG      550
50 GCACGTGAAG ACGTACAACG TGGACAAGTA TTAGCAGCTC CTGGCTCTAT      600
TACTCCACAC ACAAATTC AAGCTGATGT TTACGTTTTA TCTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC      700
TTCCGTACTA CTGACGTAAC TGGCGTTGTT CACTTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGATA ACGTAGAAAT GACTGTTGAA TTAATCGCTC      800
55 CAATCGCGAT TGAAGACGG      819

```

2) INFORMATION FOR SEQ ID NO: 982

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982

```

15 CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
   CACATCCTTC TTTCACGTCA GGTTGGTGTT AAACACCTTA TCGTCTTCAT      100
   GAACAAGATC GACTTGGTTG ATGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
   TGGAAATCCG TGACCTCTTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
   CCAGTTATCC AAGGTTTCAGC TCTTAAAGCT CTTGAAGGTG ATACTAAGTA      250
20 CGAAGACATC ATCATGGAAT TGATGAACAC TGTGATGAG TACATCCCAG      300
   AACCAGAACG TGATACTGAC AAACCTCTTC TTCTTCCAGT CGAAGACGTA      350
   TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
   TACTGTTCGT GTCAACGATG AAATCGAAAT CGTTGGTATC AAAGAAGAAA      450
   TCCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCGGTAA ACAGCTTGAC      500
25 GAAGGTCTTG CAGGGGACAA CGTAGGTGTA CTTCTTCGTG GTATCCAACG      550
   TGATGAAATC GAACGTGGTC AAGTTATCGC TAAACCAGGT TCAATCAACC      600
   CACACACTAA ATTCAAGGGT GAAGTTTACA TCCTTACTAA AGAAGAAGGT      650
   GGACGTCACA CTCCATTCTT CAACAACACTAC CGTCCACAGT TCTACTTCCG      700
   TACAAC TGACGTTTCA CAATCGAAGT TCCAGCAGGT ACTGAAATGG      750
30 TAATGCCTGG TGATAACGTA ACTATCGACG TTGAGTTGAT CCACCCAATC      800
   GCCGTTGAAC AAGG                                     814

```

35 2) INFORMATION FOR SEQ ID NO: 983

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 983

```

50 CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG      50
   CACATCCTTC TTTCACGTCA GGTTGGTGTT AAACACCTTA TCGTCTTCAT      100
   GAACAAAGTT GACTTGGTTG ACGACGAAGA ATTGCTTGAA TTGGTTGAAA      150
   TGGAAATCCG TGACCTATTG TCAGAATACG ACTTCCCAGG TGACGATCTT      200
55 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCC CTTGAAGGTG AACTAAATA      250
   CGAAGACATC GTTATGGAAT TGATGAACAC AGTTGATGAG TACATCCCAG      300
   AACCAGAACG TGACACTGAC AAACCATTCG TTCTTCCAGT CGAAGACGTA      350
   TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG      400
   TATCGTTAAA GTCAACGACG AAATCGGAAA CGTTGGTATC AAAGAAGAAA      450
60 CTCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCGGTAA ACAACTTGAC      500

```

GAAGGTCTTG CCGGAGATAA TG TAGGTGTC CTTCTTCGTG GTGTTCAACG 550
TGATGAAATC GAACGTGGAC AAGTTATTGC TAAACCAGGT TCAATCAACC 600
CACACACTAA ATTCAAAGGT GAAGTTTACA TCCTTACTAA AGAAGAAGGT 650
GGACGTCACA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700
5 TACTACTGAC GTTACAGGTT CAATCGAACT TCCAGCAGGT ACTGAAATGG 750
TAATGCCTGG TGATAACGTG ACAATCGACG TTGAGTTGAT CCACCCAATC 800
GCCGTAGAAC 810

10

2) INFORMATION FOR SEQ ID NO: 984

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
20
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus mitis*
(B) STRAIN: ATCC 903

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984

TCCTTGTAGT AGCTTCAACT GACGGACCAA TGCCACAAAC TCGTGAGCAC 50
ATCCTTCTTT CACGTCAGGT TGGTGTTAAA CACCTTATCG TCTTCATGAA 100
CAAGATCGAC TTGGTTGATG ACGAAGAATT GCTTGAATTG GTTGAAATGG 150
30 AAATCCGTGA CCTCTTGTC AATACGACT TCCCAGGTGA CGATCTTCCA 200
GTTATCCAAG GTTCAGCTCT TAAAGCTCTT GAAGGTGATA CTAAGTACGA 250
AGACATCATC ATGGAATTGA TGAACACTGT TGATGAGTAC ATCCCAGAAC 300
CAGAACGTGA TACTGACAAA CCTCTTCTTC TTCCAGTCGA AGACGTATTC 350
TCAATCACTG GTCGTGGTAC AGTTGCTTCA GGACGTATCG ACCGTGGTAC 400
35 TGTTTCGTGTC AACGATGAAA TCGAAATCGT TGGTATCAAA GAAGAAATCC 450
AAAAAGCAGT TGTTACTGGT GTTGAAATGT TCCGTAAACA GCTTGACGAA 500
GGTCTTGCA GGGACAACGT AGGTGTACTT CTTCTGTTGA TCCAACGTGA 550
TGAAATCGAA CGTGGTCAAG TTATCGCTAA ACCAGGTTCA ATCAACCCAC 600
ACACTAAATT CAAGGGTGAA GTTTACATCC TTACTAAAGA AGAAGGTGGA 650
40 CGTCACACTC CATTCTTCAA CAACTACCGT CCACAGTTCT ACTTCCGTAC 700
AAGTACGCTT ACAGGTTCAA TCGAACTTCC AGCAGGTACT GAAATGGTAA 750
TGCCTGGTGA TAACGTAAC ATCGACGTTG AGTTGATCCA CCCAATCGCC 800
GTTGAACAAG GTACTAC 817

45

2) INFORMATION FOR SEQ ID NO: 985

- (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 798 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
55
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus oralis*
(B) STRAIN: ATCC 35037
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985

	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTTCTTT	CACGTCAGGT	50
	TGGTGTTAAA	CACCTTATTG	TCTTCATGAA	CAAAATTGAC	TTGGTAGACG	100
5	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	AAATCCGTGA	CCTCTTGTC	150
	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	GTTATCCAAG	GTTCAGCTCT	200
	TAAAGCTCTT	GAAGGTGACT	CTAAATACGA	AGACATCATT	ATGGAATTGA	250
	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	CAGAACGTGA	CACTGAAAAA	300
	CCATTGCTTC	TTCCAGTCGA	AGACGTATTG	TCAATCACTG	GACGTGGTAC	350
10	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	TGTTCTGTGC	AACGACGAAA	400
	TCGAAATCGT	TGGTATCAAA	GAAGAACTC	AAAAAGCAGT	TGTTACTGGT	450
	GTTGAAATGT	TCCGTAAACA	ACTTGACGAA	GGTCTTGCCG	GAGATAACGT	500
	AGGTGTCTT	CTTCGTGGTG	TTCAACGTGA	CGAAATCGAA	CGTGGACAAG	550
	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	ACACTAAATT	TAAAGGTGAA	600
15	GTCTACATCC	TTACTAAAGA	AGAAGGTGGA	CGTCACACTC	CATTCTTCAA	650
	CAACTACCGT	CCACAATTCT	ACTTCCGTAC	TACTGACGTT	ACAGGTTCAA	700
	TCGAACCTCC	TGCAGGTACT	GAAATGGTAA	TGCCTGGTGA	TAACGTGACT	750
	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	GTAGAACAAG	GTACTACA	798

20

2) INFORMATION FOR SEQ ID NO: 986

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 815 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-05

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986

	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
	CTTCTTTCAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
40	AGTTGACTTG	GTTGACGACG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	ATTGTCAGAA	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	200
	ATCCAAGGTT	CAGCACTTAA	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	250
	CATCGTTATG	GAATTGATGA	ACACAGTTGA	TGAGTATATT	CCAGAACCAG	300
	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	350
45	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	400
	TAAAGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	CTTGCTGGAG	ATAACGTAGG	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	550
	AATCGAACGT	GGACAAGTTA	TCGCTAAACC	AGGTTCAATC	AACCCACACA	600
50	CTAAATTCAA	AGGTGAAGTC	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	700
	TGACGTTACA	GGTTCAATCG	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	GACGTTGAGT	TGATTCAACC	AATCGCCGTA	800
	GAACAAGGTA	CTACA				815

55

2) INFORMATION FOR SEQ ID NO: 987

60 (i) SEQUENCE CHARACTERISTICS:

549

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987

	CGGACAATCT	TGGTTGTTTC	TGCTACGGAT	GGCCCAATGC	CTCAAACCTCG	50
15	TGAACACATT	TTACTTTCTC	GCCAAGTAGG	CGTGAAATAT	TTGATTGTTT	100
	TCTTGAACAA	AACAGATTTA	GTCGATGATG	AAGAATTAAT	TGATCTAGTA	150
	GAAATGGAAAG	TTCGTGAACT	ATTAAGCGAA	TATGGATTTC	CAGGTGATGA	200
	TACACCTGTT	ATCAAAGGAT	CAGCATTAAG	AGCATTACAA	GGTGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ACACAGTCGA	TGAATACATC	300
20	CCAACACCAG	AACGTGATAC	GGACAAACCA	TTATTGTTAC	CCGCCGAAGA	350
	TGTATTTTCA	ATTACTGGAC	GTGGAACAGT	AGCATCTGGT	CGGATTGACC	400
	GTGGGGCTGT	TAGAGTCGGT	GACGAAATCG	AAATCGTAGG	GATCAAACCA	450
	GAAACGCAAA	GAGCCGTAGT	AACAGGAGTT	GAAATGTTCC	GCAAAACGCT	500
	TGATTACGGT	GAAGCAGGGG	ATAACGTAGG	TGTGTTATTA	CGTGGGATTC	550
25	AAAGAGAAGA	CATCGAACGT	GGCCAAGTGA	TTGCCAAACC	TGTTCAATT	600
	ACACCTCATA	CTAAATTCAA	AGCAGAAGTT	TAGGTTTGA	CTAAAGAAGA	650
	AGGCGGACGT	CATACACCAT	TCTTCAATAA	TTATCGACCA	CAATTTTATT	700
	TCCGCACAAC	TGACGTAACA	GGAACAATTG	TTTTGCCAGA	AGGAACGGAA	750
	ATGGTCATGC	CTGGCGACAA	CGTAACGATC	GATGTAGAAT	TGATTCATCC	800
30	TGTTGCTATT	GAAAACGGGA	CGACTTTCTC	CA		832

2) INFORMATION FOR SEQ ID NO: 988

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988

50	TGGTGCGATC	TTAGTTGTTT	CTGCGACAGA	TGGACCAATG	CCTCAAACCTC	50
	GCGAGCATAT	CCTTTTATCA	CGTCAAGTTG	GTGTAAAATA	TTTGATTGTA	100
	TTTTTGAATA	AAGTTGATTT	GGTCGATGAT	GAAGAATTGA	TCGATCTTGT	150
	AGAAATGGAA	GTTCGTGAAT	TACTGAATGA	ATATGGTTTC	CCAGGTGATG	200
	ACACACCTGT	CATCAAAGGC	TCTGCATTGA	AAGCATTGCA	AGGTGACCCA	250
55	GAAGCAGAAG	CTGCGATCAA	TGAATTGATG	GAAACAGTGG	ATGACTATAT	300
	CCCAACACCA	GAACGTGATA	CCGACAAACC	ATTGCTTTTA	CCAGTTGAAG	350
	ATGTTTTTCTC	AATCACTGGT	CGCGGAACGG	TAGCATCTGG	TCGTATCGAC	400
	CGTGGAGCCG	TTCGTGTCGG	TGATGAAATC	GAGATCATCG	GAATCAAACC	450
	TGAAACGAAA	AAAGCGGTTG	TGACAGGGGT	AGAGATGTTT	CGTAAAACGT	500
60	TAGATTATGG	CGAAGCTGGA	GATAACGTAG	GAATCTTGTT	ACGTGGTATC	550

550

	CAAAGAGAAG	ATATTGAACG	TGGACAAGTA	ATTGCGAAAC	CTGGTTCAAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGCGGACG	TCATACACCA	TTCTTCAATA	ACTACCGCCC	ACAATTTTAT	700
	TTCCGCACAA	CAGATGTAAC	AGGTACGATC	GTGTTGCCAG	AAGGAACAGA	750
5	AATGGTCATG	CCTGGAGACA	ACGTAACCAT	CGAGGTAGAG	TTGATCCATC	800
	CAGTGGCAAT	CGAACAAGGA	ACGACTTTCT	CTATT		835

10 2) INFORMATION FOR SEQ ID NO: 989

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989

25	TGCGATCTTA	GTA GTATCTA	CTACTGATGG	ACCAATGCCT	CAAACACGTG	50
	AGCACATTTT	GTTATCACGC	CAAGTAGGTG	TTAAATACTT	GATCGTCTTC	100
	TTGAACAAAG	TTGATTAGT	CGACGATGAA	GAATTGATTG	ATTTAGTTGA	150
	AATGGAAGTA	CGTGAGTTAC	TTTCAGAATA	TGGTTTCCCA	GGCGATGATA	200
30	TTCCTGTTCT	TAAAGGTTCA	GCTCTGAAAG	CTTTAGAAGG	CGATCCTGAA	250
	CAAGAACAAG	TAATCATGGA	CCTAATGGAT	ACGGTTGACG	AATATATCCC	300
	AACACCAGAA	CGTGACACTG	ACAAACCATT	CTTGTTACCA	GTGGAAGATG	350
	TTTTCTCAAT	CACAGGACGT	GGGACTGTTG	CATCTGGTCG	TATTGATCGT	400
	GGGGAAGTTA	AAGTCGGTGA	CGAAGTTGAA	ATTATCGGGA	TCAAACCTGA	450
35	AGTTCAAAAG	GCTGTCGTAA	CTGGACTTGA	AATGTTCCGT	AAAACATTGG	500
	ATTATGGTGA	AGCTGGAGAT	AACGTTGGGG	TTCTATTACG	TGGTATTACA	550
	CGTGATGAAA	TCCAACGTGG	TCAAGTATTA	GCTAAACCAG	GTTCAATTAC	600
	ACCACATACG	AAATTCAGTG	CAGAAGTTTA	TGTGTTGACG	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTG	TTTAACAACG	ATCGTCCTCA	ATTCTACTTC	700
40	CGTACAACAG	ACGTTACCGG	TAATATCGTG	TTGCCAGAAG	GTACTGAAAT	750
	GGTCATGCCT	GGCGATAACG	TAACAATCGA	CGTTGAATTA	ATCCATCCAA	800
	TCGCCGTAGA	AAAAGGAACA	ACTTCTCTCA	TT		832

45 2) INFORMATION FOR SEQ ID NO: 990

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9440

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990

GGATCCTGTA TATGCACAAA AACTAGGTGT TAACATCGAT GAATTACTAT 50
 TATCACAACC TGATACAGGG GAGCAAGGTT TAGAAATCGC AGAAGCACTT 100
 GTACGAAGTG GTGCGGTTGA TATTATCGTA ATTGACTCTG TAGCAGCTCT 150
 5 TGTA 154

2) INFORMATION FOR SEQ ID NO: 991

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991

25 GCCATTGCAG AGGCACAGAA GCAGGGCGGT ATTGCAGCCT TCATTGATGC 50
 TGAGCACGCC TTCGACCGTT TCTATGCAGA GAAGTTAGGT GTGGATGTTG 100
 ATAACCTTTG GGTTCACAG CCAGACAATG GTGAGCAGGC TTTAGAGATT 150
 GCCGACCAGC TGATTCGCTC TTCCGCTATT GACATTCTCG TTGTCGACTC 200
 AGTTGCAGCC TTGACTCCAA AGAAGGAGAT TGAGGGTGAC ATGGGTGACT 250
 30 CTGCAGTAGG TTTACAAGCA CGACTGATGA GTCAGGCATT GCGTAAACTT 300
 ACCTCAACAA TCGCAAAAAC TAATACTTGC TGCATCTTCA TCAACCAGTT 350
 GCGTGAGAAG ATTGGTGTGA TGTTTGGTAA TCCA 384

35

2) INFORMATION FOR SEQ ID NO: 992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R760

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992

ACACGTGAAC ACATCTTGTT ATCACGTAAC GTTGGTGTAC CATAATCGT 50
 TGTTTTCTTA AACAAAATGG ATATGGTTGA TGACGAAGAA TTAGTAGAAT 100
 TAGTTGAAAT GGAAGTTCGT GACTTATTGT CAGAATATGA CTTCCCAGGC 150
 55 GACGATGTTC CTGTAATCGC TGGTTCGTCT TTGAAAGCTC TTGAAGGCGA 200
 TGCTTCATAC GAAGAAAAAA TCATGGAATT AATGGCTGCA GTTGACGAAT 250
 ACGTTCCAAC TCCAGAACGT GACACTGACA AACCATTGAT GATGCCAGTC 300
 GAAGACGTAT TCTCAATCAC TGGACGTGGT ACTGTTGCTA CAGGCCGTGT 350
 TGAACGTGGA CAAGTTCGCG TTGGTGACGA AGTTGAAATC GTTGGTATTG 400
 60 CTGAAGAAAC TGCTAAAACA ACTGTAACGT GTGTTGAAAT GTTCCGTAAA 450

TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	TGCTACGTGG	500
TGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	AAAGCTGGTA	550
CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	TTTAACAAAA	600
GAAGAAGCTG	GACGTCATAC	ACCA			624

5

2) INFORMATION FOR SEQ ID NO: 993

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (C) ACCESSION NUMBER: extracted from U40453

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993

ATGGAAAACA	ATAAAAAAGT	ATTGAAGAAA	ATGGTATTTT	TTGTTTTAGT	50
GACATTTCTT	GGACTAACAA	TCTCGCAAGA	GGTATTTGCT	CAACAAGACC	100
CCGATCCAAG	CCAACCTCAC	AGATCTAGTT	TAGTTAAAAA	CCTTCAAAAT	150
ATATATTTTC	TTTATGAGGG	TGACCCGTGT	ACTCACGAGA	ATGTGAAATC	200
TGTTGATCAA	CTTTTATCTC	ACGATTTAAT	ATATAATGTT	TCAGGGCCAA	250
ATTATGATAA	ATTAAAAACT	GAACCTAAGA	ACCAAGAGAT	GGCAACTTTA	300
TTTAAGGATA	AAAACGTTGA	TATTTATGGT	GTAGAATATT	ACCATCTCTG	350
TTATTTATGT	GAAAATGCAG	AAAGGAGTGC	ATGTATCTAC	GGAGGGGTAA	400
CAAATCATGA	AGGGAATCAT	TTAGAAATTC	CTAAAAAGAT	AGTCGTAAAA	450
GTATCAATCG	ATGGTATCCA	AAGCCTATCA	TTTGATATTG	AAACAAATAA	500
AAAAATGGTA	ACTGCTCAAG	AATTAGACTA	TAAAGTTAGA	AAATATCTTA	550
CAGATAATAA	GCAACTATAT	ACTAATGGAC	CTTCTAAATA	TGAAACTGGA	600
TATATAAAGT	TCATACCTAA	GAATAAAGAA	AGTTTTTGGT	TTGATTTTTT	650
CCCTGAACCA	GAATTTACTC	AATCTAAATA	TCTTATGATA	TATAAAGATA	700
ATGAAACGCT	TGACTCAAAC	ACAAGCCAAA	TTGAAGTCTA	CCTAACAACC	750
AAGTAA					756

40

2) INFORMATION FOR SEQ ID NO: 994

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994

55 TGGACTAACA ATCTCGCAAG AGG

23

2) INFORMATION FOR SEQ ID NO: 995

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995
10 ACATTCTCGT GAGTAACAGG GT 22

15 2) INFORMATION FOR SEQ ID NO: 996,

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996
 ACAAATCATG AAGGGAATCA TTTAG 25

30 2) INFORMATION FOR SEQ ID NO: 997

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997
 CTAATTCTTG AGCAGTTACC ATT 23

45 2) INFORMATION FOR SEQ ID NO: 998

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998
60 GGAGGGGTAA CAAATCATGA AGG 23

2) INFORMATION FOR SEQ ID NO: 999

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999
15 TTGACCTTGT TGATGACGAA GAG 23

2) INFORMATION FOR SEQ ID NO: 1000

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000
30 TTAGTGTGTG GGTGATTGA ACT 23

35 2) INFORMATION FOR SEQ ID NO: 1001

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001
AAGAGTTGCT TGAATTAGTT GAG 23

50

2) INFORMATION FOR SEQ ID NO: 1002

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: Genomic DNA
60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: ATCC 700294

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002

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AACATGATCA CTGGTGCCGC TCAAATGGAC GGAGCTATCC TTGTAGTTGC      50
TTCAACTGAT GGACCAATGC CACAAACTCG TGAGCACATC CTTCTTTCAC      100
GTCAGGTTGG TGTTAAACAC CTTATCGTGT TCATGAACAA AGTTGACCTT      150
10 GTTGATGACG AAGAGTTGCT TGAATTAGTT GAGATGGAAA TTCGTGACCT      200
TCTTTCAGAA TACGATTTC CAGGTGATGA CCTTCCAGTT ATCCAAGGTT      250
CAGCTCTTAA AGCTCTTGAA GGCGACACTA AATTTGAAGA CATCATCATG      300
GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC      350
TGACAAACCA TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC      400
15 GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTACTGT TCGTGTC AAC      450
GACGAAATCG AAATCGTTGG TATCAAAGAA GAAACTAAAA AAGCTGTTGT      500
TACTGGTGTG GAAATGTTCC GTAAACAAC TGAACGAAGGT CTTGCAGGAG      550
ACAACGTAGG TATCCTTCTT CGTGGTGTTT AACGTGACGA AATCGAACGT      600
GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCCACACA CTAAATTCAA      650
20 AGGTGAAGTA TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT      700
TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACAAC TGACGTAACA      750
GGTTCAATCG AACTTCCAGC AGGTACAGAA ATGGTTATGC CTGGTGATAA      800
CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA GAACAAGGTA      850
CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT          894
25

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2) INFORMATION FOR SEQ ID NO: 1003

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 40 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003

```

AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTAC      50
45 TATTATCACA GCCTGATACA GGGGAGCAAG GATTAGAAAT CGCGGAAGCA      100
CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC      150
TCTTGTACCG AAAGCAGAGA TTGAAGGCGA CATGGGTGAC TCACACGTAG      200
GTTTACAAGC ACGTTTAATG TCACAAGCAC TTCGTAAGCT TTCAGGAGCA      250
ATCAACAAAT CAAAACAAT TGCAATCTTT ATTAACCAAA TTCGTGAAAA      300
50 AGTTGGGGTT ATGTTCCGAA ACCCAGAAAC AA          332

```

2) INFORMATION FOR SEQ ID NO: 1004

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004

```

10 ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAAC TC CGATCAATAC      50
   GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
   TTCAAATGGT AAAGTCATCG CCCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
   ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGA CTGGGGT      200
   TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
15 TTATGATTCC ACTGCAACTA TGCTTAATGA TATTCCTTAT AACTATCCGG      300
   GAACAAGCAG ACCTGTCTAC AACTGGGATA GAGCATATTT CGGTAATATT      350
   ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
   TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
   GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTC AAGTAATACA      500
20 ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550
   TTATGCTGCC TTTGCAAATG GTGGCACTTA CTATAAACCA ATGTATATCC      600
   ATAAAGTCGT CTTCA GTGAT GGAAGTAAAA AAGAGTTCTC TAATGTCGGA      650
   ACTCGTGCCA TGAAGGAAAC GACAGCCTAT ATGATGACCG ACATGATGAA      700
   AACAGTCTTG ACTTATGGAA CTGGGCGTGG AGCCTATCTT CCTTGGCTTC      750
25 CTCAAGCTGG TAAAACAGGA ACCTCTAACT ATACAGATGA GGAAGTTGAA      800
   AACCACATCA AGAACACTGG CTATGTAGCT CCAGATGAAA TGTTTGTTGG      850
   TTATACTCGT AAGTATTCTA TGGCTGTATG GACAGGTTAT TCGAATCGTT      900
   TAACTCCTAT CGTTGGAGAT GGTTCCTAG TTGCAGCTAA AGTTTATCGC      950
   TCAATGATAA CGTATCTATC AGAAGATACT CATCCAGAAG ACTGGACGAT      1000
30 GCCAGACGGA CTTTTCAGAA ACGGGGAATT TGTATTCAAA AATGGAGCTC      1050
   GCCCAATATG GACTGAACCC TCTACTCAAC AATCCTCAAC AGCTGAAAGT      1100
   TCAAGCTCAT CATCAGATAG TTCAACTTCA CAGTCTAGCT CAACCACTCC      1150
   AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT      1200
   CAAATACAAC CC                                     1212
35

```

2) INFORMATION FOR SEQ ID NO: 1005

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005

```

55 AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA ATACGTCTCT      50
   TACCCTGACG ATGATTGCA AGTCGCATCT ACGGTCGTAG ATGTTTCAAA      100
   TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA AGTAACGTTT      150
   CATTTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGACTG GGGTTCTGCT      200
   ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG GTGTTTATGA      250
   TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT CCGGGAACAA      300
60 GCACACCTGT CTACAACTGG GATAGAGCAT ATTCGGTAA TATTACTCTG      350

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	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
5	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACTGC	TTACATGATG	ACCGAAATGA	TGAAAACTGT	700
	CTTGGCATAc	GGAActGGTC	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
10	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCTGTAT	TAAAAATGGT	GCTCGTTCTA	1050
15	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	TC				1212

20

2) INFORMATION FOR SEQ ID NO: 1006

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
40	TTCAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
45	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCCAACG	GTGGAATTTA	CCACAAACCC	ATGTATATCA	600
50	ATAAGGTCGT	CTTCAGTGAC	GGTAGTAAAA	AAGAATTTTC	AGATGTAGGT	650
	ACACGAGCTA	TGAAAGAAAC	AACTGCTTAC	ATGATGACCG	AAATGATGAA	700
	AACTGTCTTG	GCATACGGAA	CTGGTCGTGG	AGCCTATCTC	CCATGGTTAG	750
	CGCAAGCTGG	TAAGACAGGT	ACTTCTAACT	ACACAGATGA	TGAAATTGAA	800
	AAACACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTT	850
55	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTGTC	TGAAGGAAGC	AATCCAGAGG	ATTGGAATAT	1000
	ACCAGAGGGG	CTCTACAGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1050
	GTTCTACGTG	GAGCTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1100
60	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAACT	CAACCACTCC	1150

AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
CAAATACAAC CCC 1213

5

2) INFORMATION FOR SEQ ID NO: 1007

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1218 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-04

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007

ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
CTCAAGCTGG	TAAACACTGG	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	850
TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
GCCAGACGGA	CTTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
CAAATACAAC	CCCTGATC				1218

50 2) INFORMATION FOR SEQ ID NO: 1008

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1223 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008

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5   GTAGACCAAG AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA      50
   ATACGTCTCT TACCCTGACG ATGATTGCA AGTCGCATCT ACGGTCGTAG      100
   ATGTTTCAAA TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA      150
   AGTAACGTTT CATTGTTGAC CAACCAAGCT GTGGAAACCA ATCGTGACTG      200
10  GGGTTCTGCT ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG      250
   GTGTTTATGA TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT      300
   CCGGGAACAA GCACACCTGT CTACAACCTGG GATAGAGCAT ATTTTCGGTAA      350
   TATTACTCTG CAATATGCTC TTCAACAATC ACGAAATGTC ACAGCCGTTG      400
   AGACTTTGAA TAAGGTCGGT CTAGATAGAG CTAAAACCTT CCTTAATGGT      450
15  CTTGGTATCG ACTATCCAAG CATGCATTAT GCAAACGCCA TTTCAAGTAA      500
   TACAACAGAA TCTAATAAAC AATACGGAGC AAGTAGTGAA AAAATGGCTG      550
   CTGCTTATGC TGCCTTTGCA AATGGTGGCA CTTACTATAA ACCAATGTAT      600
   ATCCATAAAG TCGTCTTCAG TGATGGGAAGT AAAAAAGAGT TCTCTAATGT      650
   CGGAACTCGT GCCATGAAGG AAACGACAGC CTATATGATG ACCGACATGA      700
20  TGAAAACAGT CTTGACTTAT GGAAGTGGGC GTGGAGCCTA TCTTCCTTGG      750
   CTTCTCAAG CTGGTAAAAC AGGAACCTCT AACTATACAG ATGAGGAAGT      800
   TGAAAACCAAC ATCAAGAACA CTGGCTATGT AGCTCCAGAT GAAATGTTTG      850
   TTGGTTATAC TCGTAAGTAT TCTATGGCTG TATGGACAGG TTATTCTGAAT      900
   CGTTTAACTC CTATCGTTGG AGATGGTTTC CTAGTTGCAG CTAAAGTTTA      950
25  TCGCTCAATG ATAACGTATC TATCAGAAGA TACTCATCCA GAAGACTGGA      1000
   CGATGCCAGA CGGACTTTTC AGAAACGGGG AATTTGTATT CAAAAATGGA      1050
   GCTCGCCCAA TATGGACTGA ACCCTCTACT CAACAATCCT CAACAGCTGA      1100
   AAGTTCAAGC TCATCATCAG ATAGTTCAAC TTCACAGTCT AGCTCAACCA      1150
   CTCCAAGCAC AAATAATAGT ACGACTACCA ATCCTAACAA TAATACGCAA      1200
30  CAATCAAATA CAACCCCTGA TCA                                     1223

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2) INFORMATION FOR SEQ ID NO: 1009

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1214 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009

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50  ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAACTC CGATCAATAC      50
   GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
   TTCAAATGGT AAAGTCATCG CCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
   ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGAAGGGGT      200
   TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
55  TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG      300
   GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CCGTAATATT      350
   ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
   TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
   GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTC AAGTAATACA      500
60  ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550

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	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
5	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
10	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCT				1214
15						

2) INFORMATION FOR SEQ ID NO: 1010

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010

	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	CTACAACTCC	GATCAATACG	50
35	TCTCTTACCC	TGACGATGAT	TTGCAAGTCG	CATCTACGGT	CGTAGATGTT	100
	TCAAATGGTA	AAGTCATCGC	ACAACCTGGT	GCTCGTCATC	AAGCAAGTAA	150
	TGTTTTCATT	GGTACCAACC	AGGCCGTAGA	AACCAATCGT	GACTGGGGAT	200
	CATCAATGAA	ACCAATCACT	GACTATGCTC	CCGCTTTAGA	ATATGGAGTC	250
	TATGACTCTA	CTGCTTCTAT	TGTACATGAT	GTCCCTTATA	ACTATCCTGG	300
40	CACTGATACT	CCACTCTACA	ACTGGGATCA	TGTCTACTTT	GGAAACATTA	350
	CAATCCAGTA	TGCTCTTCAA	CAATCACGAA	ATGTCACAGC	CGTTGAGACT	400
	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	ACCTTCCTTA	ATGGTCTTGG	450
	TATCGACTAT	CCAAGCATGC	ATTATGCAAA	CGCCATTTC	AGTAACACAA	500
	CTGAATCCAA	CAAAAAATAT	GGTGCAAGTA	GTGAAAAAAT	GGCTGCTGCC	550
45	TACGCTGCTT	TTGCTAATGG	TGGTATTTAT	CACAAACCAA	TGTATATCAA	600
	TAAAATCGTC	TTTAGTGATG	GTAGCGAAAA	AGAATTTTCT	GATGCTGGTA	650
	CACGAGCTAT	GAAAGAGACT	ACTGCCTATA	TGATGACTGA	AATGATGAAA	700
	ACTGTTTTAA	CTTACGGAAC	AGGACGTGGA	GCCTACCTAC	CATGGCTTCC	750
	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	800
50	AGTATATCAA	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	850
	TATACCCGTA	AATATGCAAT	GGCTGTTTGG	ACAGGATACT	CAAAATCGTCT	900
	AACTCCAATC	ATCGGAGATG	GTTTCCTTGT	TGCTGGTAAA	GTCTATCGTT	950
	CAATGATAAC	TTACCTTTCT	GAAGATGACC	AACCTGGAGA	TTGGACAATG	1000
	CCAGATGGCT	TGTATAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	1050
55	TTCTACGTGG	AGCTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	1100
	CAAGCTCATC	ATCAGATAGT	TCAACTTCAC	AGTCTAACTC	AACCACTCCA	1150
	AGCACAAATA	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	1200
	AAATACAACC	CCTGATCAAC	AAA			1223

60

2) INFORMATION FOR SEQ ID NO: 1011

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1207 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-08

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
20	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCTGGTAA	TATTACTCTG	350
25	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCA	AATGGTGGCA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
30	TCGTCTTCAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	CGGAACTCGT	650
	GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	TGAAAACAGT	700
	CTTGACTTAT	GGAACCTGGC	GTGGAGCCTA	TCTTCCTTGG	CTTCCTCAAG	750
	CTGGTAAAAC	AGGAACCTCT	AACTATACAG	ATGAGGAAGT	TGAAAACCAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
35	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGCCCAA	1050
	TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	AAGTTCAAGC	1100
40	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCC					1207

45 2) INFORMATION FOR SEQ ID NO: 1012

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1201 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 55 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-09
- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
5	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTGG	GATAGAGCAT	ATTTTCGGTAA	TATTACTCTG	350
	CAATATGCTC	TTCAACAATC	ACGAAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
10	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
15	GCTATGAAAG	AAACAACCTGC	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAATC	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTTCGAAT	CGTTTAACTC	900
20	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGTTCTA	1050
	CGTGGAACCT	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
25	AAATAATAGT	ACGACTACCG	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	C					1201

30 2) INFORMATION FOR SEQ ID NO: 1013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013

45	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATCTAC	AACTCCGATC	50
	AATACGTCTC	TTACCCTGAC	GATGATTTGC	AAGTCGCATC	TACGGTCGTA	100
	GATGTTTCAA	ATGGTAAAGT	CATCGCACAA	CTTGGTGCTC	GTCATCAAGC	150
	AAGTAATGTT	TCATTTCGGTA	CCAACCAGGC	CGTAGAAACC	AATCGTGACT	200
50	GGGGATCATC	AATGAAACCA	ATCACTGACT	ATGCTCCCGC	TTTAGAATAT	250
	GGAGTCTATG	ACTCTACTGC	TTCTATTGTA	CATGATGTCC	CTTATAACTA	300
	TCCTGGCACT	GATACTCCAC	TCTACAACCTG	GGATCATGTC	TACTTTGGAA	350
	ACATTACAAT	CCAGTATGCT	CTTCAACAAT	CACGAAATGT	CACAGCCGTT	400
	GAGACTTTGA	ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TCCTTAATGG	450
55	TCTTGGTATC	GACTATCCAA	GCATGCATTA	TGCAACGCC	ATTTCAAGTA	500
	ACACAACCTGA	ATCCAACAAA	AAATATGGTG	CAAGTAGTGA	AAAAATGGCT	550
	GCTGCCTACG	CTGCTTTTGC	TAATGGTGGT	ATTTATCACA	AACCAATGTA	600
	TATCAATAAA	ATCGTCTTTA	GTGATGGTAG	CGAAAAAGAA	TTTCTGATG	650
	CTGGTACACG	AGCTATGAAA	GAGACTACTG	CCTATATGAT	GACTGAAATG	700
60	ATGAAAACCTG	TTTTAACTTA	CGGAACAGGA	CGTGGAGCCT	ACCTACCATG	750

	GCTTCCACAA	GCAGGTAAGA	CAGGTACTTC	TAACATACT	GACGAAGAAA	800
	TTGAAAAGTA	TATCAAGAAC	ACTGGCTACG	TAGCTCCAGA	TGAAATGTTT	850
	GTGGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
5	ATCGCTCTAT	GATGACCTAC	CTGTCTGAAG	GAAGCAATCC	AGAGGATTGG	1000
	AATATACCAG	AGGGGCTCTA	CAGAAATGGA	GAATTCGTAT	TTAAAAATGG	1050
	TGCTCGTTCT	ACGTGGAGCT	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAGCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
10	ACAATCAAAT	ACAACCCCTG				1220

2) INFORMATION FOR SEQ ID NO: 1014

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014

30	CAAAAACATC	TGTGGGATAT	TTACAATACA	GACGAATACG	TTGCCTATCC	50
	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	TGTTGATGTT	TCTAACGGTA	100
	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	TGTTTCCTTC	150
	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	200
	ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	250
35	CTGCTACTAT	CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACC	300
	CCTGTTTATA	ACTGGGATAG	GGGCTACTTT	GGCAACATCA	CCTTGCAATA	350
	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	CGTGGAAACT	CTAAACAAGG	400
	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTCGG	AATCGACTAC	450
	CCAAGTATTC	ACTACTCAAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	500
40	CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	550
	TTGCAAATGG	TGGAACCTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	600
	TTTAGTGATG	GGAGTGAAAA	AGAGTTCTCT	AATGTCGGAA	CTCGTGCCAT	650
	GAAGGAAACG	ACAGCCTATA	TGATGACCGA	CATGATGAAA	ACTGTCTTAG	700
	TATACGGAAT	CGGACGTGGA	GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	750
45	AAAACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	AGTATATCAA	800
	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	TATACCCGCA	850
	AATATGCAAT	GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	900
	GTAGGCGATG	GCCTTACGGT	CGCTGCTAAA	GTTTACCGCT	CTATGATGAC	950
	CTACCTGTCT	GAAGGAAGCA	ATCCAGAGGA	TTGGAATATA	CCAGAGGGGC	1000
50	TCTACAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	TTCTACGTGG	1050
	AACTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	CAAGCTCATC	1100
	ATCAGATAGT	TCAACTTCAC	AGTCTAGCTC	AACCACTCCA	AGCACAAATA	1150
	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	AAATACAAC	1199

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2) INFORMATION FOR SEQ ID NO: 1015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 bases

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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
15	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTGG	GATAGAGCAT	ATTTTCGGTAA	TATTACTCTG	350
20	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
25	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTGC	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
30	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
35	TCATCATCAG	ATAGTTCAAC	TTACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	T				1211

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2) INFORMATION FOR SEQ ID NO: 1016

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1222 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016

	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCACAAC	TTGGTGCTCG	TCATCAAGCA	150
60	AGTAATGTTT	CATTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	200

	GGGATCATCA	ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	250
	GAGTCTATGA	CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	300
	CCTGGCACTG	ATACTCCACT	CTACAACCTG	GATCATGTCT	ACTTTGGAAA	350
	CATTACAATC	CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
5	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAAACCTT	CCTTAATGGT	450
	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAAACGCCA	TTTCAAGTAA	500
	CACAACTGAA	TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAAATGGCTG	550
	CTGCCTACGC	TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	600
	ATCAATAAAA	TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	650
10	TGGTACACGA	GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	700
	TGAAAACCTGT	TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	750
	CTTCCACAAG	CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	800
	TGAAAAGTAT	ATCAAGAACA	CTGGCTACGT	AGCTCCAGAT	GAAATGTTTG	850
	TGGGTTATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	900
15	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
	TCGCTCTATG	ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	1000
	ATATACCAGA	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	1050
	GCTCGTTCTA	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	1150
20	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
	CAATCAAATA	CAACCCCTGA	TC			1222

25 2) INFORMATION FOR SEQ ID NO: 1017

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017

40	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	50
	AATACGTTGC	CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	100
	GATGTTTCTA	ACGGTAAAGT	CATTGCCAG	CTAGGAGCAC	GCCATCAGTC	150
	AAGTAATGTT	TCCTTCGGAA	TTAACCAAGC	AGTAGAAACA	AACCGCGACT	200
45	GGGGATCAAC	TATGAAACCG	ATCACAGACT	ATGCTCCTGC	CTTGGAGTAC	250
	GGTGTCTACG	ATTCAACTGC	TACTATCGTT	CACGATGAGC	CCTATAACTA	300
	CCCTGGGACA	AATACCCCTG	TTTATAACTG	GGATAGGGGC	TACTTTGGCA	350
	ACATCACCTT	GCAATACGCC	CTGCAACAAT	CGCGAAACGT	CCCAGCCGTG	400
	GAAACTCTAA	ACAAGGTCGG	ACTCAACCGC	GCCAAGACTT	TCCTAAATGG	450
50	TCTCGGAATC	GACTACCCAA	GTATTCACTA	CTCAAAATGCC	ATTTCAAGTA	500
	ACACAACCGA	ATCAGACAAA	AAATATGGAG	CAAGTAGTGA	AAAGATGGCT	550
	GCTGCTTACG	CTGCCTTTGC	AAATGGTGGA	ACTTACTATA	AACCAATGTA	600
	TATCCATAAA	GTCGTCTTTA	GTGATGGGAG	TGAAAAAGAG	TTCTCTAATG	650
	TCGGAACCTG	TGCCATGAAA	GAAACAACCTG	CTTACATGAT	GACCGAAATG	700
55	ATGAAAACCTG	TCCTGGCATA	CGGAAGTGGT	CGTGGAGCCT	ATCTCCCATG	750
	GTTAGCGCAA	GCTGGTAAGA	CAGGTACTTC	TAACTACACA	GATGATGAAA	800
	TTGAAAAACA	CATCAAGAAC	ACTGGCTATG	TAGCTCCAGA	TGAAATGTTT	850
	GTTGGTTATA	CTCGTAAGTA	TTCTATGGCT	GATGGACAG	GTTATTGCAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
60	ATCGCTCAAT	GATAACGTAT	CTATCAAAAG	ATACTCATCC	AGAAGACTGG	1000

	ACGATGCCAG	ACGGACTTTT	CAGAAACGGG	GAATTTGTAT	TCAAAAATGG	1050
	AGCTCGTTCT	ACGTGGAAC	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAACCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
5	ACAATCAAAT	ACAACCCCTG	ATCAACAAA			1229

2) INFORMATION FOR SEQ ID NO: 1018

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018

25	ATGTAGACCA	AGAGGCTCAA	AAACGTCTGT	GGGATATCTA	CAACTCCGAT	50
	CAATACGTCT	CTTACCCTGA	CGATGATTG	CAAGTCGCAT	CTACGGTCGT	100
	AGATGTTTCA	AATGGTAAAG	TCATCGCCCA	ACTTGGAGCT	CGTCACCAAG	150
	CAAGTAACGT	TTCATTTGGT	ACCAACCAAG	CTGTGGAAAC	CAACCGTGAC	200
	TGGGGATCAA	GCATGAAACC	AATCACTGAT	TATGCCCCAG	CCTTAGAATA	250
30	TGGTGTATAT	GATTCCACTG	CAACTATGGT	TAATGATATT	CCTTATAACT	300
	ATCCGGGCAC	AAGCACACCT	GTCTACAAC	GGGATCGAGC	ATATTTTGGT	350
	AATATTAGCC	TGCAATATGC	CCTTCAACAA	TCTCGTAACG	TGCCTGCCGT	400
	TGAAACACTA	AACAAGGTG	GTTTAGATAG	AGCCAAAAC	TTCCTAAATG	450
	GTTTGGGAAT	TGACTATCCA	AGTATTCAT	ACTCAAATGC	TATTTCAAGT	500
35	AATACAAC	AATCTAGTAA	ACAGTACGGG	GCAAGCAGTG	AGAAAATGGC	550
	TGCGGCTTAC	GCTGCATTCG	CTAATGGCGG	TATTTACCAC	AAACCAATGT	600
	ACATCAATA	AGTTGTCTTT	AGTGATGGTA	GCGAAAAAGA	ATTTTCTGAT	650
	GCTGGTACAC	GAGCTATGAA	AGAGACTACT	GCCTATATGA	TGACTGAAAT	700
	GATGAAAAC	GTTTTAACTT	ACGGAACAGG	ACGTGGAGCC	TACCTACCAT	750
40	GGCTTCCACA	AGCAGGTAAG	ACAGGTACTT	CTAACTATAC	TGACGACGAA	800
	ATTGAAAAGT	ATATCAAGAA	CACTGGCTAC	GTAGCTCCAG	ATGAAATGTT	850
	TGTGGGTAT	ACTCGTAAAG	ATTCTATGGC	TGTATGGACT	GGATACTCAA	900
	ATCGTTTAAC	TCCAATCATT	GGAGATGGTT	TCCTAGTTGC	TGCCAAAGTT	950
	TATCGCTCAA	TGATATCGTA	TCTATCAGAA	GATGACCATC	CTGGAGATTG	1000
45	GACAATGCCT	GAGGGAGTAT	ACAGAAGTGG	AGAATTCGTA	TTTAAAAATG	1050
	GTGCTCGTTC	TACGTGGAGC	TCCCCTGCTC	CACAACAACC	CCCATCAACT	1100
	GAAAGTTCAA	GCTCATCATC	AGATAGTTCA	ACTTCACAGT	CTAGCTTAAC	1150
	CACTCCAAGC	ACAAATAATA	GTACGACTAC	CAATCCTAAC	AACAATACGC	1200
	AACAATCAAA	TACAACCCCT	GATCA			1225

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2) INFORMATION FOR SEQ ID NO: 1019

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019

	GCCTCTATTT	CAAAGGAGAT	GCCTGGCATT	AGTATTTCTA	CTTCTTGGGA	50
10	TCGAAAGGTT	TTGGAACTT	CCCTTTCTTC	TATAGTAGGG	AGTGTATCCA	100
	GTGAAAAGC	TGGTCTCCCA	GCGGAAGAAG	CAGAATCCTA	TCTTAAAAAA	150
	GGCTATTCTC	TAAATGACCG	TGTTGGAACC	TCCTATTGGG	AAAAGCAATA	200
	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
15	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCTTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
20	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTC	CAAGGTTTCA	CTCCAATTTA	650
	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTGGA	800
25	AACAGCTATG	GGAAAACCTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAAA	900
	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTTCGTG	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
30	AAGGGAGGAC	TGGGTGACTT	GATTCAGCAA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGCAC	CAAGGTTTTT	1150
	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTCA	1200
	AATGGTGCCT	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
35	CATCTGATAA	TCCCCAAATC	GCTGTGCGAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
	GTATCAAAAA	TACCATCCAA	TGAAC TAGAA	AGGAAATTA		1439

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2) INFORMATION FOR SEQ ID NO: 1020

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1441 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020

	GCCTCTATTT	CAAAGGAGAT	GCCTGGCATT	AGTATTTCTA	CTTCTTGGGA	50
	TCGAAAGGTT	TTGGAACTT	CCCTTTCTTC	TATAGTAGGG	AGTGTATCCA	100
	GTGAAAAGC	TGGTCTCCCA	GCGGAAGAAG	CAGAATCCTA	TCTTAAAAAA	150
60	GGCTATTCTC	TAAATGACCG	TGTTGGAACC	TCCTATTGGG	AAAAGCAATA	200

	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
5	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTTCA	CTCCAATTTA	650
10	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGGAAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
	AACAGCTATG	GGAAAACCTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAAA	900
15	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAAATAATG	1000
	GTGTTTCGTG	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
	AAGGGAGGAC	TGGGTGACTT	GATTCAGCAA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGCAC	CAAGGTTTTT	1150
20	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCTTTTTCA	1200
	AATGGTGCCT	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
	CATCTGATAA	TCCCCAAATC	GCTGTGCGAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
25	GTATCAAAAA	TACCATCCAA	TGAAC TAGAA	AGGAAATTAT	G	1441

2) INFORMATION FOR SEQ ID NO: 1021

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021

45	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
50	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCGG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
55	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
60	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800

	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
5	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
10	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATT	1396

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2) INFORMATION FOR SEQ ID NO: 1022

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022

	AAAGGAGATG	CCTGGCATT	GTATTTCTAC	TTCTTGGGAT	CGAAAGGTTT	50
	TGGAAACTTC	CCTTTCTTCT	ATAGTAGGGA	GTGTATCCAG	TGAAAAAGCT	100
	GGTCTCCCAG	CGGAAGAAGC	AGAATCCTAT	CTTAAAAAAG	GCTATTCTCT	150
35	AAATGACCGT	GTTGGAACCT	CCTATTTGGA	AAAGCAATAT	GAAGAGACCT	200
	TACAAGGAAA	ACGCTCGGTA	AAAGAAATCC	ATCTGGATAA	ATATGGCAAT	250
	ATGGAAGCG	TGGACACAAT	TGAGGAAGGT	AGTAAGGGAA	ACAATATCAA	300
	ACTGACCATT	GATTGGCCCT	TCCAAGATAG	CGTGGATGCT	TTGCTGAAAA	350
	GTTATTTCAA	TTCCGAGCTA	GGAAATGGTG	GAGCTAAATA	TTCTGAAGGT	400
40	GTCTATGCAG	TCGCCCTTAA	CCCAAAAACA	GGTGCTGTTT	TATCCATGTC	450
	AGGGATCAAA	CATGACCTGA	AAACGGGAGA	GTTGACTCCT	GATTCCTTGG	500
	GAACGGTAAC	CAATGTCTTT	GTCCCAGGTT	CGGTTGTCAA	GGCTGCGACC	550
	ATCAGCTCAG	GTTGGGAAAA	TGGTGTTTTA	TCAGGAAACC	AAACCTTAAC	600
	AGATCAGCCT	ATTGTTTTCC	AAGGTTTCAGC	TCCAATTTAT	TCTTGGTATA	650
45	AATTGGCATA	TGGATCTTTT	CCTATTACAG	CTGTGGAAGC	CTTGAGATAT	700
	TCATCCAATG	CTTACATGGT	TCAAACCGCT	CTTGGAATCA	TGGGCCAGAC	750
	CTATCAACCA	AATATGTTTG	TTGGAACCAG	CAATTTGGAA	ACAGCTATGG	800
	GAAAACCTCG	TGCGACCTTT	GGCGAATATG	GCTTGGGGGC	TGCGACCGGA	850
	ATTGACCTAC	CAGATGAATC	TACTGGATTT	GTTCCCAAAG	AGTATAGCTT	900
50	TGCTAATTAC	ATCACCAATT	CCTTTGGGCA	GTTTGATAAC	TATACGCCCA	950
	TGCAGTTGGC	TCAGTATGTA	GCAACTATTG	CAAATAATGG	TGTTCTGTGT	1000
	GCTCCTCGTA	TTGTTGAAGG	CATTTATGGT	AATAATGATA	AGGGAGGACT	1050
	GGGTGACTTG	ATTGAGCAAC	TGCAACCGAC	AGAGATGAAT	AAGGTCAATA	1100
	TATCCGACTC	CGATATGAGC	ATCTTGCACC	AAGGTTTTTA	TCAGGTTGCC	1150
55	CATGGTACTA	GTGGATTGAC	AACTGGACGT	GCCTTTTCAA	ATGGTGCCTT	1200
	GGTATCCATT	AGCGGAAAAA	CAGGTACAGC	CGAAAGCTAT	GTGGCAGATG	1250
	GTCAGCAAGC	AACCAATACC	AATGCGGTGG	CCTATGCCCC	ATCTGATAAT	1300
	CCCCAAATCG	CTGTCGCAGT	GGTCTTTCCT	CATAATACCA	ATCTAACAAA	1350
	TGGTGTAGGA	CCTTCCATTG	CGCGTGACAT	TATCAATCTG	TATCAAAAAT	1400
60	ACCATCCAAT	GAAC TAGAAA	GGAAATTA			1428

2) INFORMATION FOR SEQ ID NO: 1023

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023

20	TGCCTCTATT	TCAAAGGAGA	TGCCTGGCAT	TAGTATTTCT	ACTTCTTGGG	50
	ATCGAAAGGT	TTTGGAAACT	TCCCTTTCTT	CTATAGTAGG	GAGTGTATCC	100
	AGTGAAAAAG	CTGGTCTCCC	AGCGGAAGAA	GCAGAATCCT	ATCTTAAAAA	150
	AGGCTATTCT	CTAAATGACC	GTGTTGGAAC	CTCCTATTTG	GAAAAGCAAT	200
	ATGAAGAGAC	CTTACAAGGA	AAACGCTCGG	TAAAAGAAAT	CCATCTGGAT	250
25	AAATATGGCA	ATATGGAAAG	CGTGGACACA	ATTGAGGAAG	GTAAGAGGG	300
	AAACAATATC	AAACTGACCA	TTGATTTGGC	CTTCCAAGAT	AGCGTGGATG	350
	CTTTGCTGAA	AAGTTATTTT	AATTCCGAGC	TAGGAAATGG	TGGAGCTAAA	400
	TATTCTGAAG	GTGTCTATGC	AGTCGCCCTT	AACCCAAAAA	CAGGTGCTGT	450
	TTTATCCATG	TCAGGGATCA	AACATGACCT	GAAAACGGGA	GAGTTGACTC	500
30	CTGATTCCTT	GGGAACGGTA	ACCAATGTCT	TTGTCCCAGG	TTCGGTTGTC	550
	AAGGCTGCGA	CCATCAGCTC	AGGTTGGGAA	AATGGTGTTT	TATCAGGAAA	600
	CCAAACCTTA	ACAGATCAGC	CTATTGTTTT	CCAAGTTTCA	GCTCCAATTT	650
	ATTCTTGGA	TAAATTGGCA	TATGGATCTT	TTCCTATTAC	AGCTGTGGAA	700
	GCCTTGGAGT	ATTCATCCAA	TGCTTACATG	GTTCAAACCG	CTCTTGGAAT	750
35	CATGGGCCAG	ACCTATCAAC	CAAATATGTT	TGTTGGAACC	AGCAATTTGG	800
	AAACAGCTAT	GGGAAAACCT	CGTGCGACCT	TTGGCGAATA	TGGCTTGGGG	850
	GCTGCGACCG	GAATTGACCT	ACCAGATGAA	TCTACTGGAT	TTGTTCCCAA	900
	AGAGTATAGC	TTTGCTAATT	ACATACCAAA	TTCTTTTGGG	CAGTTTGATA	950
	ACTATACGCC	CATGCAGTTG	GCTCAGTATG	TAGCAACTAT	TGCAAATAAT	1000
40	GGTGTTCTGT	TGGCTCCTCG	TATTGTTGAA	GGCATTATAT	GTAATAATGA	1050
	TAAGGGAGGA	CTGGGTGACT	TGATTTCAGC	ACTGCAACCG	ACAGAGATGA	1100
	ATAAGGTCAA	TATATCCGAC	TCCGATATGA	GCATCTTGCA	CCAAGGTTTT	1150
	TATCAGGTTG	CCCATGGTAC	TAGTGGATTG	ACAACCTGGAC	GTGCCTTTTC	1200
	AAATGGTGCC	TTGGTATCCA	TTAGCGGAAA	AACAGGTACA	GCCGAAAGCT	1250
45	ATGTGGCAGA	TGGTCAGCAA	GCAACCAATA	CCAATGCGGT	GGCCTATGCC	1300
	CCATCTGATA	ATCCCCAAAT	CGCTGTCGCA	GTGGTCTTTC	CTCATAATAC	1350
	CAATCTAACA	AATGGTGTAG	GACCTTCCAT	TGCGCGTGAC	ATTATCAATC	1400
	TGTATCAAAA	ATACCATCCA	ATGAACTAGA	AAGGAAATTA	TG	1442

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2) INFORMATION FOR SEQ ID NO: 1024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

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571

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAAG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACTGACC	ATTGATTGCG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCTAA	400
	ATATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCTG	450
	TTTTATCCAT	GTGAGGGATC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCAG	GTTCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CAGGTGGGGA	AAATGGTGTT	TTATCAGGAA	600
20	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTT	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAACT	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCTA	900
	AAGAGTATAG	CTTTGCTAAT	TACATCACCA	ATTCCTTTGG	GCAGTTTGAT	950
	AACTATACAC	CCATGCAGTT	GGCTCAGTAT	GTAACAATA	TTGCAATAA	1000
	TGGTGTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTGAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGCATCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCCCATGGTA	CTAGTGGATT	GACAACTGGA	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACAGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGCA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AATGAAGTAG	AAAGGAAATT	ATGCT	1445

40 2) INFORMATION FOR SEQ ID NO: 1025

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025

55	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATCGAAAAG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTAG	GGAGTGTATC	100
	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAATCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTGGGAA	CCTCGTATTT	GGAAAAGCAA	200
60	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250

	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACCTGACC	ATTGATTG	CCTTCCAAGA	TAGCGTGGAT	350
	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCCAA	400
	GTATTCTGAG	GGTGTGTATG	CAGTCGCCCT	TAACCCCAAA	ACAGGTGCTG	450
5	TTTTGTCTAT	GTCAGGACTC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCTT	TGGGAACGGT	AACCAATGTC	TTTGTCCCAG	GTTTCGGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CTGGCTGGGA	AAATGGTGTT	TTATCAGGAA	600
	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTC	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
10	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGAA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAAC	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAG	CTTTGCTAAT	TACATCACCA	ATGCCTTTGG	GCAGTTTGAT	950
15	AACATACGC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTCCG	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGGAG	ACTGGGTGAC	TTGATTCAGC	AACTGCAACC	GACAGAGATG	1100
	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTATCTTGC	ACCAAGGATT	1150
	TTACCAAGTA	TCGCATGGAA	CTAGTCCCCT	TACGACAGGA	CGGGCGTTTT	1200
20	CAGATGGCGC	CACTGTTTCT	ATCAGTGGTA	AGACCGGTAC	AGGTGAAAGC	1250
	TATGTAGCTG	GTGGTCAAGA	AGCTAATAAT	ACCAATGCCG	TGGCCTATGC	1300
	TCCAACAGAA	AATCCTCAAA	TTGCAGTTGC	AGTAGTCTTT	CCTCATAATA	1350
	CCAATTTAAC	CAAAAATGTT	GGGCCAGCAA	TTGCTCGCGA	CATTATCAAT	1400
25	TTATATAACC	AACACCATCC	AATGAATTAG	AAAGGAAGCC	A	1441

2) INFORMATION FOR SEQ ID NO: 1026

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-08
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
45	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
50	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
55	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
60	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGCGCA	ATATGGCTTG	850

	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
5	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
10	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTA	1443

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2) INFORMATION FOR SEQ ID NO: 1027

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-09

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
35	AAAAGGCTAT	TCTCTAAATG	ATCGTGTAGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACTGA	CCATTGATTT	GGCTTTCCAA	GATAGCGTGG	350
	ATGCTTTACT	GAAAAGTTAT	TTCAATTCCG	AGCTAGAAAA	TGGTGGAGCC	400
40	AAGTATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGGA	TTAAACATGA	CTTGAAAACG	GGAGATTTAA	500
	CACCTGATTC	CTTGGAACA	GTAACCAATG	TCTTTGTCCC	GGGTTCTGTT	550
	GTCAAGGCGG	CGACCATCAG	CTCTGGTTGG	GAGAATGGAG	TCTTATCAGG	600
	AAATCAGACC	TTGACAGACC	AACCGATTGT	CTTCCAAGGT	TCAGCTCCGA	650
45	TTAATTCTTG	GTACACTCAG	GCTTACGATT	CATTTCGGAT	TACAGCGGTG	700
	GAAGCCTTGG	AGTATTCTTC	TAATGCCTAT	ATGGTCCAAA	CAGCTCTAGG	750
	TCTTATGGGG	CAGACCTACC	AACCCAATAT	GTTTGTGCGC	ACCAGCAATC	800
	TAGAGTCTGC	TATGGGGAAA	TTGCGTTCAA	CCTTTGGTGA	ATATGGCTTG	850
	GGCTCTGCGA	CTGGGATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
50	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTG	GAAGGCATTT	ATGGCAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
55	TTTTATCAGG	TTGCTCATGG	GACTAGCGGA	TTGACAACAG	GTCGTGCCTT	1200
	TTCCAATGGT	GCAGCTGTAT	CCATTAGTGG	AAAAACAGGT	ACCGCCGAAA	1250
	GTTATGTAGC	AGGTGGCCAA	GAAGCCAACA	ATACTAATGC	TGTAGCCTAT	1300
	GCACCATCAG	ATAATCCTCA	AATAGCTGTT	GCTGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GATATTATCA	1400
60	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAT	TTA	1443

2) INFORMATION FOR SEQ ID NO: 1028

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACCTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCTCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAG	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTGTT	GACTTCTTAC	CTGGAAAAAC	200
	AATACGAGGA	AACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAGTATTCTG	AAGGCGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGACTTGA	500
30	CGCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGGTCAGTA	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	TAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGTTG	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CCTCGTGCGA	CCTTTGCGCA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGC	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
45	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTT	GCAGTGGTCT	TTCTTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAACT	AGAAAGGAAA	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1029

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATAGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTTG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAAGCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTAGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAGAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGATAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACTGACC	ATTGATTGAG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTACTGA	AAAGTTATTT	CAATTCTGAG	CTAGAAAATG	GTGGAGCCAA	400
	GTATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCGG	450
	TTTTGTCTAT	GTCAGGGATT	AAACATGACT	TGAAAACGGG	AGAGTTGACG	500
	CCTGATTCTT	TGGGAACGGT	AACCAATGTC	TTTGTTCCAG	GTTTCGGTTGT	550
	CAAGGCGGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGAGTC	TTGTCAGGAA	600
20	ACCAGCCCTT	GACAGACCAG	TCCATTGTCT	TCCAAGGTTT	AGCTCCCATC	650
	AATTCTTGGT	ATACTCAGGC	TTACGGTTCA	TTCCCTATCA	CAGCGGTCCA	700
	AGCTCTGGAG	TATTCATCCA	ATGCTTATAT	GGTCCAAACA	GCCTTAGGTC	750
	TTATGGGGCA	GACCTATCAA	CCCAATATGT	TTGTCGGCAC	CAGCAATCTA	800
	GAGTCTGCTA	TGGGTAAATT	GCGTTCAACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACT	GGGATTGATC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAA	CTTTGCCAAT	TTCATTACCA	ATGCCTTTGG	GCAGTTTGAT	950
	AACTATACCC	CAATGCAATT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTTCG	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTCAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTGTCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCTCATGGGA	CTAGTGGGTT	GACAACTGGC	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACGGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGGA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AAT			1423

40 2) INFORMATION FOR SEQ ID NO: 1030

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1447 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030

55	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTGAG	AACCTCCTAT	TTGGAAAAGC	200
60	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250

	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
5	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
10	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
15	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAAT	1000
	AATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
20	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAAC	AGAAAGGAAA	TTATGCT	1447
25						

2) INFORMATION FOR SEQ ID NO: 1031

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1446 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-13
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACCTCTTG	50
45	GGATAGAAAG	GTTTTGGAAA	CTTCTCTTTC	TTCTATAGTA	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
	AAAGGCTATT	CTCTAAATGA	CCGTGTTGGG	ACTTCTTACC	TGGAAAAACA	200
	ATACGAGGAA	ACCTTACAAG	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
50	GGAAACAATA	TCAAACCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCTA	400
	AGTATTCTGA	AGGCGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGACTTGAC	500
	GCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGGTCAGTAG	550
55	TTAAGGCCGC	TACCATCAGC	TCAGGTGGG	AAAATGGTGT	TTTATCAGGA	600
	AACCAAACCT	TAACAGATCA	GCCTATTGTT	TTCCAAGGTT	CAGCTCCAAT	650
	TTATTCTTGG	TATAAATTGG	CATATGGATC	TTTTCTTATT	ACAGCTGTGG	700
	AAGCCTTGGA	GTATTCATCT	AATGCTTACA	TGGTTCAAAC	CGCTCTTGGA	750
	ATCATGGGCC	AGACCTATCA	ACCAAATATG	TTTGTGGA	CCAGCAATTT	800
60	GGAAACAGCT	ATGGGAAAAC	TTCGTGCGAC	CTTTGGCGAA	TATGGCTTGG	850

	GGGCTGCGAC	CGGAATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
	AAAGAGTATA	GCTTTGCTAA	TTACATTACT	AATGCCTTTG	GGCAGTTTGA	950
	TAACATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCC	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	1050
5	GATAAGGGAG	GACTGGGTGA	CTTGATTTCAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	1150
	TTTATCAGGT	TGCCCATGGT	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CCTTGGTATC	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	1250
	CTATGTGGCA	GATGGTCAGC	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	1300
10	CCCCATCTGA	TAATCCCCAA	ATCGCTGTTG	CAGTGGTCTT	TCCTCATAAT	1350
	ACCAATCTAA	CAAATGGTGT	AGGACCTTCC	ATTGCGCGTG	ACATTATCAA	1400
	TCTGTATCAA	AAATACCATC	CAATGAACTA	GAAAGGAAAT	TATGCT	1446

15

2) INFORMATION FOR SEQ ID NO: 1032

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	50
	GGATAGAAAG	GTTTTGGAAG	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
35	AAAGGCTATT	CTCTAAATGA	TCGTGTTGGA	ACCTCCTATT	TGGAAAAGCA	200
	ATATGAAGAG	ACCTTACAAG	GGAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGTGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
	GGAAACAATA	TCAAGCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCCA	400
40	AGTATTCTGA	GGGTGTGTAT	GCAGTCGCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGAGTTGAC	500
	TCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	550
	TCAAGGCTGC	GACCATCAGC	TCTGGCTGGG	AAAATGGAGT	CTTATCAGGA	600
	AACCAGACCT	TGACAGACCA	GTCCATTGTC	TTTCAAGGTT	CAGCTCCCAT	650
45	CAATTCTTGG	TATACTCAGG	CTTACGGTTC	ATTCCCTATC	ACAGCAGTCC	700
	AAGCTCTGGA	GTATTCATCT	AATGCCTATA	TGGTCCAAAC	AGCTTTAGGT	750
	CTTATGGGGC	AGACCTACCA	ACCTAATATG	TTTGTGCGCA	CCAGCAACCT	800
	AGAGTCTGCT	ATGGGGAAAT	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	850
	GTTCTGCGAC	CGGGATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
50	AAAGACTATA	GCTTTGCTAA	TTACATCACC	AATGCCTTTG	GGCAGTTTGA	950
	TAACATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCC	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGAAATAAT	1050
	GATAAGGGAG	GCCTAGGCGA	CTTGATTTCAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCTGATAT	GAGTATTTTG	CACCAAGGTT	1150
55	TTTATCAGGT	TGCTCATGGG	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CAGCGGTATC	CATTAGTGGA	AAAACAGGTA	CTGCCGAAAG	1250
	TTATGTTGAG	GGTGGTCAAG	AAGCTAACAA	TACTAATGCT	GTGGCCTATG	1300
	CACCATCAGA	TAATCCTCAA	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	1350
	ACCAACCTTA	CAAATGGTGT	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	1400
60	CCTCTATAAC	CAACATCATC	CAATGAATTA	GAAAGGAACA	TATGCT	1446

2) INFORMATION FOR SEQ ID NO: 1033

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCGTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAGCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCC	400
	AAGTATTCTG	AGGGTGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
30	CTCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTGCGTT	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAA	1000
40	GATGGTGTTT	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCTCATGG	GACTAGTGGA	TTGACAACTG	GACGTGCTTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGTGG	GAAAACAGGT	ACTGCCGAAA	1250
45	GTTATGTTGC	AGGTGGTCAA	GAAGCCAACA	ATACCAACGC	GGTGGCCTAT	1300
	GCCCCATCAG	ATAATCCTCA	AATCGCTGTT	GCCGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TTGGACCTTC	TATTGCACGC	GATATTATCA	1400
	ACCTCTATAA	CCAACACCAT	CCAATGAATT	AGAAAGGAAC	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1034

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-01

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034

	GGAAACTGCA	GAGGTCAAGG	GGATTGATTT	TACAACCAGT	CCCAATCGTA	50
	GTTATCCAAA	CGGACAATTT	GCTTCTAGTT	TTATCGGACT	AGCTCAGCTC	100
10	CATGAAAATG	AAGATGGCAG	CAAGAGCTTA	CTGGGAACCT	CTGGAATGGA	150
	GAGTTCCTTG	AACAGTATTC	TTGCAGGGAC	AGACGGTATT	ATTACCTATG	200
	AAAAAGACCG	TGTAGGAAAT	ATCGTACCAG	GTACAGAACT	GGTATCGCAA	250
	CAAACTGTGG	ATGGCAAGGA	TGTTTATACA	ACATTGTCTA	GTCCGCTACA	300
	ATCTTTTCATG	GAAACTCAGA	TGGATGCCTT	TCTAGAAAAA	GTAAAAGGTA	350
15	AGTATATGAC	CGCGACCTTG	GTCAGTGCAA	AGACCGGTGA	AATCCTCGCT	400
	ACCACCCAAC	GACCTACCTT	TAATGCAGAT	ACTAAAGAAG	GAATCACTGA	450
	GGACTTTGTT	TGGCGTGATA	TTCTTTATCA	AAGTAACTAT	GAACCAGGAT	500
	CAGCCATGAA	GGTTATGACG	TTAGCTTCTT	CTATTGATAA	TAATACCTTC	550
	CCAAGTGGAG	AATACTTCAA	TAGCAGTGAA	TTCAAAATAG	CGGATGCGAC	600
20	GACTCGAGAT	TGGGATGTTA	ATGATGGTTT	GACTACTGGT	GGGATGATGA	650
	CTTTCTTACA	AGGTTTCGCT	CACTCCAGTA	ATGTTGGAAT	GAGTCTACTT	700
	GAACAAAAAA	TGGGAGATGC	TACTTG GTTG	GATTATCTAA	AACGCTTTAA	750
	ATTTGGGGTT	CCAACCTCGCT	TTGGCTTGAC	AGATGAATAC	GCTGGTCAAC	800
	TTCCAGCTGA	TAATATTGTT	AGTATTGCTC	AAAGCTCATT	TGGGCAAGGA	850
25	ATTTCACTGA	CACAAACACA	AATGCTTCGT	GCCTTTACAG	CTATTGCTAA	900
	TGATGGAGTT	ATGCTGGAGC	CAAAATTTAT	AAGTGCTATT	TATGATACTA	950
	ACAATCAGTC	TGTACGTAAG	TCACAAAAAG	AAATAGTAGG	AAATCCTGTT	1000
	TCCAAAGAGG	CAGCAAGCAC	AACTCGAAAT	CACATGATCT	TAGTTGGGAC	1050
	GGACCCTCTA	TATGGAAC TA	TGTATAATCA	CTACACAGGA	AAGCCAATTA	1100
30	TAACAGTTCC	TGGACAAAAT	GTAGCAGTTA	AATCCGGTAC	GGCTCAAATC	1150
	GCTGATGAGA	AAAATGGAGG	ATACTTG GTT	GGTTCTACCA	ATTATATTTT	1200
	CTCAGTTGTG	ACTATGAATC	CTGCTGAAAA	TCCTGATTTT	ATCTTGATATG	1250
	TAACGGTTCA	ACAGCCTGAG	CATTATTCAG	GTATCCAGTT	GGGAGAATTT	1300
	GCCACCCCAA	TCTTGAGCG	GGCTTCAGCT	ATGAAAGAAT	CTCTCAATCT	1350
35	TCAATCTCCA	GCCAAAAATT	TAGATAAAGT	TACGACAGAA	TCTTCTTATG	1400
	CAATGCCTAG	CATCAAGGAT	ATTTCACCTG	GTGAGTTGGC	GGAAGCCTTA	1450
	CGCCGAAATA	TTGTGCAACC	AATCGTTGTA	GGTACTGGAA	CAAAGATTAA	1500
	AGAGACTTCT	GTAGAAGAAG	GGACCAATCT	TGCACCAAAC	CAACAAGTTC	1550
	TCCTTTTATC	GGATAAGGTA	GAAGAAATTC	CAGACATGTA	TGGCTGGAAA	1600
40	AAAGAGACTG	CCGAGACCTT	TGCTAAATGG	TTGGATATTG	AACTGGAATT	1650
	TGAAGGTTCA	GGTTCCGTTG				1670

45 2) INFORMATION FOR SEQ ID NO: 1035

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1683 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035

60

	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	CAACCAGTCC	50
	CAATCGTAGT	TACCCAAATG	GACAATTTGC	TTCTAGTTTT	ATCGGTCTAG	100
	CTCAGCTCCA	TGAAAATGAA	GATGGAAGCA	AGAGTTTGCT	GGGAACCTCT	150
	GGAATGGAGA	GTTCCCTGAA	CAGTATTCTT	GCAGGGACAG	ACGGCATTAT	200
5	TACCTATGAA	AAGGATCGTC	TGGGCAATAT	TGTACCCGGA	ACAGAACAAG	250
	TTTCCCAACA	AACGGTGGAT	GGCAAGGATG	TTTACACAAC	CATTTCCAGC	300
	CCCCTCCAGT	CCTTCATGGA	AACTCAGATG	GATGCCTTTC	TAGAAAAAGT	350
	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	ACCGGTGAAA	400
	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	TAAAGAAGGA	450
10	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	GTAACATATGA	500
	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	ATTGATAATA	550
	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	CAAAATAGCG	600
	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	CTACTGGTGG	650
	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	GTTGGAATGA	700
15	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGTTGGA	TTATCTAAAA	750
	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	ATGAATACGC	800
	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	AGCTCATTGG	850
	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	CTTTACAGCT	900
	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	GTGCTATTTA	950
20	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	ATAGTAGGAA	1000
	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	CATGATCTTA	1050
	GTTGGGACGG	ACCCTCTATA	TGGAACATG	TATAATCACT	ACACAGGAAA	1100
	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	TCCGGTACGG	1150
	CTCAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGTTTGG	TTCTACCAAT	1200
25	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	CTGATTTTAT	1250
	CTTGATATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	ATCCAGTTGG	1300
	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	GAAAGAATCT	1350
	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	CGACAGAATC	1400
	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	GAGTTGGCGG	1450
30	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	TACTGGAACA	1500
	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	CACCAAACCA	1550
	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTTCA	GACATGTATG	1600
	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	GGATATTGAA	1650
35	CTGGAATTTG	AAGGTTCAAG	TTCCGTTGTT	CAG		1683

2) INFORMATION FOR SEQ ID NO: 1036

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 50 (B) STRAIN: StrR-03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036

	TCAAAAAAGA	ATTGGAAACT	GCAGAGGTCA	AGGGGATTGA	TTTTACAACC	50
55	AGTCCCAATC	GTAGTTACCC	AAATGGACAA	TTTGCTTCTA	GTTTATACGG	100
	TCTAGCTCAG	CTCCATGAAA	ATGAAGATGG	AAGCAAGAGT	TTGCTGGGAA	150
	CCTCTGGAAT	GGAGAGTTCC	TTGAACAGTA	TTCTTGACAG	GACAGACGGC	200
	ATTATTACCT	ATGAAAAGGA	TCGTCTGGGC	AAATATTGTAC	CCGGAACAGA	250
	ACAAGTTTCC	CAACAAACGG	TGGATGGCAA	GGATGTTTAC	ACAACCATT	300
60	CCAGCCCCCT	CCAGTCCTTC	ATGGAACTC	AGATGGATGC	CTTTCTAGAA	350

	AAAGTAAAAG	GTAAGTATAT	GACCGCGACC	TTGGTCAGTG	CAAAGACCGG	400
	TGAAATCCTC	GCTACCACCC	AACGACCTAC	CTTTAATGCA	GATACTAAAG	450
	AAGGAATCAC	TGAGGACTTT	GTTTGGCGTG	ATATTCTTTA	TCAAAGTAAC	500
	TATGAACCAG	GATCAGCCAT	GAAGGTTATG	ACGTTAGCTT	CTTCTATTGA	550
5	TAATAATACC	TTCCCAAGTG	GAGAATACTT	CAATAGCAGT	GAATTCAAAA	600
	TAGCGGATGC	GACGACTCGA	GATTGGGATG	TTAATGATGG	TTTGACTACT	650
	GGTGGGATGA	TGACTTTCTT	ACAAGGTTTC	GCTCACTCCA	GTAATGTTGG	700
	AATGAGTCTA	CTTGAACAAA	AAATGGGAGA	TGCTACTTGG	TTGGATTATC	750
	TAAAACGCTT	TAAATTTGGG	GTTCCAATC	GCTTTGGCTT	GACAGATGAA	800
10	TACGCTGGTC	AACTTCCAGC	TGATAATATT	GTTAGTATTG	CTCAAAGCTC	850
	ATTTGGGCAA	GGAATTTTCA	TGACACAAAC	ACAAATGCTT	CGTGCCTTTA	900
	CAGCTATTGC	TAATGATGGA	GTTATGCTGG	AGCCAAAATT	TATAAGTGCT	950
	ATTTATGATA	CTAACAATCA	GTCTGTACGT	AAGTCACAAA	AAGAAATAGT	1000
	AGGAAATCCT	GTTTCCAAAG	AGGCAGCAAG	CACAACTCGA	AATCACATGA	1050
15	TCTTAGTTGG	GACGGACCCT	CTATATGGAA	CTATGTATAA	TCACTACACA	1100
	GGAAAGCCAA	TTATAACAGT	TCCTGGACAA	AATGTAGCAG	TTAAATCCGG	1150
	TACGGCTCAA	ATCGCTGATG	AGAAAAATGG	AGGATACTTG	GTTGGTTCTA	1200
	CCAATTATAT	TTTCTCAGTT	GTGACTATGA	ATCCTGCTGA	AAATCCTGAT	1250
	TTTATCTTGT	ATGTAACGGT	TCAACAGCCT	GAGCATTATT	CAGGTATCCA	1300
20	GTTGGGAGAA	TTTGCCACCC	CAATCTTGGA	GCGGGCTTCA	GCTATGAAAG	1350
	AATCTCTCAA	TCTTCAATCT	CCAGCCAAAA	ATTTAGATAA	AGTTACGACA	1400
	GAATCTTCTT	ATGCAATGCC	TAGCATCAAG	GATATTTTAC	CTGGTGAGTT	1450
	GGCGGAAGCC	TTACGCCGAA	ATATTGTGCA	ACCAATCGTT	GTAGGTACTG	1500
	GAACAAAGAT	TAAAGAGACT	TCTGTAGAAG	AAGGGACCAA	TCTTGCACCA	1550
25	AACCAACAAG	TTCTCCTTTT	ATCGGATAAG	GTAGAAGAAA	TTCCAGACAT	1600
	GTATGGCTGG	AAAAAAGAGA	CTGCCGAGAC	CTTTGCTAAA	TGGTTGGATA	1650
	TTGAAC TGGA	ATTTGAAGGT	TCAGGTTCCG	TT		1682

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2) INFORMATION FOR SEQ ID NO: 1037

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1681 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-04

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037

	CAAAAAAGAA	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAATCG	TAGTTATCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TACTGGGAAC	150
50	CTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGTA	200
	TTATTACCTA	TGAAAAAGAC	CGTGTAAGAA	ATATCGTACC	AGGTACAGAA	250
	CTGGTATCGC	AACAACTGT	GGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
55	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
60	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700

	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
5	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCTTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
10	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	AGCCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
15	AATCTTCTTA	TGCAATGCCT	CAGCTCAAGG	ATATTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	ACCAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
20	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	T		1681

2) INFORMATION FOR SEQ ID NO: 1038

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038

40	AAAAAAGAAT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTATCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	ACTGGGAACC	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGTAT	200
	TATTACCTAT	GAAAAAGACC	GTGTAGGAAA	TATCGTACCA	GGTACAGAAC	250
45	TGGTATCGCA	ACAAACTGTG	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
	AGTCCGCTAC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
50	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
55	AAACGCTTTA	AATTTGGGGT	TCCAACCTCGC	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCACTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
60	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050

	TTAGTTGGGA	CGGACCCTCT	ATATGGA	ACT	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	1250
5	TATCTTGAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCT	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	1500
10	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	1550
	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	1650
	GAACTGGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCA	1685

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2) INFORMATION FOR SEQ ID NO: 1039

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1679 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039

	AAAAGAATTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGACTA	100
35	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTAC	TGGGAACCTC	150
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
40	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
45	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGATGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
50	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
55	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAAATC	TGCTGAAAAT	CCTGATTTTA	1250
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTG	CCACCCAAT	CTTGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
60	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400

	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550
	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
5	GGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1650
	ACTGGAATTT	GAAGGTTTCAG	GTTCCGTTG			1679

10 2) INFORMATION FOR SEQ ID NO: 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double,
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040

25	TAAAAAGGAT	CTAAAAGACG	CTAGTGTTGA	AGGAATTGAC	TTCACAACCTA	50
	GCCCTAATAG	AAGCTATCCA	AATGGACAAT	TCGCTTCTAG	TTTTATTGGT	100
	TTGGCCCAAC	TCCATGAAAA	TGAGGATGGT	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGGATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
30	TTATTACCTA	TGAAAAAGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
35	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AAATGCAAGT	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGAAGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
40	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTCACT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
45	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
50	CAATTATATT	TTCTCAGCTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGAGG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTCAAC	TGGTGAGTTG	1450
55	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAAC TGGA	TTTGAAGGTT	CAGGTTCCGT	CGTTC		1685

2) INFORMATION FOR SEQ ID NO: 1041

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041

	GTCTATCAAA	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	50
20	CAACCAGTCC	CAATCGTAGT	TATCCAAACG	GACAATTTGC	TTCTAGTTTT	100
	ATCGGACTAG	CTCAGCTCCA	TGAAAATGAA	GATGGCAGCA	AGAGCTTACT	150
	GGGAACCTCT	GGAATGGAGA	GTTCTTGAA	CAGTATTCTT	GCAGGGACAG	200
	ACGGTATTAT	TACCTATGAA	AAAGACCGTG	TAGGAAATAT	CGTACCAGGT	250
	ACAGAACTGG	TATCGCAACA	AACTGTGGAT	GGCAAGGATG	TTTATACAAC	300
25	ATTGTCTAGT	CCGCTACAAT	CTTTCATGGA	AACTCAGATG	GATGCCTTTC	350
	TAGAAAAAGT	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	400
	ACCGGTGAAA	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	450
	TAAAGAAGGA	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	500
	GTA ACTATGA	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	550
30	ATTGATAATA	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	600
	CAAAATAGCG	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	650
	CTACTGGTGG	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	700
	GTTGGAATGA	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTG GTTGA	750
	TTATCTAAAA	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	800
35	ATGAATACGC	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	850
	AGCTCATTTG	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	900
	CTTTACAGCT	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	950
	GTGCTATTTA	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	1000
	ATAGTAGGAA	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	1050
40	CATGATCTTA	GTTGGGACGG	ACCCTCTATA	TGGA ACTATG	TATAATCACT	1100
	ACACAGGAAA	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	1150
	TCCGGTACGG	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	1200
	TTCTACCAAT	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	1250
	CTGATTTTAT	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	1300
45	ATCCAGTTGG	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	1350
	GAAAGAATCT	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	1400
	CGACAGAATC	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	1450
	GAGTTGGCGG	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	1500
	TACTGGAACA	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	1550
50	CACCAAACCA	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTTCA	1600
	GACATGTATG	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	1650
	GGATATTGAA	CTGGAATTTG	AAGGTT CAGG	TTCCGTTGTT	CAGAAG	1696

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2) INFORMATION FOR SEQ ID NO: 1042

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-09

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	GCTGGGAACC	150
15	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGCAT	200
	TATTACCTAT	GAAAAGGATC	GTCTGGGAAA	TATTGTCCCC	GGAACGGAAC	250
	AAGTTTCCCA	ACAAACTGTA	GATGGCAAGG	ATGTTTATAC	GACTATTTCC	300
	AGCACCCCTT	AGTCCTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
20	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
25	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTG GTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACTCGC	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCCTTTACA	900
30	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
35	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGAGAG	GGGCTTCAGC	TATGAAAGAC	1350
	TCTCTCAATC	TTCAAACAAC	AGCTAAAGCT	TTGGAGCAAG	TAAGTCAACA	1400
40	AAGTCCCTTA	CCTATGCCTA	GTGTCAAGGA	TATTTACACCT	GGTGATTTAG	1450
	CAGAAGAATT	CGGTCGCAAT	CTTGTAACAAC	CCATCGTTGT	GGGAACAGGA	1500
	ACGAAGATTA	AAAACAGTTC	TGCTGAAGAA	GGGAAGAATC	TTGCCCCGAA	1550
	TCAGCAAGTC	CTTATCTTAT	CTGATAAAGT	AGAGGAAGTT	CCAGATATGT	1600
	ATGGTTGGAC	AAAGGAGACT	GCTGAGACCC	TTGCTAAGTG	GCTCAATATA	1650
45	GAACCTGAAT	TTCAAGGTTC	GGGTTCTACT	GTGCAGAAG		1689

2) INFORMATION FOR SEQ ID NO: 1043

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1690 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

55

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043

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5  CAAAAAAGAG TTGGAAACTG CAGAGGTCAA GGGGATTGAT TTTACAACCA      50
   GTCCTAATCG TAGTTACCCA AACGGACAAT TTGCTTCTAG TTTTATCGGT      100
   CTAGCTCAAC TCCATGAAAA TGAAGATGGA AGCAAGAGTT TGCTGGGAAC      150
   TTCTGGAATG GAGAGTTCCT TGAACAGTAT TCTTGCAGGG AAAGACGGTA      200
   TTATTACTTA TGAAAAGGAT CGTCTGGGTA ATATTGTCCC TGGAAACAGAA      250
10  CAAGTTTCCC AACAAACGGT AGATGGCAAG GATGTTTATA CAACATTGTC      300
   TAGTCCGCTC CAATCTTTCA TGGAAACTCA GATGGATGCC TTTCTAGAAA      350
   AAGTAAAGG TAAGTATATG ACCGCGACCT TGGTCAGTGC AAAGACCGGT      400
   GAAATCCTCG CTACCACCCA ACGACCTACC TTTAATGCAG ATACTAAAGA      450
   AGGAATCACT GAGGACTTTG TTTGGCGTGA TATTCTTTAT CAAAGTAACT      500
15  ATGAACCAGG ATCAGCCATG AAGGTTATGA CGTTAGCTTC TTCTATTGAT      550
   AATAATACCT TCCCAAGTGG AGAATACTTC AATAGCAGTG AATTCAAAT      600
   AGCGGATGCG ACGACTCGAG ATTGGGATGT TAATGATGGT TTGACTACTG      650
   GTGGGATGAT GACTTTCTTA CAAGGTTTCG CTCACTCCAG TAATGTTGGA      700
   ATGAGTCTAC TTGAACAAAA AATGGGAGAT GCTACTTGGT TGGATTATCT      750
20  AAAACGCTTT AAATTTGGGG TTCCAACTCG CTTTGGCTTG ACAGATGAAT      800
   ACGCTGGTCA ACTTCCAGCT GATAATATTG TTAGTATTGC TCAAAGCTCA      850
   TTTGGGCAAG GAATTTCACT GACACAAACA CAAATGCTTC GTGCCTTTAC      900
   AGCTATTGCT AATGATGGAG TTATGCTGGA GCCAAAATTT ATAAGTGCTA      950
   TTTATGATAC TAACAATCAG TCTGTACGTA AGTCACAAAA AGAAATAGTA     1000
25  GGAAATCCTG TTTCCAAAGA GGCAGCAAGC ACAACTCGAA ATCACATGAT     1050
   CTTAGTTGGG ACGGACCCTC TATATGGAAC TATGTATAAT CACTACACAG     1100
   GAAAGCCAAT TATAACAGTT CCTGGACAAA ATGTAGCAGT TAAATCCGGT     1150
   ACGGCTCAAA TCGCTGATGA GAAAAATGGA GGATACTTGG TTGGTTCTAC     1200
   CAATTATATT TTCTCAGTTG TGAATATGAA TCCTGCTGAA AATCCTGATT     1250
30  TTATCTTGTA TGTAACGGTT CAACAGCCTG AGCATTATTC AGGTATCCAG     1300
   TTGGGAGAAT TTGCCACCCC AATCTTGAGG CGGGCTTCAG CTATGAAAGA     1350
   ATCTCTCAAT CTTCAATCTC CAGCCAAAAA TTTAGATAAA GTTACGACAG     1400
   AATCTTCTTA TGCAATGCCT AGCATCAAGG ATATTTACC TGGTGAGTTG     1450
   GCGGAAGCCT TACGCCGAAA TATTGTGCAA CCAATCGTTG TAGGTACTGG     1500
35  AACAAAGATT AAAGAGACTT CTGTAGAAGA AGGGACCAAT CTTGCACCAA     1550
   ACCAACAAGT TCTCCTTTTA TCGGATAAGG TAGAAGAAAT TCCAGACATG     1600
   TATGGCTGGA AAAAAGAGAC TGCCGAGACC TTTGCTAAAT GGTGGATAT      1650
   TGAAC TGAAAGGTT CAGGTTCCGT TGTTCAGAAG      1690

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2) INFORMATION FOR SEQ ID NO: 1044

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044

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AGTTGGAAAC TGCAGAGGTC AAGGGGATTG ATTTTACAAC CAGTCCTAAT      50
CGTAGTTACC CAAACGGACA ATTTGCTTCT AGTTTATCG GACTAGCTCA      100
60  GCTCCATGAA AATGAAGATG GCAGCAAGAG CTTGCTGGGA ACCTCTGGGA      150

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	TGGAGAGTTC	TTTAAATAGA	ATTCTTGCAG	GGACAGACGG	CATTATTACC	200
	TATGAAAAGG	ATCGTCTGGG	AAATATTGTC	CCCGGAACGG	AACAAGTTTC	250
	CCAACAAACG	GTAGATGGCA	AGGATGTTTA	TACGACTATT	TCCAGCACCC	300
	TTCAGTCCTT	CATGGAGACC	CAGATGAATG	CCTTTCAAGA	AAAAGTAAAA	350
5	GGCAAGTATA	TGACGGCTAC	CTTGGTCAGT	GCTAAAACAG	GGGAAATTCT	400
	TGCAACAACG	CAACGGCCGA	CCTTCGATGC	TGATACTAAG	GAAGGACTTA	450
	CCAAGGACTT	TGTTTGGCGT	GATATCCTCT	ATCAAAGTAA	CTATGAGCCA	500
	GGGTCAACCA	TGAAGGTCAT	GACGCTTGCT	GCTGCTATTG	ATAATAACAC	550
	TTTCCCAGGA	GGAGAAGTTT	TCAATAGTAG	TGAATTAAAA	ATAGCGGATG	600
10	CGACAATTCG	AGATTGGGAT	GTTAATGATG	GTTTGACGAC	TGGTGGGATG	650
	ATGACTTTCT	TACAAGGTTT	CGCTCACTCC	AGTAATGTTG	GAATGAGTCT	700
	ACTTGAACAA	AAAATGGGAG	ATGCTACTTG	GTTGGATTAT	CTAAACCGCT	750
	TTAAGTTTGG	GGTGCCGACG	CGTTTTGGTC	TGACTGATGA	GTATTCAGGT	800
	CAATTGCCTG	CAGATAATAT	TGTTAATATT	GCCATGAGTG	CATTTGGTCA	850
15	GGGGATTTC	GTGACCCAGA	CGCAAATGAT	TCGTGCCTTT	ACAGCTATTG	900
	CTAATGATGG	TGTTATGCTG	GAGCCTAAAT	TTATTAGTGC	CATTTATGAT	950
	CCAAATGATC	AAACTGCTCG	GAAATCTCAA	AAAGAAATTG	TGGGAAATCC	1000
	TGTTTCTAAA	GATGCAGCTA	GTCTAACTCG	GACTAACATG	ATTTTGGTAG	1050
	GGACGGATCC	GGTTTATGGA	ACCATGTATA	ACCACAGCAC	AGGTAAGCCA	1100
20	ACTGTAACTG	TTCCTGGGCA	AAATGTAGCC	CTCAAGTCTG	GTACGGCTCA	1150
	GATTGCTGAC	GAGAAAAATG	GTGGTTATCT	AGTCGGGTTA	ACCAACTATA	1200
	TTTTCTCGGC	TGTATCGATG	AATCCGGCTG	AAAATCCTGA	TTTTATCTTG	1250
	TATGTAAACG	TACAGCAACC	TGAACATTAT	TCAGGTATCC	AGTTGGGAGA	1300
	ATTTGCCACC	CCAATCTTGG	AGCGGGCTTC	AGCTATGAAA	GAATCTCTCA	1350
25	ATCTTCAATC	TCCAGCCAAG	AATTTAGATA	AAGTTACGAC	AGAATCTTCT	1400
	TATGCAATGC	CTAGCATCAA	GGATATTTCA	CCTGGTGAGT	TGGCGGAAGC	1450
	CTTACGCCGA	AATATTGTGC	AACCAATCGT	TGTAGGTACT	GGAACAAAGA	1500
	TTAAAGAGAC	TTCTGTAGAA	GAAGGGACCA	ATCTTGCACC	AAACCAACAA	1550
	GTTCTCCTTT	TATCGGATAA	GGTAGAAGAA	ATTCCAGACA	TGTATGGCTG	1600
30	GAAAAAAGAG	ACTGCTGAAA	CCTTTGCTAA	ATGGTTGGAT	ATTGAGCTGG	1650
	AATTTGAAGG	GTCAGGTT				1668

35 2) INFORMATION FOR SEQ ID NO: 1045

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045

50	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	GTCCCAATCG	50
	TAGTTACCCA	AATGGACAAT	TTGCTTCTAG	TTTTATCGGT	CTAGCTCAGC	100
	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	CTCTGGAATG	150
	GAGAGTTTCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	200
55	TGAAAAGGAT	CGTCTGGGCA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	250
	AACAAACGGT	GGATGGCAAG	GATGTTTACA	CAACCATTTC	CAGCCCCCTC	300
	CAGTCCTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	AAGTAAAAGG	350
	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	GAAATCCTCG	400
	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	AGGAATCACT	450
60	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	ATGAACCAGG	500

	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	AATAATACCT	550
	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	AGCGGATGCG	600
	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	GTGGGATGAT	650
	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	ATGAGTCTAC	700
5	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	AAAACGCTTT	750
	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	ACGCTGGTCA	800
	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	TTTGGGCAAG	850
	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	AGCTATTGCT	900
	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	TTTATGATAC	950
10	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	GGAAATCCTG	1000
	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCACATGAT	CTTAGTTGGG	1050
	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	GAAAGCCAAT	1100
	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	GCGGCTCAAA	1150
	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTCTTAC	CAATTATATT	1200
15	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	TTATCTTGTA	1250
	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	TTGGGAGAAT	1300
	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	ATCTCTCAAT	1350
	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	AATCTTCTTA	1400
	TGCAATGCCT	AGCATCAAGG	ATATTTCAAC	TGGTGAGTTG	GCGGAAGCCT	1450
20	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	AACAAAGATT	1500
	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCAACCA	ACCAACAAGT	1550
	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	TATGGCTGGA	1600
	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	TGAACTGGAA	1650
	TTTGAAGGTT	CAGGTTCCGT	TGTTCAGAAG			1680
25						

2) INFORMATION FOR SEQ ID NO: 1046

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1689 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
45	TCCTAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGTC	100
	TAGCTCAACT	CCATGAAAAT	GAAGATGGAA	GCAAGAGTTT	GCTGGGAACT	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAAGGA	AAGACGGTAT	200
	TATTACTTAT	GAAAAGGATC	GTCTGGGTAA	TATTGTCCCT	GGAACAGAAC	250
	AAGTTTCCCA	ACAAACGGTA	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
50	AGTCCGCTCC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
55	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGCTTGA	CAGATGAATA	800
60	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850

	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
5	TTAGTTGGGA	CGGACCCTCT	ATATGGAAT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
10	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
15	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAAT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAACTGGAAT	TTGAAGGTTT	AGGTTCCGTT	GTTTACAAG		1689

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2) INFORMATION FOR SEQ ID NO: 1047

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1690 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

	CAAAAAGAA	TTGGAAGCTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAACCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TGCTGGGAAC	150
40	TTCTTGAATG	GAGAGTTTCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	200
	TTATTACCTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTACA	CAACCATTTC	300
	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	GATGGATGCT	TTTCAAGAGA	350
	AGGTAAAAGG	AAAGTACACG	ACAGCGACTT	TGGTCAGTGC	TAAAACAGGG	400
45	GAAATTCTGG	CAACAACGCA	ACGACCGACC	TTTGATGCAG	ATACAAAAGA	450
	AGGCATTACA	GAGGACTTTG	TTTGGCGTGA	TATCCTTTAC	CAAAGTAACT	500
	ATGAGCCAGG	TTCCCCTATG	AAAGTGATGA	TGTTGGCTGC	TGCTATTGAT	550
	AATAATACCT	TTCCAGGGGG	AGAAGTCTTC	AATAGTAGTG	AGTTAAAAAT	600
	TGCAGATGTC	ACGATTCGAG	ATTGGGACGT	CAATGAAGGA	TTGACTGGTG	650
50	GCAGAATGAT	GACCTTTTCT	CAAGGGTTCG	CTCACTCAAG	TAACGTTGGG	700
	ATGACGCTTC	TTGAGCAAAA	GATGGGAGAT	GCTACATGGC	TTGATTATCT	750
	AAATCGCTTT	AAATTTGGTG	TTCCGACTCG	TTTTGGCTTG	ACGGATGAAT	800
	ATGCAGGCCA	ACTTCCAGCT	GACAATATCG	TAAATATTGC	TCAGAGTTCA	850
	TTTGGACAAG	GGATTTTCAGC	GACCCAGACG	CAAATGATTC	GTGCCTTCAC	900
55	GGCTATTGCC	AACGATGGAG	TCATGTTAGA	ACCTAAATTT	ATCAGTGCCA	950
	TTTATGATCC	AAATGATCAA	ACTGCTCGGA	AATCACAAAA	AGAAGTTGTG	1000
	GGAAATCCTG	TGTCTAAAGA	TGCAGCGAGC	TTGACGCGAA	CGCATATGGT	1050
	TTTAGTCGGT	ACCGATCCAG	TATATGGAAC	TATGTATAAT	CATAAGACAG	1100
	GGAAACCAAC	TGTAACGTGT	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	1150
60	ACGGCTCAGA	TTGCCGATGA	GAAAAATGGA	GGTTACTTAG	TTGGTACGAC	1200

	CAATTACATT	TTTTCGGCTG	TATCGATGAA	CCCTGCTGAA	AATCCTGATT	1250
	TTATTCTCTA	TGTGACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATTTCAG	1300
	TTGGGGGAAT	TTGCCAATCC	TATCTTGGA	AGGGCAGTGG	CTATGAAAGA	1350
	TTCCCTTAAC	CTCCAATCTA	CCGCTAAAAC	GTTAAATCAG	GTAACCAATC	1400
5	AAAGCGCTTA	TGCCATGCCT	AGCATCAAGG	ACATTTTACC	TGGCGATTG	1450
	GCGGAAGCCT	TACGTCGCAA	TATTGTGCAA	CCAATCGTTG	TAGGAACAGG	1500
	AACAAAAATT	AAAGAATCAT	CTGTAGAAGA	AGGGACGGAT	CTTGACACCTA	1550
	ACCAGCAAGT	TCTTCTCTTA	TCTGATAAAG	CAGAGGAAGT	TCCAGATATG	1600
	TATGGTTGGA	CAAAAGAGAC	TGCTGAGACC	TTTGCTAAGT	GGCTCAATAT	1650
10	AGAACTTGAA	TTTGAAGGTT	CGGGCTCTAC	TGTGCAGAAG		1690

2) INFORMATION FOR SEQ ID NO: 1048

15

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1682 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

30	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTACCCAAAC	GGACAATTTG	CTTCTAGCTT	TATTGGCTTA	100
	GCCCAACTTC	ATGAAAATGA	GGATGGTAGT	AAGAGTTTGT	TAGGGACTTC	150
	TGGTTTGGAG	AGTTCTTTAA	ATACCATTCT	TGCTGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
35	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
40	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAAGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
45	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
50	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
55	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
60	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550

AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
GGCTGGAAAA	AAGAGACTGC	TGAAACCTTT	GCTAAATGGT	TGGATATTGA	1650
GTTGGAATTT	GAAGGTTTCA	GTTCCGTCGT	TC		1682

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2) INFORMATION FOR SEQ ID NO: 1049

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1241 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R690
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

GCAGCGTTGC	GTGATACCGT	TGAAAAAACC	ATTAAAAACT	GTTTGGATTT	50
TGAAAGGAGA	CAGGAGCATG	AATAGAATAA	AAGTTGCAAT	ACTGTTTGGG	100
GGTTGCTCAG	AGGAGCATGA	CGTATCGGTA	AAATCTGCAA	TAGAGATAGC	150
CGCTAACATT	AATAAAGAAA	AATACGAGCC	GTTATACATT	GGAATTACGA	200
AATCTGGTGT	ATGGAAAATG	TGCGAAAAAC	CTTGCGCGGA	ATGGGAAAAC	250
GACAATTGCT	ATTGAGCTGT	ACTCTCGCCG	GATAAAAAAA	TGCACGGATT	300
ACTTGTTAAA	AAGAACCATG	AATATGAAAT	CAACCATGTT	GATGTAGCAT	350
TTTCAGCTTT	GCATGGCAAG	TCAGGTGAAG	ATGGATCCAT	ACAAGGTCTG	400
TTTGAATTGT	CCGGTATCCC	TTTTGTAGGC	TGCGATATTC	AAAGCTCAGC	450
AATTTGTATG	GACAAATCGT	TGACATACAT	CGTTGCGAAA	AATGCTGGGA	500
TAGCTACTCC	CGCCTTTTGG	GTTATTAATA	AAGATGATAG	GCCGGTGGCA	550
GCTACGTTTA	CCTATCCTGT	TTTTGTTAAG	CCGGCGCGTT	CAGGCTCATC	600
CTTCGGTGTG	AAAAAAGTCA	ATAGCGCGGA	CGAATTGGAC	TACGCAATTG	650
AATCGGCAAG	ACAATATGAC	AGCAAAATCT	TAATTGAGCA	GGCTGTTTCG	700
GGCTGTGAGG	TCGGTTGTGC	GGTATTGGGA	AACAGTGCCG	CGTTAGCTGT	750
TGGCGAGGTG	GACCAAATCA	GGCTGCAGTA	CGGAATCTTT	CGTATTCATC	800
AGGAAGTCGA	GCCGGAAAAA	GGCTCTGAAA	ACGCAGTTAT	AACCGTTCCC	850
GCAGACCTTT	CAGCAGAGGA	GCGAGGACGG	ATACAGGAAA	CGGCAAAAAA	900
AATATATAAA	GCGCTCGGCT	GTAGAGGTCT	AGCCCGTGTG	GATATGTTTT	950
TACAAGATAA	CGGCCGCATT	GTAAGTGAACG	AAGTCAATAC	TCTGCCCGGT	1000
TTCACGTCAT	ACAGTCGTTA	TCCCCGTATG	ATGGCCGCTG	CAGGTATTGC	1050
ACTTCCCGAA	CTGATTGACC	GCTTGATCGT	ATTAGCGTTA	AAGGGGTGAT	1100
AAGCATGGAA	ATAGGATTTA	CTTTTTTAGA	TGAAATAGTA	CACGGTGTTC	1150
GTTGGGACGC	TAAATATGCC	ACTTGGGATA	ATTCACCGG	AAAACCGGTT	1200
GACGGTTATG	AAGTAAATCG	CATTGTAGGG	ACATACGAAT	T	1241

50

2) INFORMATION FOR SEQ ID NO: 1050

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

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TCACACCGCA TACGGCCTAT TATACCGAGC AAGCGTTGCG TGATACCGTT      50
GAAAAAACCA TTAAAAACTG TTTGGATTTT GAAAGGAGAC AGGAGCATGA      100
ATAGAATAAAA AGTTGCAATA CTGTTTGGGG GTTGCTCAGA GGAGCATGAC      150
10 GTATCGGTAA AATCTGCAAT AGAGATAGCC GCTAACATTA ATAAAGAAAA      200
ATACGAGCCG TTATACATTG GAATTACGAA ATCTGGTGTA TGGAAAATGT      250
GCGAAAAACC TTGCGCGGAA TGGGAAAACG ACAATTGCTA TTCAGCTGTA      300
CTCTCGCCGG ATAAAAAAT GCACGGATTA CTTGTAAAA AGAACCATGA      350
ATATGAAATC AACCATGTTG ATGTAGCATT TTCAGCTTTG CATGGCAAGT      400
15 CAGGTGAAGA TGGATCCATA CAAGGTCTGT TTGAATTGTC CGGTATCCCT      450
TTTGTAGGCT GCGATATTCA AAGCTCAGCA ATTTGTATGG ACAAATCGTT      500
GACATACATC GTTGCGAAAA ATGCTGGGAT AGCTACTCCC GCCTTTTGGG      550
TTATTAATAA AGATGATAGG CCGGTGGCAG CTACGTTTAC CTATCCTGTT      600
TTTGTTAAGC CGGCGCGTTC AGGCTCATCC TTCGGTGTGA AAAAAGTCAA      650
20 TAGCGCGGAC GAATTGGACT ACGCAATTGA ATCGGCAAGA CAATATGACA      700
GCAAAATCTT AATTGAGCAG GCTGTTTCGG GCTGTGAGGT CGGTTGTGCG      750
GTATTGGGAA ACAGTGCCGC GTTAGCTGTT GGCGAGGTGG ACCAAATCAG      800
GCTGCAGTAC GGAATCTTTC GTATTCATCA GGAAGTCGAG CCGGAAAAAG      850
GCTCTGAAAA CGCAGTTATA ACCGTTCCCG CAGACCTTTC AGCAGAGGAG      900
25 CGAGGACGGA TACAGGAAAC GGCAAAAAAA ATATATAAAG CGCTCGGCTG      950
TAGAGGTCTA GCCCGTGTGG ATATGTTTTT ACAAGATAAC GGCCGCATTG      1000
TACTGAACGA AGTCAATACT CTGCCCAGTT TCACGTCATA CAGTCGTTAT      1050
CCCCGTATGA TGGCCGCTGC AGGTATTGCA CTTCCCGAAC TGATTGACCG      1100
CTTGATCGTA TTAGCGTTAA AGGGGTGATA AGCATGGAAA TAGGATTTAC      1150
30 TTTTTTAGAT GAAATAGTAC ACGGTGTTTC TTGGGACGCT AAATATGCCA      1200
CTTGGGATAA TTTCACCGGA AAACCGGTTG ACGGTTATGA AGTAAATCG      1249

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35 2) INFORMATION FOR SEQ ID NO: 1051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R481

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

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TATACCGAGC AAGCGTTGCG TGATACCGTT GAAAAAACCA TTAAAAACTG      50
TTTGGATTTT GAAAGGAGAC AGGAGCATGA ATAGAATAAA AGTTGCAATA      100
CTGTTTGGGG GTTGCTCAGA GGAGCATGAC GTATCGGTAA AATCTGCAAT      150
AGAGATAGCC GCTAACATTA ATAAAGAAAA ATACGAGCCG TTATACATTG      200
55 GAATTACGAA ATCTGGTGTA TGGAAAATGT GCGAAAAACC TTGCGCGGAA      250
TGGGAAAACG ACAATTGCTA TTCAGCTGTA CTCTCGCCGG ATAAAAAAT      300
GCACGGATTA CTTGTAAAA AGAACCATGA ATATGAAATC AACCATGTTG      350
ATGTAGCATT TTCAGCTTTG CATGGCAAGT CAGGTGAAGA TGGATCCATA      400
CAAGGTCTGT TTGAATTGTC CGGTATCCCT TTTGTAGGCT GCGATATTCA      450
60 AAGCTCAGCA ATTTGTATGG ACAAATCGTT GACATACATC GTTGCGAAAA      500

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	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	550
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	600
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	650
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	700
5	GCTGTTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	750
	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	800
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	850
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	900
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	950
10	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1000
	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1050
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1100
	AGGGGTGATA	AGCATGGAAA	TAGGATTAC	TTTTTTAGAT	GAAATAGTAC	1150
	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1200
15	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAATT	1250
	GGCTTGAATC	GCTTTTTGAA	GG			1272

20 2) INFORMATION FOR SEQ ID NO: 1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

35	TCCCCCGGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGAATTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
40	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
45	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
50	GCAAAATCTT	AATTGAGCAG	GCTGTTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
55	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	1200
60	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTA		1237

2) INFORMATION FOR SEQ ID NO: 1053

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1263 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

20	CATACGGCCT ATTATACCGA GCAAGCGTTG CGTGATACCG TTGAAAAAAC	50
	CATTAAAAAC TGTTTGGATT TTGAAAGGAG ACAGGAGCAT GAATAGAATA	100
	AAAGTTGCAA TACTGTTTGG GGGTTGCTCA GAGGAGCATG ACGTATCGGT	150
	AAAATCTGCA ATAGAGATAG CCGCTAACAT TAATAAAGAA AAATACGAGC	200
	CGTTATACAT TGGAATTACG AAATCTGGTG TATGGAAAAT GTGCGAAAAA	250
25	CCTTGCGCGG AATGGGAAAA CGACAATTGC TATTCAGCTG TACTCTCGCC	300
	GGATAAAAAA ATGCACGGAT TACTTGTTAA AAAGAACCAT GAATATGAAA	350
	TCAACCATGT TGATGTAGCA TTTTCAGCTT TGCATGGCAA GTCAGGTGAA	400
	GATGGATCCA TACAAGGTCT GTTTGAATTG TCCGGTATCC CTTTTGTAGG	450
	CTGCGATATT CAAAGCTCAG CAATTTGTAT GGACAAATCG TTGACATACA	500
30	TCGTTGCGAA AAATGCTGGG ATAGCTACTC CCGCCTTTTG GGTTATTAAT	550
	AAAGATGATA GGCCGGTGGC AGCTACGTTT ACCTATCCTG TTTTGTGTTAA	600
	GCCGGCGCGT TCAGGCTCAT CCTTCGGTGT GAAAAAAGTC AATAGCGCGG	650
	ACGAATTGGA CTACGCAATT GAATCGGCAA GACAATATGA CAGCAAAATC	700
	TTAATTGAGC AGGCTGTTTC GGGCTGTGAG GTCGGTTGTG CGGTATTGGG	750
35	AAACAGTGCC GCGTTAGCTG TTGGCGAGGT GGACCAAATC AGGCTGCAGT	800
	ACGGAATCTT TCGTATTCAT CAGGAAGTCG AGCCGGAAAA AGGCTCTGAA	850
	AACGCAGTTA TAACCGTTCC CGCAGACCTT TCAGCAGAGG AGCGAGGACG	900
	GATACAGGAA ACGGCAAAAA AAATATATAA AGCGCTCGGC TGTAGAGGTC	950
	TAGCCCCGTG GGATATGTTT TTACAAGATA ACGGCCGCAT TGTACTGAAC	1000
40	GAAGTCAATA CTCTGCCCCG TTTACGTCAT TACAGTCGTT ATCCCCGTAT	1050
	GATGGCCGCT GCAGGTATTG CACTTCCCGA ACTGATTGAC CGCTTGATCG	1100
	TATTAGCGTT AAAGGGGTGA TAAGCATGGA AATAGGATTT ACTTTTTTAG	1150
	ATGAAATAGT ACACGGTGTT CGTTGGGACG CTAAATATGC CACTTGGGAT	1200
	AATTTACCGG GAAAACCGGT TGACGGGTAT GAAAGTAAAT CGCATTGTAG	1250
45	GGACATTCTGA ATT	1263

2) INFORMATION FOR SEQ ID NO: 1054

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1232 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

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5  CGGCCTATTA TNCCGAGCAA GCGTTGCGTG ATACCGTTGA AAAAACCATT      50
   AAAAACTGTT TGGATTTTGA AAGGAGACAG GAGCATGAAT AGAATAAAAG      100
   TTGCAATACT GTTTGGGGGT TGCTCAGAGG AGCATGACGT ATCGGTAAAA      150
   TCTGCAATAG AGATAGCCGC TAACATTAAT AAAGAAAAAT ACGAGCCGTT      200
   ATACATTGGA ATTACGAAAT CTGGTGTATG GAAAATGTGC GAAAAACCTT      250
10  GCGCGGAATG GGAAAACGAC AATTGCTATT CAGCTGTACT CTCGCCGGAT      300
   AAAAAAATGC ACGGATTACT TGTAAAAAAG AACCATGAAT ATGAAATCAA      350
   CCATGTTGAT GTAGCATTTT CAGCTTTGCA TGGCAAGTCA GGTGAAGATG      400
   GATCCATACA AGGTCTGTTT GAATTGTCCG GTATCCCTTT TGTAGGCTGC      450
   GATATTCAAA GCTCAGCAAT TTGTATGGAC AAATCGTTGA CATAATCGT      500
15  TGCGAAAAAT GCTGGGATAG CTACTCCCGC CTTTGGGTT ATTAATAAAG      550
   ATGATAGGCC GGTGGCAGCT ACGTTTACCT ATCCTGTTTT TGTTAAGCCG      600
   GCGCGTTCAG GCTCATCCTT CGGTGTGAAA AAAGTCAATA GCGCGGACGA      650
   ATTGGACTAC GCAATTGAAT CGGCAAGACA ATATGACAGC AAAATCTTAA      700
   TTGAGCAGGC TGTTCGGGC TGTGAGGTCG GTTGTGCGGT ATTGGGAAAC      750
20  AGTGCCCGCT TAGTTGTTGG CGAGGTGGAC CAAATCAGGC TGCAGTACGG      800
   AATCTTTCGT ATTCATCAGG AAGTCGAGCC GGAAAAAGGC TCTGAAAACG      850
   CAGTTATAAC CGTTCCCGCA GACCTTTCAG CAGAGGAGCG AGGACGGATA      900
   CAGGAAACGG CAAAAAAAT ATATAAAGCG CTCGGCTGTA GAGGTCTAGC      950
   CCGTGTGGAT ATGTTTTTAC AAGATAACGG CCGCATTGTA CTGAACGAAG      1000
25  TCAATACTCT GCCCGGTTTC ACGTCATACA GTCGTTATCC CCGTATGATG      1050
   GCCGCTGCAG GTATTGCACT TCCCGAACTG ATTGACCGCT TGATCGTATT      1100
   AGCGTTAAAG GGGTGATAAG CATGGAAATA GGATTACTT TTTTAGATGA      1150
   AATAGTACAC GGTGTTGCTT GGGACGCTAA ATATGCCACT TGGGATAATT      1200
   TCACCGGAAA ACCGTTGAC GGTATAAGT AA                      1232
30

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2) INFORMATION FOR SEQ ID NO: 1055

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35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1218 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
40
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Enterococcus gallinarum
45  (B) STRAIN: R684

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

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50  TACCGAGCAA GCGTTGCGTG ATACCGTTGA AAAAACCATT AAAAACTGTT      50
   TGGATTTTGA AAGGAGACAG GAGCATGAAT AGAATAAAAG TTGCAATACT      100
   GTTTGGGGGT TGCTCAGAGG AGCATGACGT ATCGGTAAAA TCTGCAATAG      150
   AGATAGCCGC TAACATTAAT AAAGAAAAAT ACGAGCCGTT ATACATTGGA      200
   ATTACGAAAT CTGGTGTATG GAAAATGTGC GAAAAACCTT GCGCGGAATG      250
   GGAAAACGAC AATTGCTATT CAGCTGTACT CTCGCCGGAT AAAAAAATGC      300
55  ACGGATTACT TGTAAAAAAG AACCATGAAT ATGAAATCAA CCATGTTGAT      350
   GTAGCATTTT CAGCTTTGCA TGGCAAGTCA GGTGAAGATG GATCCATACA      400
   AGGTCTGTTT GAATTGTCCG GTATCCCTTT TGTAGGCTGC GATATTCAAA      450
   GCTCAGCAAT TTGTATGGAC AAATCGTTGA CATAATCGT TGCGAAAAAT      500
   GCTGGGATAG CTACTCCCGC CTTTGGGTT ATTAATAAAG ATGATAGGCC      550
60  GGTGGCAGCT ACGTTTACCT ATCCTGTTTT TGTTAAGCCG GCGCGTTCAG      600

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	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	ATTGGACTAC	650
	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	TTGAGCAGGC	700
	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	AGTGCCGCGT	750
	TAGCTGTTGG	CGAGGTGGAC	CAAAATCAGGC	TGCAGTACGG	AATCTTTCGT	800
5	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	CAGTTATAAC	850
	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	CAGGAAACGG	900
	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	CCGTGTGGAT	950
	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	TCAATACTCT	1000
	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	GCCGCTGCAG	1050
10	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	AGCGTTAAAG	1100
	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	AATAGTACAC	1150
	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAAAT	TCACCGGAAA	1200
	ACCGGTTGAC	GGTTAGAA				1218

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2) INFORMATION FOR SEQ ID NO: 1056

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: R688
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

	AATCACACCG	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	50
	TTGAAAAAAC	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	100
35	GAATAGAATA	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	150
	ACGTATCGGT	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	200
	AAATACGAGC	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAT	250
	GTGCGAAAAA	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	300
	TACTCTCGCC	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	350
40	GAATATGAAA	TCAACCATGT	TGATGTAGCA	TTTTTCAGCTT	TGCATGGCAA	400
	GTCAGGTGAA	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	450
	CTTTTGTAGG	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	500
	TTGACATACA	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	550
	GGTTATTAAT	AAAGATGATA	GGCCGGTGCG	AGCTACGTTT	ACCTATCCTG	600
45	TTTTTGTAA	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	650
	AATAGCGCGG	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	700
	CAGCAAAATC	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	750
	CGGTATTGGG	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	800
	AGGCTGCAGT	ACGGAATCTT	TCGTATTCAT	CAGGAAGTCG	AGCCGGAAAA	850
50	AGGCTCTGAA	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	900
	AGCGAGGACG	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	950
	TGTAGAGGTC	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	1000
	TGTACTGAAC	GAAGTCAATA	CTCTGCCCCG	TTTCACGTCA	TACAGTCGTT	1050
	ATCCCCGTAT	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	1100
55	CGCTTGATCG	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	1150
	ACTTTTTTAG	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	1200
	CACTTGGGAT	AATTTACCGG	GAAAACCGGT	TGACGGTTAT	GAAGTAAATC	1250
	GCATTGTAGG	GACAT				1265

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2) INFORMATION FOR SEQ ID NO: 1057

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1269 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus flavescens*
- (B) STRAIN: R689

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
20	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
25	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
30	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
35	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCCTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
40	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	1250
	ATTGTAGGGA	CATACGAAT				1269

45

2) INFORMATION FOR SEQ ID NO: 1058

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1169 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R420

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
5	ATTCTCCAGA	ATACTCAGTG	TCACTAACCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTAACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
10	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
15	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750
	TTGACGATTG	TGCTTGTGA	TGCGATTCTT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
20	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTTCGTCAC	950
	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
25	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTGCTA				1169

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

45	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
	ATTCTCCAGA	ATACTCAGTG	TCACTAGCCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTGACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
50	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
55	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
60	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750

TTGACGATTG GTGCTTGTGA TGC GATTCTT CTTGTCGACG GTTTTTTTTGA 800
 TTTTGAAGAG AAATACCAAT TAATCAGCGC CACGATCACT GTCCCAGCAC 850
 CATTGCCTCT CGCGCTTGAA TCACAGATCA AGGAGCAGGC ACAGCTGCTT 900
 TATCGAAACT TGGGATTGAC GGGTCTGGCT CGAATCGATT TTTTCGTCAC 950
 5 CAATCAAGGA GCGATTTATT TAAACGAAAT CAACACCATG CCGGGATTTA 1000
 CTGGGCACTC CCGCTACCCA GCTATGATGG CGGAAGTCGG GTTATCCTAC 1050
 GAAATATTAG TAGAGCAATT GATTGCACTG GCAGAGGAGG ACAAACGATG 1100
 AACACATTAC AATTGATCAA TAAAAACCAT CCATTGAAAA AAAATCAAGA 1150
 GCCCCCGCAC TTAGTG 1166
 10

2) INFORMATION FOR SEQ ID NO: 1060

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1028 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus casseliflavus*
 25 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

AACATGAAAA AAATCGCCTT ATTTTTGGAG GCAATTCACC GGAATACACC 50
 30 GTTTCCTTTAG CTTTCAAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC 100
 CTATGACTAC GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT 150
 GGTACTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG 200
 TTGGATACGA AACATAAACA GAAAATACAG CCGCTATTCG AAGGAAACGG 250
 CTTTTGGCTA AGTGAAGAGC AGCAAACGTT GGTACCTGAT GTTTTATTTT 300
 35 CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT 350
 GAATTGATGA AGCTGCCTTA TGTAGGCTGC GGGGTGGCAG GTTCTGCCTT 400
 ATGTATGAAC AAATGGCTGC TGCATCAAGC TGCAGCAGCC ATTGGCGTAC 450
 AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGAACAA 500
 ATCGAAGCTT TTATCCAGAC CCATGGCTTC CCAGTTTCTT TTAAGCCTAA 550
 40 TGAAGCGGGC TCCTCAAAAG GGATCACTAA AGTCACCTGC GTTGAAGAAA 600
 TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTCCGC AGTGCTCCTA 650
 CAAAAAATA TTGCCGGTGT TGAGATCGGT TGCGGTATTT TGGGCAACGA 700
 CTCTTTGACT GTCGGTGCTT GTGACGCCAT TTCATTAGTA GACGGCTTTT 750
 TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAAAT CACCGTCCCT 800
 45 GCGCCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT 850
 GCTCTATCGT AGTCTTGGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTTG 900
 TCACGGAGCG AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC 950
 TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGG TCGGCTTATC 1000
 CTATCAAGAA CTACTACAAA AACTGCTT 1028
 50

2) INFORMATION FOR SEQ ID NO: 1061

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 5 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

```

10 AATATGAAAA AAATCGCCTT ATTTTGGAG GCAATTCACC GGAGTACGCC      50
   GTTTCCTTTAG CCTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
   CGATGACTAT GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
   GGTATTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
   TTGGATACGA AACATAAACA GAAAATCCAG CCGCTTTTGT AAGGAAACGG      250
   CTTTTGGCTA AGTGAAGAGC AACAAACGTT GGTTCCTGAT GTTTTATTTT      300
15 CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
   GAATTGATGA AACTACCTTA TGTAGGCTGC GGGGTGGCAG CCTCTGCCTT      400
   ATGTATGAAC AAATGGCTGC TGCATCAAGC AGCAGAAGCG ATTGGCGTAC      450
   AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGATCAA      500
   ATCGAAGCTT TTATCCAGAC CCATGGCTTT CCGGTTTTTT TTAAGCCTAA      550
20 TGAAGCGGGC TCCTCAAAAG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
   TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTTCAGC AGTGCTCCTA      650
   CAAAAAATA TTGCCGGTGT TGAGATCGGT TCGCGTATTT TGGGCAACGA      700
   CTCTTTGACT GTCGGTGCTT GTGACGCTAT TTCATTAGTA GACGGCTTTT      750
   TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAGAT CACCGTTCCT      800
25 GCACCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
   GCTCTATCGT AGTCTTTGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTT      900
   TCACGGATCA AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
   TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGA TCGGCTTATC     1000
   CTATCAAGAA CTACTACAAA AACTGCTTGT     1030
30

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2) INFORMATION FOR SEQ ID NO: 1062

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 45 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

```

50 AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
   CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
   CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
   TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
   TGTTGGATAC GAAACATAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
   GGCTTTTGGC TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
55 TCCCATTATG CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
   TTGAATTGAT GAAGCTGCCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
   TTATGTATGA ACAAATGGCT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
   ACAAAGTGCT CCTACGATTC TCTTGACAAA TCAAGCCAAC CAGCAAGAAC      500
   AAATCGAAGC TTTTATCCAG ACCCATGGCT TCCCAGTTTT CTTTAAGCCT      550
60 AATGAAGCGG GCTCCTCAAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600

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AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC 650
 TACAAAAAAA TATTGCCGCT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC 700
 GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTTCATTAG TAGACGGCTT 750
 TTTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC 800
 5 CTGCGCCATT GCCTGAAACG ATTGAAACCA AGGTCAAAGA ACAAGCTCAG 850
 CTGCTCTATC GTAGTCTTGG TCTTAAAGGT CTTGCTCGCA TCGACTTTTT 900
 TGTCACGGAG CGAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG 950
 GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCCGCTTA 1000
 TCCTATCAAG AACTACTACA AAAACTGCTT G 1031
 10

2) INFORMATION FOR SEQ ID NO: 1063

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus casseliflavus*
 25 (B) STRAIN: R775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

AACATGAAAA AAATCGCCAT TATTTTTTGA GGCAATTCAC CGGAATACAC 50
 30 CGTTTTCTTTA GCTTCAGCAA CTAGCGCAAT CGAAGCACTC CAATCATCTC 100
 CCTATGACTA CGACCTCTCT TTGATCGGGA TCGCCCCAGA TGCTATGGAT 150
 TGGTACTTGT ATACAGGAGA ACTGGAAGAAC ATCCGACAAG ACACGTGGTT 200
 GTTGATACG AAACATAAAC AGAAAAATACA GCCGCTATTT GAAGGAAACG 250
 GCTTTTGGCT AAGTGAAGAG CAGCAAACGT TAGTACCTGA TATTTTATTT 300
 35 CCCATTATGC ATGGCAAATA CGGGGAAGAT GGCAGTATCC AAGGATTGTT 350
 TGAATTGATG AACTACCTT ATGTAGGTTG CGGGGTGGCA GGTCTGCCT 400
 TATGTATGAA CAAATGGCTG CTGCATCAAG CTGCAGCAGC CATTGGCGTA 450
 CAAAGTGCTC CTACGATTCT CTTGACAAAT CAAGCCAACC AGCAAGAACA 500
 AATCGAAGCT TTTATCCAGA CCCATGGCTT CCCAGTTTTT TTTAAGCCTA 550
 40 ATGAAGCGGG CTCTTCAAAA GGGATCACTA AAGTCACCTG CGTTGAAGAA 600
 ATCGCTTCTG CCTTAAAAAA AGCCTTTACT TATTGTTCCG CAGTGCTCCT 650
 AAAAAAAAT ATTGCCGGTG TTGAGATCGG TTGCGGTATT TTGGGCAACG 700
 ACTCTTTGAC TGTCGGTGCT TGTGACGCCA TTTCATTAGT AGACGGCTTT 750
 TTCGATTTTG AAGAAAAGTA CCAGCTGATC AGCGCCAAAA TCACCGTCCC 800
 45 TGCGCCATTG CCTGAAACGA TTGAAACCAA GGTCAAAGAA CAAGCTCAGC 850
 TGCTCTATCG TAGTCTTGGT CTTAAAGGTC TTGCTCGCAT CGACTTTTTT 900
 GTCACGGATC AAGGAGAACT ATAATTGAAT GAAATCAATA CTATGCCGGG 950
 CTTTACGAGT CACTCCCGTT ATCCTGCCAT GATGGCAGCG GTCGGCTTAT 1000
 CCTATCAAGA ACTACTACAA AACTGCTTG 1030
 50

2) INFORMATION FOR SEQ ID NO: 1064

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1032 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

```

10 AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
   CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
   CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
   TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
   TGTGGATAC  GAAACAGAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
   GGCTTTTGGT TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTATT      300
15 TCCCATTATG CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
   TTGAATTGAT GAAGCTACCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
   TTATGTATGA ACAAATGGTT GCTGCATCAA CATTGGCGT  CCATTGGCGT      450
   ACAAAGTGCT CCTACGATTC TCTTGACAAA TCACGCCAAC CAGCAAGAAC      500
   AAATCGAAGC TTTTATCCAG ACCCATGGCT TTCCAGTTTT CTTTAAGCCT      550
20 AATGAAGCGG GTTCCTCAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600
   AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC      650
   TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC      700
   GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTCATTAG  TAGACGGCTT      750
   TTTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC      800
25 CTGCGCCATT GCCTGAAACG ATTGAAACTA AGGTCAAAGA ACAAGCTCAG      850
   CTGCTCTATC GTAGTCTTGG ACTTAAAGGT CTTGCTCGCA TCGACTTTTT      900
   TGTACGGAT  CAAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG      950
   GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTTCGGTTA     1000
   TCCTATCAAG AACTACTACA AAAACTACTT GT                          1032
30

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2) INFORMATION FOR SEQ ID NO: 1065

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1034 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Enterococcus flavescens*
(B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

```

50 AAAACATGA AAAAATCGC CATTATTTT GGAGGCAATT CACCGGAATA      50
   CACCGTTTCT TTAGCTTCAG CAACTAGCGC AATCGAAGCA CTCCAATCAT      100
   CTCCCTATGA CTACGACCTC TCTTTGATCG GGATCGCCCC AGATGCTATG      150
   GATTGGTACT TGTATACAGG AGAACTGGAA AACATCCGAC AAGACACGTG      200
   GTTGTGGAT  ACGAAACATA AACAGAAAAT ACAGCCGCTA TTCGAAGGAA      250
   ACGGCTTTTG GCTAAGTGAA GAGCAGCAA CGTTGGTACC TGATGTTTTA      300
55 TTTCCCATTA TGCATGGCAA ATACGGGGAA GATGGCAGTA TCCAAGGATT      350
   GTTGAATTG  ATGAAGCTGC CTTATGTAGG CTGCGGGGTG GCAAGTCTG      400
   CCTTATGTAT GAACAAATGG CTGCTGCATC AAGCTGCAGC AGCCATTGGC      450
   GTACAAAGTG CTCCTACGAT TCTCTTGACA AATCAAGCCA ACCAGCAAGA      500
   ACAAATCGAA GCTTTTATCC AGACCCATGG CTTTCCAGTT TTCTTTAAGC      550
60 CTAATGAAGC GGGCTCCTCA AAAGGGATCA CTAAAGTCAC CTGCGTTGAA      600

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GAAATCGCTT CTGCCTTAAA AGAAGCCTTT ACTTATTGTT CCGCAGTGCT 650
 CCTACAAAAA AATATTGCCG GTGTTGAGAT CGGTTGCGGT ATTTTGGGCA 700
 ACGACTCTTT GACTGTCGGT GCTTGTGACG CCATTTTCATT AGTAGACGGC 750
 TTTTTCGATT TTGAAGAAAA GTACCAGCTG ATCAGCGCCA AAATCACCGT 800
 5 CCCTGCGCCA TTGCCTGAAA CGATTGAAAC CAAGGTCAAA GAACAAGCTC 850
 AGCTGCTCTA TCGTAGTCTT GGTCTTAAAG GTCTTGCTCG CATCGACTTT 900
 TTTGTCACGG ATCAAGGAGA ACTATACTTG AATGAAATCA ATACTATGCC 950
 GGGCTTTACG AGTCACTCCC GCTATCCTGC CATGATGGCA GCGGTCGGCT 1000
 TATCCTATCA AGAACTACTA CAAAACTGC TTGT 1034
 10

2) INFORMATION FOR SEQ ID NO: 1066

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1012 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 25 (B) STRAIN: R760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

CATGAAAAAA ATCGCCATTA TTTTGGAGG CAATTCACCG GAATACACCG 50
 30 TTTCTTTAGC CTCAGCAACT AGCGCAATCG AAGCACTCCA ATCATCTCCC 100
 TATGATTACG ACCTCTCTTT GATCGGGATC GCCCCAGATG CTATGGATTG 150
 GTA CTTGTAT ACAGGAGAAC TGGAAAACAT CCGACAAGAC ACGTGGTTGT 200
 TGGATACGAA ACATACACAG AAAATCCAGC CACTTTTGA AGGAAACGGC 250
 TTTTGGATAA GTGAAGCGCA GCAAACGTTG GTACCTGATG TTTTATTTCC 300
 35 CATTATGCAT GGTAAATACG GGAAGATGG CAGTATCCAA GGATTGTTTG 350
 AATTGATGAA GCTGCCTTAT GTAGGCTGTG GGGTGGCAGC CTCTGCCTTA 400
 TGTATGAACA AATGGTTATT GCATCAAGCA GCAGCAGCGA TTGGCGTACA 450
 AAGCGCTCCT ACGATTCTCT TGACAAATCA AGCCAACCAG CAAAGACAAA 500
 TCGAAGCCTT TATCCAGACC CATGGCTTTC CAGTTTTCTT TAAGCCTAAT 550
 40 GAAGCGGGCT CCTCAAAAGG GATCACAAAA GTAACCTGTG TTGAAGAAAT 600
 CGCTCCTGCC TTGAAGGAAG CCTTCGCTTA TTGTTCCGCA GTGCTCTTAC 650
 AAAAAAATAT CGCTGGCGTT GAGATTGGTT GCGGTATCTT AGGCAACGAC 700
 TCTTTGACTG TCGGTGCTTG TGACGCTATT TCATTAGTAG ACGGCTTTTT 750
 CGATTTTGAA GAAAAGTACC AGTTGATCAG CGCCAAAATC ACCGTCCTCG 800
 45 CGCCATTGCC TGAAACGATT GAAACCAAAG TCAAAGAACA AGCTCAGCTG 850
 CTCTATCACA GTCTTGGTCT TAAAGGACTT GCTCGCATCG ACTTTTTTGT 900
 CACGGATCAA GGAGAACTAT ACTTGAATGA AATCAATACT ATGCCGGGCT 950
 TTACGAGTCA CTCCCGCTAT CCTGCCATGA TGGCAGCGGT CGGCTTATCC 1000
 TATCAAGAAT TA 1012
 50

2) INFORMATION FOR SEQ ID NO: 1067

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 721 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 5 (B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

```

10 CTTACGCTTT ATCGATTAGA CACGGGNAGC TTGTCCAATG GGRAGCCGAT 50
   TTGATTTTAT GGATGAACGC TCTCATCATG CGGCAAATGG AATATCATGC 100
   AATGAAGCGC AAAATCGCAG ACGTTTGCGC TCCATCATGG AAAACAGTGG 150
   GTTTGAAGCA TATAGCCTCG AATGGTGGCA CTATGTATTA AGAGACGAAC 200
   CATACCCCAA TAGCTATTTT GATTTCCCCG TTAAATAAAC TTTTAACCGT 250
   TGCACGGACA AACTATATAA GCTAACTCTT TCGGCAGGAA ACCCGACGTA 300
15 TGTAAGTGGT TCTTAGGGAA TTTATATATA GTAGATAGTA TTGAAGATGT 350
   AAGGCAGAGC GATATTGCGG TCATTATCTG CGTGCGCTGC GGCAAGATAG 400
   CCTGATAATA AGACTGATCG CATAGAGGGG TGGTATTTC AACC GCCCAT 450
   TGTCAACAGG CAGTTCAGCC TCGTTAAATT CAGCATGGGT ATCACTTATG 500
   AAAATTTCATC TACATTGGTG ATAATAGTAA ATCCAGTAGG GCGAAATAAT 550
20 TGACTGTAAT TTACGGGGCA AAACGGCACA ATCTCAAACG AGATTGTGCC 600
   GTTTAAGGGG AAGATTCTAG AAATATTTCA TACTTCCAAC TATATAGTTA 650
   AGGAGGAGAC TGAAAATGAA GAAGTTGTTT TTTTATTGT TATTGTTATT 700
   CTTAATATAC TTAGGTTATT G 721

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2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 40 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

```

45 ATTTTTAAGG ATGAACGCTC TTCATCATGC GGCAAATGGA ATATCATGCA 50
   ATGAAGCGCA AAATCGCAGA CGTTTGCGCT CCATCATGGA AAACAGTGGG 100
   TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC TATGTATTAA GAGACGAACC 150
   ATACCCCAAT AGCTATTTTG ATTTCCCCGT TAAATAAACT TTTAACCGTT 200
   GCACGGACAA ACTATATAAG CTAACCTCTT CGGCAGGAAA CCCGACGTAT 250
   GTAAGTGGT CTTAGGGAAT TTATATATAG TAGATAGTAT TGAAGATGTA 300
   AGGCAGAGCG ATATTGCGGT CATTATCTGC GTGCGCTGCG GCAAGATAGC 350
50 CTGATAATAA GACTGATCGC ATAGAGGGGT GGTATTTTCA ACCGCCCAT 400
   GTCAACAGGC AGTTCAGCCT CGTTAAATTC AGCATGGGTA TCACTTATGA 450
   AAATTTCATCT ACATTGGTGA TAATAGTAAA TCCAGTAGGG CGAAATAATT 500
   GACTGTAATT TACGGGGCAA AACGGCACAA TCTCAAACGA GATTGTGCCG 550
   TTTAAGGGGA AGATTCTAGA AATATTTTCA ACTTCCAAC TATATAGTTA 600
55 GGAGGAGACT GAAAATGAAG AAGTTGTTT TTTTATTGTT ATTGTTATTC 650
   TTAATATACT TAGGTTAT 668

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60 2) INFORMATION FOR SEQ ID NO: 1069

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069

15 CGGCAAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTRAGCTT 50
 GTACCAATGG GAAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC 100
 GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT 150
 CCATCATGGA AAACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC 200
 20 TATGTATTAA GAGACGAACC ATACCCCAAT AGCTATTTTG ATTTCCCCGT 250
 TAAATAAACT TTTAACCGTT GCACGGACAA ACTATATAAG CTAACCTTTT 300
 CGGCAGGAAA CCCGACGTAT GTAACGGT CTTAGGGAAT TTATATATAG 350
 TAGATAGTAT TGAAGATGTA AGGCAGAGCG ATATTGCGGT CATTATCTGC 400
 GTGCGCTGCG GCAAGATAGC CTGATAATAA GACTGATCGC ATAGAGGGGT 450
 25 GGTATTTTAC ACCGCCCAT GTCAACAGGC AGTTCAGCCT CGTTAAATTC 500
 AGCATGGGTA TCACTTATGA AAATTCATCT ACATTGGTGA TAATAGTAAA 550
 TCCAGTAGGG CGAAATAATT GACTGTAATT TACGGGGCAA AACGGCACAA 600
 TCTCAAACGA GATTGTGCCG TTTAAGGGGA AGATTCTAGA AATATTTTCAT 650
 ACTTCCAACAT ATATAGTTAA GGAGGAGACT GAAAATGAAG AAGTTGTTTT 700
 30 TTTTATTGTT ATTGTTATTC TTAATATACT TAGGTTATGA CTACGTTAAT 750
 GAAANCCTGA 760

35 2) INFORMATION FOR SEQ ID NO: 1070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070

50 AAAAGGAATA CGGGGCTTTC AAAAATCCAA GCCATAACCC GCGGGCAAGT 50
 GCCATTTGAT TCTTACGCTT TAATCGATTA GACACGGGTA AGCTTGTAAC 100
 AATGGGGAAC CGATTTGATT TTAATGNATG AACGCTCTTC ATCATGCGGC 150
 AAATGGAATA TCATGCAATG AAGCGCAAAA TCGCAGACGT TTGCGCTCCA 200
 55 TCATGGAAAA CAGTGGGTTT GAAGCATATA GCCTCGAATG GTGGCACTAT 250
 GTATTAAGAG ACGAACCATA CCCCAATAGC TATTTTGATT TCCCCGTTAA 300
 ATAACTTTT AACCGTTGCA CGGACAAACT ATATAAGCTA ACTCTTTCGG 350
 CAGGAAACCC GACGTATGTA ACTGGTTCTT AGGGAATTTA TATATAGTAG 400
 ATAGTATTGA AGATGTAAGG CAGAGCGATA TTGCGGTCAT TATCTGCGTG 450
 60 CGCTGCGGCA AGATAGCCTG ATAATAAGAC TGATCGCATA GAGGGGTGGT 500

ATTTCACACC GCCCATTGTC AACAGGCAGT TCAGCCTCGT TAAATTCAGC 550
ATGGGTATCA CTTATGAAAA TTCATCTACA TTGGTGATAA TAGTAAATCC 600
AGTAGGGCGA AATAATTGAC TGTAATTTAC GGGGCAAAAC GGCACAATCT 650
CAAACGAGAT TGTGCCGTTT AAGGGGAAGA TTCTAGAAAT ATTTCACTACT 700
5 TCCAACATA TAGTTAAGGA GGAGACTGAA AATGAAGAAG TTGTTTTTTT 750
TTATTGTTAT TGTATTCTT AATATACTTA GGTTATGACT ACGTTAATGA 800
A 801

10

2) INFORMATION FOR SEQ ID NO: 1071

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 711 bases
15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R684

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

TTGTACCAAT GGGGAGCCGA TTTGATTTTA TGGATGAACG CTCTCATCAT 50
GCGGCAAATG GAATATCATG CAATGAAGCG CAAAATCGCA GACGTTTGCG 100
CTCCATCATG GAAAACAGTG GGTTTGAAGC ATATAGCCTC GAATGGTGGC 150
30 ACTATGTATT AAGAGACGAA CCATACCCCA ATAGCTATTT TGATTTCCCC 200
GTTAAATAAA CTTTTAACCG TTGCACGGAC AACTATATA AGCTAACTCT 250
TTCGGCAGGA AACCCGACGT ATGTAAGTGG TTCTTAGGGA ATTTATATAT 300
AGTAGATAGT ATTGAAGATG TAAGGCAGAG CGATATTGCG GTCATTATCT 350
GCGTGCGCTG CGGCAAGATA GCCTGATAAT AAGACTGATC GCATAGAGGG 400
35 GTGGTATTTT ACACCGCCCA TTGTCAACAG GCAGTTCAGC CTCGTAAAT 450
TCAGCATGGG TATCACTTAT GAAAATTCAT CTACATTGGT GATAATAGTA 500
AATCCAGTAG GCGGAAATAA TTGACTGTAA TTTACGGGGC AAAACGGCAC 550
AATCTCAAAC GAGATTGTGC CGTTTAAGGG GAAGATTCTA GAAATATTTT 600
ATACTTCCAA CTATATAGTT AAGGAGGAGA CTGAAAATGA AGAAGTTGTT 650
40 TTTTTTATTG TTATTGTTAT TCTTAATATA CTTAGGTAT GACTACGTTA 700
ATGAAGCACT G 711

45 2) INFORMATION FOR SEQ ID NO: 1072

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R688
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072
- 60

	GCCATTGATC	TTACGCTTTA	TCGATTAGAC	ACGGGTNAGC	TTGTACCAAT	50
	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	GCGGCAAATG	100
	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	CTCCATCATG	150
	GAAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	ACTATGTATT	200
5	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	GTTAAATAAA	250
	CTTTTAACCG	TTGCACGGAC	AAACTATATA	AGCTAACTCT	TTCGGCAGGA	300
	AAACCGACGT	ATGTAAGTGG	TTCTTAGGGA	ATTTATATAT	AGTAGATAGT	350
	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	GCGTGCGCTG	400
	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	GTGGTATTTT	450
10	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	TCAGCATGGG	500
	TATCACTTAT	GAAAATTTCAT	CTACATTGGT	GATAATAGTA	AATCCAGTAG	550
	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	AATCTCAAAC	600
	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	ATACTTCCAA	650
	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	TTTTTTATTG	700
15	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	ATGAAGCACT	750
	G					751

20 2) INFORMATION FOR SEQ ID NO: 1073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

35	ATTTGATTTT	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	50
	GCAATGAAGC	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	100
	GGGTTTGAAG	CATATAGCCT	CGAATGGTGG	CACTATGTAT	TAAGAGACGA	150
	ACCATACCCC	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	200
40	GTTGCACGGA	CAAACATAT	AAGCTAACTC	TTTCGGCAGG	AAACCCGACG	250
	TATGTAAGT	GTTCTTAGGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	300
	GTAAGGCAGA	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	350
	AGCCTGATAA	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	400
	ATTGTCAACA	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	450
45	TGAAAATTCA	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	500
	ATTGACTGTA	ATTTACGGGG	CAAAACGGCA	CAATCTCAA	CGAGATTGTG	550
	CCGTTTAAGG	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	600
	TAAGGAGGAG	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	650
	TTCTTAATAT	ACTTAGGTTA	TGACTACGTT	AATGA		685

50

2) INFORMATION FOR SEQ ID NO: 1074

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 5 (B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

```

10 ATCGATTAGA CACGGGTGAG CTTGTACCAA TGGGGAGCCG ATTTGATTTT 50
   ATGGATGAAC GCTCTCATCA TGCGGCAAAT GGAATATCAT GCAATGAAGC 100
   GCAAAATCGC AGACGTTTGC GCTCCATCAT GGAAAACAGT GGGTTTGAAG 150
   CATATAGCCT CGAATGGTGG CACTATGTAT TAAGAGACGA ACCATACCCC 200
   AATAGCTATT TTGATTTCCC CGTTAAATAA ACTTTTAACC GTTGCACGGA 250
   CAAACTATAT AAGCTAACTC TTTCGGCAGG AAACCCGACG TATGTAAC TG 300
15 GTTCTTAGGG AATTTATATA TAGTAGATAG TATTGAAGAT GTAAGGCAGA 350
   GCGATATTGC GGTCAATTATC TGCCTGCGCT GCGGCAAGAT AGCCTGATAA 400
   TAAGACTGAT CGCATAGAGG GGTGGTATT T CACACCGCCC ATTGTCAACA 450
   GGCAGTTCAG CCTCGTTAAA TTCAGCATGG GTATCACTTA TGAAAATTCA 500
   TCTACATTGG TGATAATAGT AAATCCAGTA GGGCGAAAATA ATTGACTGTA 550
20 ATTTACGGGG CAAAACGGCA CAATCTCAAA CGAGATTGTG CCGTTTAAGG 600
   GGAAGATTCT AGAAATATTT CATACTTCCA ACTATATAGT TAAGGAGGAG 650
   ACTGAAAATG AAGAAGTTGT TTTTTTTATT GTTATTGTTA TTCTTAATAT 700
   ACTTAGGTTA TGAAGTACGTT AATGAAGCAC TG 732

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25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 40 (B) STRAIN: R691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

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   TCTCATCATG CGGCAAATGG AATATCATGC AATGAAGCGC AAAATCGCAG 50
   ACGTTTGC GC TCCATCATGG AAAACAGTGG GTTTGAAGCA TATAGCCTCG 100
45 AATGGTGGCA CTATGTATTA AGAGACGAAC CATACCCCAA TAGCTATTTT 150
   GATTTCCCCG TTAAATAAAC TTTTAACCGT TGCACGGACA AACTATATAA 200
   GCTAACTCTT TCGGCAGGAA ACCCGACGTA TGTAAGTGGT TCTTAGGGAA 250
   TTTATATATA GTAGATAGTA TTGAAGATGT AAGGCAGAGC GATATTGCGG 300
   TCATTATCTG CGTGCGCTGC GGCAAGATAG CCTGATAATA AGACTGATCG 350
50 CATAGAGGGG TGGTATTTCA CACCGCCCAT TGTCAACAGG CAGTTCAGCC 400
   TCGTTAAATT CAGCATGGGT ATCACTTATG AAAATTTCATC TACATTGGTG 450
   ATAATAGTAA ATCCAGTAGG GCGAAATAAT TGAAGTGAAT TTACGGGGCA 500
   AAACGGCACA ATCTCAAACG AGATTGTGCC GTTTAAGGGG AAGATTCTAG 550
   AAATATTTCA TACTTCCAAC TATATAGTTA AGGAGGAGAC TGAAAATGAA 600
55 GAAGTTGTTT TTTTATTGT TATTGTTATT CTTAATATAC TTAGGTTATG 650
   ACTACGTAA TGAAGCACTG 670

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60 2) INFORMATION FOR SEQ ID NO: 1076

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: DG131/3 serotype OX3:H8
 (C) ACCESSION NUMBER: Z36901
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

	ATGAAAATAA	TAATTTTTAG	AGTGCTAACT	TTTTTCTTTG	TTATCTTTTC	50
	TGTTAATGTG	GTTGCGAAGG	AATTTACCTT	AGATTTCTCG	ACAGCAAAGA	100
	CGTATGTAGA	TTCGCTGAAT	GTCATTCGCT	CTGCAATAGG	TACTCCATTA	150
20	CAGACTATTT	CATCAGGAGG	TACGTCTTTA	CTGATGATTG	ATAGTGGCAC	200
	AGGGGATAAT	TTGTTTGCAG	TTGATGTCAG	AGGGATAGAT	CCAGAGGAAG	250
	GGCGGTTTAA	TAATCTACGG	CTTATTGTTG	AACGAAATAA	TTTATATGTG	300
	ACAGGATTTG	TTAACAGGAC	AAATAATGTT	TTTTATCGCT	TTGCTGATTT	350
	TTCACATGTT	ACCTTTCCTG	GTACAACTGC	GGTTACATTG	TCTGGTGACA	400
25	GTAGCTATAC	CACGTTACAG	CGTGTTGCGG	GGATCAGTCG	TACGGGGATG	450
	CAGATAAATC	GCCATTCGTT	GACTACTTCT	TATCTGGATT	TAATGTCGCA	500
	TAGCGGAACC	TCACTGACGC	AGTCTGTGGC	AAGAGCGATG	TTACGGTTTG	550
	TTACTGTGAC	AGCTGAAGCT	TTACGTTTTC	GGCAAATTCA	GAGGGGATTT	600
	CGTACAACAC	TTGATGATCT	CAGTGGGCGT	TCTTATGTAA	TGACTGCTGA	650
30	AGATGTTGAT	CTTACGTTGA	ACTGGGGAAG	GTTGAGTAGT	GTCCTGCCTG	700
	ACTATCATGG	ACAAGACTCT	GTTTCGTGTTG	GAAGAATTTC	TTTTGGAAGT	750
	GTTAATGCAA	TTCTGGGTAG	CGTGGCATTG	ATACTGAATT	GTCATCATCA	800
	TGCATCGCGA	GTTGCCAGAA	TTGTACCTAA	TGAGTTTCCT	TCTATGTGCC	850
	CGGTAGATGG	AAGAGTGCGT	GGGATTACGC	ACAATAAAAT	ATTGTGGGAC	900
35	TCATCCACTC	TGGGGGCAAT	TTTGATACGC	AGGGCTATTA	GCAGTTGA	948

2) INFORMATION FOR SEQ ID NO: 1077

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1259 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: 94C serotype O48:H21
 (C) ACCESSION NUMBER: extracted from Z37725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

55	CACCTGTATA	TGAAGTGTAT	ATTATTTAAA	TGGGTACTGT	GCCTGTTACT	50
	GGGTTTTTCT	TCGGTATCCT	ATTCCCGGGA	GTTTACGATA	GACTTTTCGA	100
	CCCAACAAAG	TTATGTCTCT	TCGTTAAATA	GTATACGGAC	AGAGATATCG	150
	ACCCCTCTTG	AACATATATC	TCAGGGGACC	ACATCGGTGT	CTGTTATTAA	200
60	CCACACCCCA	CCGGGCAGTT	ATTTTGCTGT	GGATATACGA	GGGCTTGATG	250

	TCTATCAGGC	GCGTTTTGAC	CATCTTCGGC	TGATTATTGA	GCAAAATAAT	300
	TTATATGTGG	CCGGGTTCGT	TAATACGGCA	ACAAATACTT	TCTACCGTTT	350
	TTCAGATTTT	ACACATATAT	CAGTGCCCGA	TGTGACAACG	GTTTCCATGA	400
	CAACGGACAG	CAGTTATACC	ACTCTGCAAC	GTGTCCGAGC	GCTGGAACGT	450
5	TCCGGAATGC	AAATCAGTCG	TCACTCACTG	GTTTCATCAT	ATCTGGCGTT	500
	AATGGAGTTC	AGTGGTAATA	CAATGACCAG	AGATGCATCC	AGAGCAGTTC	550
	TGCGTTTTGT	CACTGTCACA	GCAGAAGCCT	TACGCTTCAG	GCAGATACAG	600
	AGAGAATTTT	GTCAGGCACT	GTCTGAAACT	GCTCCTGTGT	ATACCATGAC	650
	GCCGGGAGAC	GTGGACCTCA	CTCTGAACTG	GGGGCGAATC	AGCAATGTGC	700
10	TTCCGGAGTA	TCGGGGAGAG	GATGGTGTCA	GAGTGGGGAG	AATATCCTTT	750
	AATAATATAT	CAGCGATACT	GGGTACTGTG	GCCGTTATAC	TGAATTGCCA	800
	TCATCAGGGG	GCGCGTTCTG	TTCGCGCCGT	GAATGAAGAG	AGTCAACCAG	850
	AATGTCAGAT	AACTGGCGAC	AGGCCCGTTA	TAAAAATAAA	CAATACATTA	900
	TGGGAAAGTA	ATACAGCTGC	AGCGTTTCTG	AACAGAAAGT	CACAGTTTTT	950
15	ATATACAACG	GGTAAATAAA	GGAGTTAAGT	ATGAAGAAGA	TGTTTATGGC	1000
	GGTTTTATTT	GCATTAGTTT	CTGTTAATGC	AATGGCGGCG	GATTGTGCTA	1050
	AAGGTAAAT	TGAGTTTTCC	AAGTATAATG	AGGATGACAC	ATTTACAGTG	1100
	AAGGTTGACG	GGAAAGAATA	CTGGACCAGT	CGCTGGAATC	TGCAACCGTT	1150
	ACTGCAAAGT	GCTCAGCTGA	CAGGAATGAC	TGTCACAATC	AAATCCAGTA	1200
20	CCTGTGAATC	AGGCTCCGGA	TTTGCTGAAG	TGCAGTTTAA	TAATGACTGA	1250
	GGCATAACC					1259

25 2) INFORMATION FOR SEQ ID NO: 1078

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1079

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

19

55

2) INFORMATION FOR SEQ ID NO: 1080

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases

60

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080

10 TATAGCTACT GTCACCAGAC AATGT 25

2) INFORMATION FOR SEQ ID NO: 1081

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081

25 ATGTCAGAGG GATAGATCCA 20

2) INFORMATION FOR SEQ ID NO: 1082

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082

40 TTGARCRAAA TAATTTATAT GTG 23

45 2) INFORMATION FOR SEQ ID NO: 1083

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

TGATGATGRC AATTCAGTAT 20

60

2) INFORMATION FOR SEQ ID NO: 1084

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

15

2) INFORMATION FOR SEQ ID NO: 1085

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GTCCTGTGC GTGG

34

30

2) INFORMATION FOR SEQ ID NO: 1086

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

45 CTACTCCCGC CTTTGGGTT

20

50

2) INFORMATION FOR SEQ ID NO: 1087

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

60

5 2) INFORMATION FOR SEQ ID NO: 1088

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

20

2) INFORMATION FOR SEQ ID NO: 1089

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1090

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

AATAGCGCGG ACGAATTGGA C

21

50

2) INFORMATION FOR SEQ ID NO: 1091

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

5 AACGCGGCAC TGTTTCCCAA

20

2) INFORMATION FOR SEQ ID NO: 1092

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

20

TCGGCAAGAC AATATGACAG C

21

25 2) INFORMATION FOR SEQ ID NO: 1093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSsa-165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

40

TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
CGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACCTGCTT	200
45	TTTTAAAGTA	TAGGTATAAA	ATACAATTGA	TTAAAATAGT	250
AATCATGAAA	CAATTAACCTA	AGCCTTTATA	CTTTTACCTA	TTACTTTTTA	300
TTACAACAAC	ACTGATTGGC	GCGTTACTAT	TATATTTGCC	AATCACAGGT	350
AAACATCCTA	TTGATTTTGT	GGACGCCCGT	T		381

50

2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

GGTAAAACAG GTACTTCTAA CTA

23

5

2) INFORMATION FOR SEQ ID NO: 1095

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

20 CGATAGAAGC AGCAGGACAA

20

2) INFORMATION FOR SEQ ID NO: 1096

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

40

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAG GGATCACWAA AGTMAC

26

55

2) INFORMATION FOR SEQ ID NO: 1098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases

60

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098

10 TCTTCAAAT CGAAAAGCC GTC 23

2) INFORMATION FOR SEQ ID NO: 1099

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099

25 TCAAAGGGA TCACWAAAGT MAC 23

2) INFORMATION FOR SEQ ID NO: 1100

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100

40 GTAAAKCCCG GCATRGTRTT GATTTC 26

2) INFORMATION FOR SEQ ID NO: 1101

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

55 GACGGYTTTT TYGATTTTGA AGA 23

60 2) INFORMATION FOR SEQ ID NO: 1102

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAG ACC

23

15

2) INFORMATION FOR SEQ ID NO: 1103

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

20

30

2) INFORMATION FOR SEQ ID NO: 1104

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

GGATCAACAC AGTAGAACCG

20

45

2) INFORMATION FOR SEQ ID NO: 1105

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

50 CTCCTACGAT TCTCTTGAYA AATCA

25

2) INFORMATION FOR SEQ ID NO: 1106

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

15

CAACCGATCT CAACACCGGC AAT

23

20 2) INFORMATION FOR SEQ ID NO: 1107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

30

CTCATTTGAC TTCCTCCTTT GCT

23

35

2) INFORMATION FOR SEQ ID NO: 1108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

45

GTAAGAATCG GAAAAGCGGA AGG

23

50

2) INFORMATION FOR SEQ ID NO: 1109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

ACATCGTGAT CGCTAAAAGG AGC

23

2) INFORMATION FOR SEQ ID NO: 1110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

ACGAGAAAGA CAACAGGAAG ACC

23

2) INFORMATION FOR SEQ ID NO: 1111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

CTTTTCCGG CTCGWYTTCC TGATG

25

2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

GGCTGYGATA TTCAAAGCTC

20

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

10

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

25

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

TTTCGGGCTG TGAGGTCGGB TGHGCG

26

40

2) INFORMATION FOR SEQ ID NO: 1116

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

55

2) INFORMATION FOR SEQ ID NO: 1117

60

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: 94
 (C) ACCESSION NUMBER: U94526
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

	AAATTCGATC	CGCACTACAT	CGGAATTACA	AAAAACGGTG	TATGGAAGCT	50
	ATGCAAGAAG	CCATGTACGG	AATGGGAAGC	CGACAGTCTC	CCCGCCATAC	100
	TCTCCCCGGA	TAGGAAAACG	CATGGGCTGC	TTGTCATGAA	AGAAAGCGAA	150
20	TACGAAACAC	GGCGTATTGA	TGTGGCTTTC	CCGGTTTTGC	ATGGCAAATG	200
	CGGGGAGGAT	GGTGGCATA	AGGGGCTGTT	TGTATTGTCT	GGTATCCCCT	250
	ATGTGGGCTG	TGATATTCAA	AGCTCCGCAG	CTTGCATGGA	CAAATCACTG	300
	GCCTACATTC	TTACAAAAAA	TGCGGGCATC	GCCGTTCCCG	AATTTCAAAT	350
	GATTGATAAA	GGTGACAAGC	CGGAGGCGGG	TGCGCTTACC	TACCCTGTCT	400
25	TTGTGAAGCC	GGCACGGTCA	GGTTCGTCCT	TTGGCGTAAC	CAAAGTAAAC	450
	GGTACGGAAG	AACTTAACGC	TGCGATAGAA	GCGGCAGGAC	AATATGATGG	500
	AAAAATCTTA	ATTGAGCAAG	CGATTTCCGG	CTGTGAGGTC	GGGTGTGCGG	550
	TCATGGGGAA	CGAGGATGAT	TTGATTGTCG	GCGAAGTGGA	TCAAATCCGG	600
	CTGAGCCACG	GTATCTTCCG	CATCCATCAG	GAAAACGAGC	CGGAAAAAGG	650
30	CTCAGAAAAT	GCGATGATTA	CAGTTCCCCG	AGACATTCCG	GTCGAGGAAC	700
	GAAATCGGGT	GCAGGAAACG	GCAAAGAAAG	TATATCGGGT	GCTTGGATGC	750
	AGAGGGCTTG	CCCGTGTTGA	TCTTTTTTTT	G		800
	T					801

35

2) INFORMATION FOR SEQ ID NO: 1118

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

TTTTCWGAGC CTTTTTCCGG CTCG 24

50

2) INFORMATION FOR SEQ ID NO: 1119

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119

5 TTTCGGGCTG TGAGGTCGGB TGHGC 25

2) INFORMATION FOR SEQ ID NO: 1120

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120

20

TTTCGGGCTG TGAGGTCGGB TGHG 24

25 2) INFORMATION FOR SEQ ID NO: 1121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121

TGTTTGWATT GTCYGGYATC CC 22

40

2) INFORMATION FOR SEQ ID NO: 1122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

TGGTGCATTG CTACGTGG 18

55

2) INFORMATION FOR SEQ ID NO: 1123

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

10 TTTCGGGCTG TGAGGTCGGB TG 22

2) INFORMATION FOR SEQ ID NO: 1124

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

25 GATTGTGRTCC ACYTCGCCRA CA 22

2) INFORMATION FOR SEQ ID NO: 1125

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

40 ACTCACAAC TGGGATGGATG 20

45 2) INFORMATION FOR SEQ ID NO: 1126

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

60 TTATGGTTGT GCTGGTTGAG G 21

2) INFORMATION FOR SEQ ID NO: 1127

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA 20

15

2) INFORMATION FOR SEQ ID NO: 1128

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA 20

30

2) INFORMATION FOR SEQ ID NO: 1129

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

45 ATGATGACHG AMATGATGAA AAC 23

2) INFORMATION FOR SEQ ID NO: 1130

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130

60

5 2) INFORMATION FOR SEQ ID NO: 1131

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131

CATCTGGAGC TACRTARCCA GT

22

20

2) INFORMATION FOR SEQ ID NO: 1132

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132

AGTGAAAARA TGGCTGCTGC

20

35

2) INFORMATION FOR SEQ ID NO: 1133

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133

CATCAAGAAC ACTGGCTAYG TAG

23

50

2) INFORMATION FOR SEQ ID NO: 1134

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

5 CTAGATAGAG CTAAACCTT CCT 23

2) INFORMATION FOR SEQ ID NO: 1135

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

20

CATTATGCAA ACGCCATTTC AAG 23

25 2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

ACTTGTCCAC GTTSGATRTC T 21

40

2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

AATTAATGGC TGCWGTGAY GAA 23

55

2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 1032 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*
 (C) ACCESSION NUMBER: M75132

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

	ATGAAAAAAA	TTGCCGTTTT	ATTTGGAGGG	AATTCTCCAG	AATACTCAGT	50
	GTCACATAACC	TCAGCAGCAA	GTGTGATCCA	AGCTATTGAC	CCGCTGAAAT	100
15	ATGAAGTAAT	GACCATTGGC	ATCGCACCAA	CAATGGATTG	GTATTGGTAT	150
	CAAGGAAACC	TCGCGAATGT	TCGCAATGAT	ACTTGGCTAG	AAGATCACAA	200
	AAACTGTCAC	CAGCTGACTT	TTTCTAGCCA	AGGATTATA	TTAGGAGAAA	250
	AACGAATCGT	CCCTGATGTC	CTCTTTCCAG	TCTTGCATGG	GAAGTATGGC	300
	GAGGATGGCT	GTATCCAAGG	ACTGCTTGAA	CTAATGAACC	TGCCTTATGT	350
20	TGGTTGCCAT	GTCGCTGCCT	CCGCATTATG	TATGAACAAA	TGGCTCTTGC	400
	ATCAACTTGC	TGATAACCATG	GGAATCGCTA	GTGCTCCAC	TTTGCTTTTA	450
	TCCCCTATG	AAAACGATCC	TGCCACAATC	GATCGTTTTA	TTCAAGACCA	500
	TGGATTCCCG	ATCTTTATCA	AGCCGAATGA	AGCCGGTCT	TCAAAAGGGA	550
	TCACAAAAGT	AACTGACAAA	ACAGCGCTCC	AATCTGCATT	AACGACTGCT	600
25	TTTGCTTACG	GTTCTACTGT	GTTGATCCAA	AAGGCGATAG	CGGGTATTGA	650
	AATTGGCTGC	GGCATCTTAG	GAAATGAGCA	ATTGACGATT	GGTGCTTGTG	700
	ATGCGATTTT	TCTTGTCGAC	GGTTTTTTTG	ATTTTGAAGA	GAAATACCAA	750
	TTAATCAGCG	CCACGATCAC	TGTCCCAGCA	CCATTGCCTC	TCGCGCTTGA	800
	ATCACAGATC	AAGGAGCAGG	CACAGCTGCT	TTATCGAAAC	TTGGGATTGA	850
30	CGGGTCTGGC	TGAATCGAT	TTTTTCGTCA	CCAATCAAGG	AGCGATTTAT	900
	TTAAACGAAA	TCAACACCAT	GCCGGGATTT	ACTGGGCACT	CCCGCTACCC	950
	AGCTATGATG	GCGGAAGTCG	GGTTATCCTA	CGAAATATTA	GTAAGAGCAAT	1000
	TGATTGCACT	GGCAGAGGAG	GACAAACGAT	GA		1032

35

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1768 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: X56895

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

	GATATCGTTA	CGCTTCATGT	GCCGCTCAAT	ACGGATACGC	ACTATATTAT	50
55	CAGCCACGAA	CAAATACAGA	GAATGAAGCA	AGGAGCATTT	CTTATCAATA	100
	CTGGGCGCGG	TCCACTTGTA	GATACCTATG	AGTTGGTTAA	AGCATTAGAA	150
	AACGGGAAAC	TGGGCGGTGC	CGCATTTGAT	GTATTGGAAG	GAGAGGAAGA	200
	GTTTTTCTAC	TCTGATTGCA	CCCAAAAACC	AATTGATAAT	CAATTTTAC	250
	TTAAACTTCA	AAGAATGCCT	AACGTGATAA	TCACACCGCA	TACGGCCTAT	300
60	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAACTG	350

	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	400
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	450
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	500
	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	550
5	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	600
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	650
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	700
	CAAGGTCGTG	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	750
	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	800
10	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	850
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	900
	AGGCTCATCC	TTCCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	950
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	1000
	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	1050
15	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	1100
	GTATTCATCA	GGAAGTCGAG	CCGGA AAAAG	GCTCTGAAAA	CGCAGTTATA	1150
	ACCGTTCCCC	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	1200
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	1250
	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1300
20	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1350
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1400
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTTAGAT	GAAATAGTAC	1450
	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1500
	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAGTT	1550
25	GGCTGAATCG	CTTTTGAAGG	CAAAAGA AACT	GGCTGCTACC	CAAGGGTACG	1600
	GATTGCTTCT	ATGGGACGGT	TACCGTCCTA	AGCGTGCTGT	AAACTGTTTT	1650
	ATGCAATGGG	CTGCACAGCC	GGAAAATAAC	CTGACAAAGG	AAAGTTATTA	1700
	TCCCAATATT	GACCGAACTG	AGATGATTTC	AAAAGGATAC	GTGGCTTCAA	1750
	AATCAAGCCA	TAGCCGCG				1768
30						

2) INFORMATION FOR SEQ ID NO: 1140

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1086 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus casseliflavus*
 - 45 (C) ACCESSION NUMBER: L29638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

	GTAAGAATCG	GAAAAGCGGA	AGGAAGAAAA	ACATGAAAAA	AATCGCCATT	50
50	ATTTTTGGAG	GCAATTCACC	GGAATACACC	GTTTCTTTAG	CTTCAGCAAC	100
	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	CTATGACTAC	GACCTCTCTT	150
	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	GGTACTTGTA	TACAGGAGAA	200
	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	TTGGATACGA	AACATAAACA	250
	GAAAATACAG	CCGCTATTCT	AAGGAAACGG	CTTTTGGCTA	AGTGAAGAGC	300
55	AGCAAACGTT	GGTACCTGAT	GTTTTATTTT	CCATTATGCA	TGGCAAATAC	350
	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	GAATTGATGA	AGCTGCCTTA	400
	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	ATGTATGAAC	AAATGGCTGC	450
	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	AAAGTGCTCC	TACGATTCTC	500
	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	ATCGAAGCTT	TTATCCAGAC	550
60	CCATGGCTTC	CCAGTTTTCT	TTAAGCCTAA	TGAAGCGGGC	TCCTCAAAAG	600

	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	TCGCTTCTGC	CTTAAAAGAA	650
	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	CAAAAAAATA	TTGCCGGTGT	700
	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	CTCTTTGACT	GTCGGTGCTT	750
	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	TCGATTTTGA	AGAAAAGTAC	800
5	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	GCGCCATTGC	CTGAAACGAT	850
	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	GCTCTATCGT	AGTCTTGCTC	900
	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	TCACGGAGCG	AGGAGAACTA	950
	TACTTGAATG	AAATCAATAC	TATGCCGGGC	TTTACGAGTC	ACTCCCGCTA	1000
	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	CTATCAAGAA	CTACTACAAA	1050
10	AACTGCTTGT	CTTAGCAAAG	GAGGAAGTCA	AATGAG		1086

2) INFORMATION FOR SEQ ID NO: 1141

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3946 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 25 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: extracted from M97297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

30	ATGAATAACA	TCGGCATTAC	TGTTTATGGA	TGTGAGCAGG	ATGAGGCAGA	50
	TGCATTCCAT	GCTCTTTCGC	CTCGCTTTGG	CGTTATGGCA	ACGATAATTA	100
	ACGCCAACGT	GTCGGAATCC	AACGCCAAAT	CCGCGCCTTT	CAATCAATGT	150
	ATCAGTGTGG	GACATAAATC	AGAGATTTCC	GCCTCTATTC	TTCTTGCGCT	200
	GAAGAGAGCC	GGTGTGAAAT	ATATTTCTAC	CCGAAGCATC	GGCTGCAATC	250
35	ATATAGATAC	AACTGCTGCT	AAGAGAATGG	GCATCACTGT	CGACAATGTG	300
	GCGTACTCGC	CGGATAGCGT	TGCCGATTAT	ACTATGATGC	TAATTCTTAT	350
	GGCAGTACGC	AACGTAAAAT	CGATTGTGCG	CTCTGTGGAA	AAACATGATT	400
	TCAGGTTGGA	CAGCGACCGT	GGCAAAGTAC	TCAGCGACAT	GACAGTTGGT	450
	GTGGTGGGAA	CGGGCCAGAT	AGGCAAAGCG	GTTATTGAGC	GGCTGCGAGG	500
40	ATTTGGATGT	AAAGTGTTGG	CTTATAGTCG	CAGCCGAAGT	ATAGAGGTAA	550
	ACTATGTACC	GTTTGATGAG	TTGCTGCAAA	ATAGCGATAT	CGTTACGCTT	600
	CATGTGCCGC	TCAATACGGA	TACGCACTAT	ATTATCAGCC	ACGAACAAAT	650
	ACAGAGAATG	AAGCAAGGAG	CATTTCTTAT	CAATACTGGG	CGCGGTCCAC	700
	TTGTAGATAC	CTATGAGTTG	GTAAAGCAT	TAGAAAACGG	GAAACTGGGC	750
45	GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
	TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
	TGCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
	TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAAG	950
	GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
50	TCAGAGGAGC	ATGACGTATC	GGTAAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
	CATTAATAAA	GAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
	GTGTATGGAA	AATGTGCGAA	AAACCTTGCG	CGGAATGGGA	AAACGACAAT	1150
	TGCTATT CAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
	TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
55	CTTTGCATGG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTTGAA	1300
	TTGTCCGGTA	TCCCTTTTGT	AGGCTGCGAT	ATTCAAAGCT	CAGCAATTTG	1350
	TATGGACAAA	TCGTTGACAT	ACATCGTTGC	GAAAAATGCT	GGGATAGCTA	1400
	CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
	TTTACCTATC	CTGTTTTTGT	TAAGCCGGCG	CGTTCAGGCT	CATCCTTCGG	1500
60	TGTGAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550

	CAAGACAATA	TGACAGCAAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
	GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCGCGTTAG	TTGTTGGCGA	1650
	GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCGTATT	CATCAGGAAG	1700
	TCGAGCCGGA	AAAAGGCTCT	GAAAACGCAG	TTATAACCGT	TCCCGCAGAC	1750
5	CTTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
	TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCC	TGTGGATATG	TTTTTACAAG	1850
	ATAACGGCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
	TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
	CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTTAAAGGGG	TGATAAGCAT	2000
10	GGAAATAGGA	TTTACTTTTT	TAGATGAAAT	AGTACACGGT	GTTTCGTTGGG	2050
	ACGCTAAATA	TGCCACTTGG	GATAATTTCA	CCGGAACACC	GGTTGACGGT	2100
	TATGAAGTAA	ATCGCATTGT	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
	GAAGGCAAAA	GAAGTGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
	ACGGTTACCG	TCCTAAGCGT	GCTGTAAACT	GTTTTATGCA	ATGGGCTGCA	2250
15	CAGCCGGA	ATAACCTGAC	AAAGGAAAGT	TATTATCCCA	ATATTGACCG	2300
	AACTGAGATG	ATTTCAAAG	GATACGTGGC	TTCAAATCA	AGCCATAGCC	2350
	GCGGCAGTGC	CATTGATCTT	ACGCTTTATC	GATTAGACAC	GGGTGAGCTT	2400
	GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
	GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCCT	2500
20	CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
	TATGTATTAA	GAGACGAACC	ATACCCAAT	AGCTATTTTG	ATTTCCCCGT	2600
	TAAATAAACT	TTTAACCGTT	GCACGGACAA	ACTATATAAG	CTAACTCTTT	2650
	CGGCAGGAAA	CCCGACGTAT	GTAAGTGGTT	CTTAGGGAAT	TTATATATAG	2700
	TAGATAGTAT	TGAAGATGTA	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	2750
25	GTGCGCTGCG	GCAAGATAGC	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	2800
	GGTATTTTAC	ACCGCCCAT	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	2850
	AGCATGGGTA	TCACCTATGA	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	2900
	TCCAGTAGGG	CGAAATAATT	GACTGTAATT	TACGGGGCAA	AACGGCACAA	2950
	TCTCAAACGA	GATTGTGCCG	TTTAAGGGGA	AGATTCTAGA	AATATTTTCAT	3000
30	ACTTCCAAT	ATATAGTTAA	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	3050
	TTTTTATTGTT	ATTGTTATTC	TTAATATACT	TAGGTTATGA	CTACGTTAAT	3100
	GAAGCACTGT	TTTCTCAGGA	AAAAGTCGAA	TTTCAAAATT	ATGATCAAAA	3150
	TCCCAAAGAA	CATTTAGAAA	ATAGTGGGAC	TTCTGAAAAT	ACCCAAGAGA	3200
	AAACAATTAC	AGAAGAACAG	GTTTATCAAG	GAAATCTGCT	ATTAATCAAT	3250
35	AGTAAATATC	CTGTTCCGCA	AGAAAGTGTG	AAGTCAGATA	TCGTGAATTT	3300
	ATCTAAACAT	GACGAATTAA	TAAATGGATA	CGGGTTGCTT	GATAGTAATA	3350
	TTTATATGTC	AAAAGAAATA	GCACAAAAT	TTTCAGAGAT	GGTCAATGAT	3400
	GCTGTAAAGG	GTGGCGTTAG	TCATTTTATT	ATTAATAGTG	GCTATCGAGA	3450
	CTTTGATGAG	CAAAGTGTGC	TTTACCAAGA	AATGGGGGCT	GAGTATGCCT	3500
40	TACCAGCAGG	TTATAGTGAG	CATAATTCAG	GTTTATCACT	AGATGTAGGA	3550
	TCAAGCTTGA	CGAAATGGA	ACGAGCCCT	GAAGGAAAGT	GGATAGAAGA	3600
	AAATGCTTGG	AAATACGGGT	TCATTTTACG	TTATCCAGAG	GACAAAACAG	3650
	AGTTAACAGG	AATTCAATAT	GAACCATGGC	ATATTTCGCTA	TGTTGGTTTA	3700
	CCACATAGTG	CGATTATGAA	AGAAAAGAAT	TTCGTTCTCG	AGGAATATAT	3750
45	GGATTACCTA	AAAGAAGAAA	AAACCATTTC	TGTTAGTGTA	AATGGGGAAA	3800
	AATATGAGAT	CTTTTATTAT	CCTGTACTA	AAAATACCAC	CATTCATGTG	3850
	CCGACTAATC	TTCGTTATGA	GATATCAGGA	AACAATATAG	ACGGTGTAAT	3900
	TGTGACAGTG	TTTCCCGGAT	CAACACATAC	TAATTCAAGG	AGGTAA	3946

50

2) INFORMATION FOR SEQ ID NO: 1142

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

5

2) INFORMATION FOR SEQ ID NO: 1143

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

20 CAATTAGCTT AGCAATAGGT GTTGG

25

2) INFORMATION FOR SEQ ID NO: 1144

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

35

TGTYTTCCAA GGTTTCAGCTC

20

40 2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

AACATATTKG GTTGATAGGT

20

55

2) INFORMATION FOR SEQ ID NO: 1146

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

60

(B) TYPE: Nucleic acid

633

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

GGGATTACCT ATGCCAATAT GAT

23

10

2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

AGCTGTGTTA GCVCGAACAT CTTG

24

25

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

40

GACTTTGT TT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149

55

TCCYACWATT TCTTTTGWG

20

60 2) INFORMATION FOR SEQ ID NO: 1150

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150

TGATAATCAC ACCGCATACG

20

15

2) INFORMATION FOR SEQ ID NO: 1151

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151

TGCTGTCATA TTGTCTTGCC

20

30

2) INFORMATION FOR SEQ ID NO: 1152

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

20

45

2) INFORMATION FOR SEQ ID NO: 1153

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

60 CTCGTATGTC CCTACAATGC

20

2) INFORMATION FOR SEQ ID NO: 1154

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

15

GTTTGAAGCA TATAGCCTCG

20

20 2) INFORMATION FOR SEQ ID NO: 1155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

30

CAGTGCTTCA TTAACGTAGT C

21

35

2) INFORMATION FOR SEQ ID NO: 1156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

45

GTTGAAATGC ATCACGAACA ATT

23

50

2) INFORMATION FOR SEQ ID NO: 1157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

AAGAACGTTT CAGTTAAGGA AAT

23

5

2) INFORMATION FOR SEQ ID NO: 1158

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

20 AAGAGGTAAT GTCTGTGGT

19

2) INFORMATION FOR SEQ ID NO: 1159

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

35

TGAAGGTTTG CCAGGTGA

18

40 2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

CGTTTCTGTT AAAGAAATTA GAAG

24

55

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

10

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

25

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

40

GTTGGTTTCA ACGTTAAGAA C

21

2) INFORMATION FOR SEQ ID NO: 1164

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

55

GGTTTCAACG TCAAGAAC

18

60 2) INFORMATION FOR SEQ ID NO: 1165

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

GGTTTCAACG TGAAGAAC

18

15

2) INFORMATION FOR SEQ ID NO: 1166

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

ACGTTAAGAA TGTTTCTGTC AA

22

30

2) INFORMATION FOR SEQ ID NO: 1167

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 14 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

14

45

2) INFORMATION FOR SEQ ID NO: 1168

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

60 GAACAATTGG TTGAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1169

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: SP-665
(C) ACCESSION NUMBER: AF139883

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

20

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50	
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100	
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150	
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200	
25	TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	250	
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300	
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350	
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400	
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450	
30	GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550	
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600	
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650	
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700	
35	CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800	
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850	
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900	
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCCGA	950	
40	TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCTG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACCTGGAGC	TCGTCACCAA	1050	
GCAAGTAAAC	TTTCATTG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100	
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150	
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200	
45	TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTCCG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300	
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350	
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400	
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450	
50	CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550	
TGTCGGAAC	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600	
TGATGAAAAC	AGTCTTGACT	TATGGAAC	GGCGTGAGC	CTATCTTCCT	1650	
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700	
55	AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTTCG	1800	
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCCTAGTTG	CAGCTAAAGT	1850	
TTATCGTCAA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900	
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTTGT	ATTCAAAAAT	1950	
60	GGAGCTCGCC	CAATATGGAC	TGAACCTCT	ACTCAACAAT	CCTCAACAGC	2000

TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

5

2) INFORMATION FOR SEQ ID NO: 1170

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

20 ACGAATTGGA CTACGCAATT

20

2) INFORMATION FOR SEQ ID NO: 1171

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

35

ACGAGGATGA TTTGATTGTC

20

40 2) INFORMATION FOR SEQ ID NO: 1172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 64147
- (C) ACCESSION NUMBER: X13136

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

GATCCTCTAA	ATGATTCTCA	GGTGGCTGTT	ATTGCCTCTA	TTTCAAAGGA	50
GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	GGATAGAAAG	GTTTTGGAAA	100
CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	CCAGTGAAAA	AGCTGGTCTC	150
60 CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	AAAGGCTATT	CTCTAAATGA	200

	CCGTGTAGGA	ACCTCCTATT	TGGAAAAGCA	ATATGAAGAG	ACCTTACAAG	250
	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	ACAAATATGG	CAACATGGAA	300
	AGCGTGATA	CAATTGAGGA	AGGTAGTAAG	GGAAACAATA	TCAAGCTGAC	350
	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	TGCTTTGCTG	AAAAGTTATT	400
5	TCAATTCAGA	GTTGGGAAAT	GGTGGAGCCA	AGTATTCTGA	AGGTGTCTAT	450
	GCAGTCGCCC	TTAACCCAAA	AACAGGTGCT	GTTTTGTCTA	TGTCAGGAAT	500
	TAAACATGAC	TTGAAAACAG	GAGAGTTGAC	GCCGGATTCC	TTGGGAACGG	550
	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	TCAAAGCAGC	GACCATCAGC	600
	TCTGGTTGGG	AAAATGGAGT	CTTGTGAGGA	AATCAGACCT	TGACAGACCA	650
10	GTCCATTGTC	TTTCAAGGTT	CAGCTCCAAT	TAATTCTTGG	TATCCTGCCT	700
	TTTCTAGACC	AATGCCGATT	ACGGCGGTTT	AGGCTCTAGA	GTATTCATCC	750
	AATGCTTATA	TGGTCCAAAC	AGCCCTAGGT	CTTATGGGGC	AGACCTATCA	800
	ACCCAATATG	TTTGTGCGCA	CCAGCAATCT	AGAGTCTGCT	ATGGGGAAAT	850
	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	GTTCTGCGAC	CGGAATTGAC	900
15	CTACCAGATG	AATCTACTGG	ATTTGTTCCT	AAAGAGTATA	GCTTTGCTAA	950
	TTTCATTACC	AATGCCTTTG	GGCAGTTTGA	TAAGTATACG	CCGATGCAGT	1000
	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	ATGGTGTTCT	TGTGGCTCCT	1050
	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	GATAAGGGAG	GACTGGGTGA	1100
	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	GAATAAGGTC	AATATATCCG	1150
20	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	TTTATCAGGT	TGCCCATGGT	1200
	ACTAGTGAAT	TGACAACTGG	ACGTGCCTTT	TCAAATGGCG	CCTTGGTATC	1250
	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	CTATGTGGCA	GATGGTCAGC	1300
	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	CCCCATCTGA	TAATCCCCAA	1350
	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	ACCAACCTTA	CAAATGGTGT	1400
25	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	CCTCTATAAC	CAACATCATC	1450
	CAATGAATTA	GAAAGGAACA	TATGCTTTAT	CCAACACCTA	TTGCTAAGCT	1500
	AATTGACAGT	TATTCGAAGT	TACCGGGTAT	CGGGATTAAG	ACGGCTACCC	1550
	GTTTGGCCTT					1560

30

2) INFORMATION FOR SEQ ID NO: 1173

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2007 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: CS109
 (C) ACCESSION NUMBER: Z49096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

	GAGTCCCGAT	TGCTGAGGAT	GCAACCTCCT	ATAATGTCTA	TGCGGTCATT	50
50	GATGAGAACT	ATAAGTCAGC	AACGGGTAAG	ATTCTTTACG	TAGAAAAAAC	100
	ACAATTTAAC	AAGGTTGCAG	AGGTCTTTCA	TAAGTATCTG	GACATGGAAG	150
	AATCCTATGT	AAGAGAGCAA	CTCTCGCAAC	CTAATCTCAA	GCAAGTTTCC	200
	TTTGGAGCAA	AGGGAAATGG	GATTACCTAT	GCCAATATGA	TGACTATCAA	250
	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	300
55	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGTCTA	350
	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTGC	TGGGAACCTC	400
	TGGAATGGAG	AGTTCCCTGA	ACAGTATTCT	TGCAGGGACA	GACGGCACTA	450
	TTACCTATGA	AAAGGATCGT	CTGGGCAATA	TTGTACCCGG	AACAGAACTG	500
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	550
60	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	600

	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	650
	ATTCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	700
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	750
	AACCAGGATC	AGCCTTTAAG	GTCATGATGT	TAGCTTCTTC	TATTGATAAT	800
5	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	850
	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGAGGGTTTG	ACTACTGGTG	900
	GGATGATGAC	TTTCTCACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAACG	950
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTGGA	ATTATCTAAA	1000
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	1050
10	CTGGTCAACT	TCCAGCTGAT	AATATTGTAA	GTATTGCTCA	AAGCTCATTT	1100
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	1150
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAAATTTATA	AGTGCTATTT	1200
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1250
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1300
15	AGTTGGGACG	GACCCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1350
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1400
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1450
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1500
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1550
20	GGAGAATTTG	CCACCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1600
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1650
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1700
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1750
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1800
25	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1850
	AGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1900
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTGT	TCAGAAGCAA	GATGTTTCGA	1950
	CTAATACAGC	TATCAAAAAC	ATTAAAAAAA	TTAAATTAAC	TTTAGGAGAC	2000
	TAATATG					2007
30						

2) INFORMATION FOR SEQ ID NO: 1174

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

45 GAACGTGGTG AAGTTCGC

18

2) INFORMATION FOR SEQ ID NO: 1175

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

60

5 2) INFORMATION FOR SEQ ID NO: 1176

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

TACTGGTGTA GAAATGTTC

19

20

2) INFORMATION FOR SEQ ID NO: 1177

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

GCTCAACAAG TTCCAGATTA

20

35

2) INFORMATION FOR SEQ ID NO: 1178

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 2456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: NCTC8325
50 (C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

55	ATGAACTGAT TATACTTAAC ATTAAAAAAG ATGATAACAC CTTCTACACC	50
	TCCATATCAC AAAAATTAT AACATTATTT TGACATAAAT ACTACATTTG	100
	TAATATACTA CAAATGTAGT CTTATATAAG GAGGATATTG ATGAAAAAGA	150
	TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA	200
	TATTTTTTATG CTTCAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT	250
	TGAAGATAAA AATTTCAAAC AAGTTTATAA AGATAGCAGT TATATTTCTA	300
60	AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT	350

	AATAGTTT	AG	CGTTAA	GA	TATAAA	CATT	CAGGAT	CGTA	AAATAA	AAAAA	400
	AGTATCT	AAA	AATAAA	AAAC	GAGTAG	ATGC	TCAATA	TATAAA	ATTAAA	ACAA	450
	ACTACGG	TAA	CATTGA	TCGC	AACGTT	CAAT	TTAATT	TTTGT	TAAAGA	AAGAT	500
	GGTATGT	GGA	AGTTAG	ATTG	GGATCA	TAGC	GTCATT	TATTC	CAGGA	ATGCA	550
5	GAAAGAC	CAA	AGCATAC	ATA	TTGAAA	ATTT	AAAATC	AGAA	CGTGG	TAAAA	600
	TTTTAG	ACCG	AAACA	ATGTG	GAATTG	GCCA	ATACAG	GGAAC	ACATAT	GAGA	650
	TTAGGC	ATCG	TTCCAA	AGAA	TGTATC	TAAA	AAAGAT	TATA	AAGCA	ATCGC	700
	TAAAGA	ACTA	AGTATTT	CTG	AAGACT	TATAT	CAACA	ACAAA	TGGAT	CAAAA	750
	TTGGGT	TACAA	GATGAT	ACCT	TCGTT	CCACT	TTAAAA	ACCGT	TAAAA	AAATG	800
10	GATGA	ATATT	TAAGTG	ATTT	CGCAAA	AAAAA	TTTCAT	CTTA	CAACT	AATGA	850
	AACAG	AAAGT	CGTAA	CTATC	CTCTA	GAAAA	AGCGAC	TTCA	CATCT	ATTAG	900
	GTTAT	GTTGG	TCCC	ATTAAC	TCTGA	AGAAT	TAAAC	AAAAA	AGAAT	ATAAA	950
	GGCTAT	AAAG	ATGAT	GCAGT	TATTGG	TAAA	AAGGG	ACTCG	AAAA	ACTTTA	1000
	CGATA	AAAAAG	CTCCA	ACATG	AAGAT	GGCTA	TCGTG	TCACA	ATCGT	TGACG	1050
15	ATAAT	AGCAA	TACAAT	CGCA	CATAC	ATTAA	TAGAG	AAAAA	GAAAA	AAGAT	1100
	GGCAA	AGATA	TTCA	ACTAAC	TATTG	ATGCT	AAAGT	TCAAA	AGAGT	ATTTA	1150
	TAACA	ACATG	AAAA	ATGATT	ATGGC	TCAGG	TACTG	CTATC	CACCC	TCAAA	1200
	CAGGT	GAATT	ATTAG	CACTT	GTAAG	CACAC	CTTCAT	ATGA	CGTCT	ATCCA	1250
	TTATG	TATG	GCATG	AGTAA	CGAAG	AATAT	AATAA	ATTAA	CCGA	AGATAA	1300
20	AAAAG	AACCT	CTGCT	CAACA	AGTT	CCAGAT	TACA	ACTTCA	CCAGG	TTCAA	1350
	CTCA	AAAAAT	ATTA	ACAGCA	ATGAT	TGGGT	TAAAT	AACAA	AACAT	TAGAC	1400
	GATA	AAACAA	GTTAT	AAAAAT	CGAT	GGTAAA	GGTT	GCAAA	AAGAT	AAATC	1450
	TTGGG	TGGT	TACA	ACGTTA	CAAG	ATATGA	AGTGG	TAAAT	GGTAA	TATCG	1500
	ACTTA	AAACA	AGCA	ATAGAA	TCAT	CAGATA	ACATTT	TCTT	TGCT	AGAGTA	1550
25	GCACT	CGAAT	TAGG	CAGTAA	GAAAT	TTGAA	AAAGG	CATGA	AAAA	ACTAGG	1600
	TGTTG	TGAA	GATAT	ACCAA	GTGAT	TATCC	ATTTT	TATAAT	GCTCA	AATTT	1650
	CAAAC	AAAAA	TTTAG	ATAAT	GAAAT	ATTAT	TAGCT	GATTC	AGGTT	ACGGA	1700
	CAAGG	TGAAA	TACTG	ATTAA	CCCAG	TACAG	ATCCT	TTCAA	TCTAT	AGCGC	1750
	ATTAG	AAAAT	AATGG	CAATA	TTAAC	GCACC	TCACT	TATTA	AAAG	ACACGA	1800
30	AAAAC	AAAGT	TTGGA	AAGAAA	AATAT	TATTT	CCAA	AGAAAA	TATCA	ATCTA	1850
	TTAA	ATGATG	GTATG	CAACA	AGTCG	TAAAT	AAAAC	ACATA	AAGA	AGATAT	1900
	TTAT	AGATCT	TATG	CAAACT	TAATT	TGGCAA	ATCCG	GTA	CT	GCAGAACTCA	1950
	AAATG	AAACA	AGGAG	AAAGT	GGCAG	ACAAA	TTGGG	TGGT	TATAT	CATAT	2000
	GATA	AAGATA	ATCCA	AAACAT	GATG	ATGGCT	ATTA	ATGTTA	AAGAT	GTACA	2050
35	AGATA	AAGGA	ATGG	CTAGCT	ACAAT	GCCAA	AATCT	CAGGT	AAAGT	GTATG	2100
	ATGAG	CTATA	TGAGA	ACGGT	AATA	AAAAAT	ACGAT	ATAGA	TGAAT	AACAA	2150
	AACAG	TGAAG	CAATC	CGTAA	CGATG	GTTGC	TTCAC	TGTTT	TATT	TGAAT	2200
	TATTA	ATAAG	TGCTG	TTACT	TCTCC	CTTAA	ATACA	ATTTT	TTCAT	TTTCA	2250
	TTGT	ATGTTG	AAAGT	GACAC	TGTA	ACGAGT	CCATTT	TCTT	TTTT	TATGGA	2300
40	TTTCT	TATTTT	GTAAT	TTTCAG	CGATA	ACGTA	CAATG	TATTA	CCTGG	TATAC	2350
	AGTTT	AATAA	ATTTA	ACGTT	ATTC	ATTTGT	GTTCT	CGCTA	CAACT	TCTTC	2400
	TCCGT	ATTTA	CCTT	CCTTCTA	CCCATA	AATTT	AAATG	ATATT	GAAAG	TGTAT	2450
	GCATGC										2456

45

2) INFORMATION FOR SEQ ID NO: 1179

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

60 ATTTGGTGAC GGGTGACTTT

20

2) INFORMATION FOR SEQ ID NO: 1180

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180
15 TCCACCGTTG CCAATCGCA 19

2) INFORMATION FOR SEQ ID NO: 1181

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181
30 AGCAGCTTAC TAGATGCCGT 20

35 2) INFORMATION FOR SEQ ID NO: 1182

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182
AACTGCAAGA GATCCTTTGG 20

50 2) INFORMATION FOR SEQ ID NO: 1183

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2535 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: Genomic DNA
60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 175

(C) ACCESSION NUMBER: M18729

5

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	CAACAGTATG	TGGATATTAA	50
10	AAAGCAATAT	CCAGATGCTT	TTTTGCTCTT	TCGGATGGGT	GATTTTTATG	100
	AATTATTTTA	TGAGGATGCG	GTCAATGCTG	CGCAGATTCT	GGAAATTTCC	150
	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	CCGATCCCTA	TGGCGGGTGT	200
	TCCCTATCAT	TCTGCCCAAC	AGTATATCGA	TGTCTTGATT	GAGCAGGGTT	250
	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	ATCCTAAACA	AGCAGTTGGG	300
15	GTTGTAAAC	GAGAGGTTGT	TCAGGTCATT	ACGCCAGGGA	CAGTGGTCGA	350
	TAGCAGTAAG	CCGGACAGTC	AGAATAATTT	TTTGGTTTCC	ATAGACCGCG	400
	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	ATTTGGTGAC	GGGTGACTTT	450
	TATGTGACAG	GTCTTTTGGA	TTTCACGCTG	GTTTGTGGGG	AAATCCGTAA	500
	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	TGACTTGTCT	GAGGAAGAAG	550
20	AACAAATCCT	CAGCCGCCAG	ATGAATCTGG	TACTCTCTTA	TGAAAAAGAA	600
	AGCTTTGAAG	ACCTTCATTT	ATTGGATTTG	CGATTGGCAA	CGGTGGAGCA	650
	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	TCATCGGACT	CAGATGAGGG	700
	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	ACGAAATTAA	GGATTTCTTG	750
	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	AGAATGCTCG	800
25	CTCAGGTAAG	AAACAAGGCA	GTCTTTTCTG	GCTTTTGGAT	GAAACCAAAA	850
	CGGCTATGGG	GATGCGTCTC	TTGCGTTCTT	GGATTCATCG	CCCCTTGATT	900
	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	GTAGTGCAGG	TCTTTCTCGA	950
	CCATTTCTTT	GAGCGTAGTG	ACTTGACAGA	CAGTCTCAAG	GGTGTATTATG	1000
	ACATTGAGCG	CTTGGCTAGT	CGTGTCTCTT	TTGGCAAAAC	CAATCCAAAG	1050
30	GATCTCTTGC	AGTTGGCGAC	TACCTTGTCT	AGTGTGCCAC	GGATTTCGTGC	1100
	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	AGCCTATCTC	ATCGCACAAAC	1150
	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	TTAGCGCAGC	GATTGCTCCT	1200
	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	ATTATCCGGA	CTGGATTTGA	1250
	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	CAGAGAAGGG	ACTAGCTGGA	1300
35	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	ACTCTGGTAT	CAGCACGCTC	1350
	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	TATTTTCATG	TGACCAATTCT	1400
	GCAACTGGGA	AATGTGCCAG	CCCACTTTT	CCGCAAGGCG	ACGCTGAAAA	1450
	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	CCCGTATCGA	GGGAGATATG	1500
	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	GAATACGAAA	TATTTATGCG	1550
40	CATTCGTGAA	GAGGTCGGCA	AGTACATCCA	GCGTTTACAA	GCTCTAGCCC	1600
	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	GTCTGGCGGT	TGTGGCTGAA	1650
	ACCCAGCATT	TGATTCGACC	TGAGTTTGGT	GACGATTCAC	AAATTGATAT	1700
	CCGGAAAGGG	CGCCATGCTG	TCGTTGAAAA	GGTTATGGGG	GCTCAGACCT	1750
	ATATTCCAAA	TACGATTGAG	ATGGCAGAAG	ATACCAGTAT	TCAATTGGTT	1800
45	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	TATATGCGTC	AGTTAGCCAT	1850
	GACGGCGGTT	ATGGCCAGC	TGGGTTCTTA	TGTTCTTGCT	GAAAGCGCCC	1900
	ATTTACCGAT	TTTTGATGCG	ATTTTACCC	GTATCGGAGC	AGCAGATGAC	1950
	TTGGTTTCGG	GTCAGTCAAC	CTTTATGGTG	GAGATGATGG	AGGCCAATAA	2000
	TGCCATTTTC	CATGCGACCA	AGAACTCTCT	CATTCTCTTT	GATGAATTGG	2050
50	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	CTCTTGCTCA	GTCCATCATC	2100
	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	ACCCTCTTTG	CGACCCACTA	2150
	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	ACAACACTTG	GTCAATGTCC	2200
	ACGTGGCAAC	TTTGGAGCAG	GATGGGCAGG	TCACCTTCCT	TCACAAGATT	2250
	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	ATCCATGTTG	CCAAGATTGC	2300
55	TGGCTTGCCA	GCAGACCTTT	TAGCAAGGGC	GGATAAGATT	TTGACTCAGC	2350
	TAGAGAATCA	AGGAACAGAG	AGTCCTCCTC	CCATGAGACA	AACTAGTGCT	2400
	GTCAGTGAAC	AGATTTCACT	CTTTGATAGG	GCAGAAGAGC	ATCCTATCCT	2450
	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	TATGACACCT	ATGCAGGTTA	2500
	TGAATGTCTT	AGTAGAGTTA	AAACAGAAAC	TATAA		2535

60

2) INFORMATION FOR SEQ ID NO: 1184

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

15

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
20	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
25	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGATTTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
30	AAACCAATCC	AAAGGATCTC	TTG			623

2) INFORMATION FOR SEQ ID NO: 1185

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

50	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
55	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGATTTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
60	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550

CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC T 621

5

2) INFORMATION FOR SEQ ID NO: 1186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

20 (xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

TGACGGGTGA CTTTTATGTG ACAGGTCTTT TGGATTTTAC GCTGGTTTGT 50
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 25 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCAGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTGT 350
 GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400
 30 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTTGCGT TCTTGGATTCT 450
 ATCGCCCCCTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500
 CAGGTCTTTC TCGACCATT TTTGAGCGT AGTGACTTGA CAGACAGTCT 550
 CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC TT 622

35

2) INFORMATION FOR SEQ ID NO: 1187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

TGACGGGTGA CTTTTATGTG ACAGGTCTTT TGGATTTTAC GCTGGTTTGT 50
 55 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCGGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 60 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTGT 350

GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400
 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTTGCGT TCTTGGATTG 450
 ATCGCCCCCTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500
 CAGGTCTTTC TCGACCATTG CTTTGAGCGT AGTGACTTGA CAGACAGTCT 550
 5 CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC TT 622

10 2) INFORMATION FOR SEQ ID NO: 1188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

25 GGGTGACTTT TATGTAACGG GGCTATTGGA TTTCACGTTG GTTTGTGGGG 50
 AAATTTCGCA TCTCAAGGCT AGAGAAGTGG TGCTGGGTTA TGAATTGTCT 100
 GAGGAAGAAG AACAAATCCT CAGTCGTCAG ATGAATCTGG TGCTTTCTTA 150
 TGAGAAGGAA GGCTTTGAGG ACCTTCATTT ACTGGATCCA CGACTGGCAG 200
 30 CTGTGGAGCA AGCGGCAGCT AGTAAGCTCC TCCAGTATGT TCACCGGACC 250
 CAGATGCGGG AATTGAACCA CCTCAAACCA GTTATCCGCT ATGAAATCAA 300
 AGATTTCTTA CAGATGGACT ATGCGACCAA GGCTAGTCTG GATTTGTTG 350
 AGAATGCCCC TTCAGGCAAG AAGCAAGGCA GTCTTTTCTG GCTTTTAGAT 400
 GAAACCAAGA CGGCTATGGG AATGCGTCTC TTGCGTTCTT GGATTCATCG 450
 35 TCCTTTGATT GATAAGGAGC GAATCGTCCA CGGTCAAGAG GTGGTGCAGG 500
 TCTTTCTTGA CCACTTCTTT GAGCGTAGTG ATTTAACGGA CAGTCTTAAG 550
 GGTGTTTATG ATATCGAACG CTTGGCTAGT CGGGTTTCTT TTGGCAAGA 599

40 2) INFORMATION FOR SEQ ID NO: 1189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

55 (x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

GGTGACGGGT GACTTTTATG TGACAGGTCT TTTGGATTTT ACGCTGGTTT 50
 GTGGGGAAAT CCGCAATCTC AAGGCTCGAG AAGTGGTGCT GGGTTATGAC 100
 TTGTCTGAGG AAGAAGAACA GATCCTTAGT CGTCAGATGA ATCTGGTACT 150
 60 TTCCTATGAA AAAGAAGGCT TTGAAGACCT TCATTTACTG GATTCACGAT 200

TGGCAGCTGT GGAGCAAGCG GCATCTAGTA AACTGCTTCA GTATGTTTCAT 250
 CGGACTCAGA TGAGGGAATT GAACCACCTC AAGCCTGTTA TCCGCTATGA 300
 AATCAAAGAT TTTTTCGAGA TGGATTATGC GACCAAGGCT AGTCTGGATT 350
 TGGTTGAGAA TGCCCGTTCA GGCAAGAAGC AAGGTAGTCT TTTTTCGCTT 400
 5 TTGGATGAAA CCAAAACAGC TATGGGAATG CGTCTCTTGC GGTCTTGGAT 450
 TCATCGCCCC CTGATTGATA AGGAACGAAT TGTCCAACGC CAAGAAAGTTG 500
 TGCAGGTCTT TCTCGACCAT TTCTTTGAGC GTAGTGATTT GACAGACAGT 550
 CTAAGGGTG TTTATGACAT TGAGCGCTTG GCTAGTCGTG TTTCTTTTGG 600
 CAAAACCAAT CCAAAGGATC TCTT 624
 10

2) INFORMATION FOR SEQ ID NO: 1190

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 25 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

TGACGGGTGA CTTTCAGGTG ACTAGTTTGA AGGACTTTGT CTTGGTCTGC 50
 30 GGGGAAATCC GCAATTTGAA AGCTAGGGAA GTGGTGCTGG GCTATGCCTT 100
 GCCAGAAGCT GAGGAGCAGG TTTTGGCTGG ACAGATGAAC CTTTACTGT 150
 CCTATGTGGA GAAGGTTTTG GAGGATGTTC AGCTGCTGGG CGAGGAGCTG 200
 TCTCCTATGG AGCGTCAGGC AGCAGGGAAA CTGCTGGAGT ATGTGCACCG 250
 GACCCAGATG AGGGAGCTCA GCCATTTGAA GAAGGCTCAG CATTATGAAA 300
 35 TCAAGGACTT CCTGCAAATG GACTATGCCA CCAAGGCGAG TCTGGATTTG 350
 ACAGAAAATG CTCGCTCGGG CAAGAAGCAC GGCAGTCTTT ATTGGCTGAT 400
 GGACGAGACT AAGACGGCCA TGGGCGGCCG CATGCTGCGC TCTTGATCC 450
 AGCGTCCGCT GATTGATGAA GCGCGAATTA GCCAGCGACA GAATGTCGTT 500
 GAGGTTTTTC TGGATCATTT CTTTGAGCGG AGTGATTGA CGGAGAGCCT 550
 40 CAAGGGGGTC TATGATATCG AGCGGCTGGC TAGTCGGGTG TCTTTTGGC 599

2) INFORMATION FOR SEQ ID NO: 1191

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

60 TGACGGGTGA CTTTCAGGTG ACTAGTTTGA AGGACTTTGC CCTGGTCTGC 50

	GGGGAAATCC	GTAATTTGAA	GGCTAGGGAA	GTGGTGCTGG	GCTATGCTTT	100
	GCCAGAAGCT	GAGGAGCAGG	TCTTGGCTGG	ACAGATGAAT	CTTTTGCTGT	150
	CCTATGTACA	GACGGCCTTG	GACGATGTCC	AGCTGCTGGG	CGAGGAACTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCGGGGAAA	TTGCTAGAGT	ATGTGCACCG	250
5	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCCAG	CATTATGAAA	300
	TCAAGGACTT	TCTGCAAATG	GATTATGCTA	CCAAGGCGAG	TCTGGATTG	350
	ACAGAAAATG	CTCGCTCGGG	TAAGAAACAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACC	AAGACGGCCA	TGGGCGGCCG	TATGCTGCCG	TCTTGGATCC	450
	AGCGTCCGTT	GATTGATGAA	GTGCGAATTA	GCCAGCGGCA	GAATGTCGTC	500
10	GAGGTTTTTC	TGGAACATTT	CTTTGAGCGG	AGTGATTGTA	CGGAGAGCCT	550
	CAAGGGAGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGCA	600
	AGACCAATCC	AAAGGATCTC	TT			622

15

2) INFORMATION FOR SEQ ID NO: 1192

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

GGTAAAACAG GAACCTCTAA CT

22

30

2) INFORMATION FOR SEQ ID NO: 1193

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

GGTAAGACAG GTACTTCTAA CT

22

45

2) INFORMATION FOR SEQ ID NO: 1194

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

60

5 2) INFORMATION FOR SEQ ID NO: 1195

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

CATTTC AAGT AACACAACAG AATC

24

20

2) INFORMATION FOR SEQ ID NO: 1196

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTTC AAGT GTAATACAAC AGAA

24

35

2) INFORMATION FOR SEQ ID NO: 1197

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1198

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

```
10 AACGGGCGTC TCGATAGAAA AACACGTGAA AATCCCAATG ATTATAAACA      50
   ATCAATATAC GATTTTGCTG AAGCTGTAAC AAAAGGTATT AAGGAACAAA      100
   CAAATAAAAA TTAATAGGCA ACTTAACCAG AATCGTTAAA ACTATATGAC      150
   GATTCTGGTT TTTTAAATTC AAAAAGTTT CTAAAAAATT TACTTGCTTC      200
   TTAAAGTAT AGGTATGAAA TACAATTGAT TAAAATAGTA AAGGAAATGA      250
   ATCATGAAAC AATTAATAA GCCTTTATAC TTTTACCTAT TACTTTTAT      300
15  TACAACAACG CTGATTGGCG CGTTACTATT ATATTGCCA ATCACAKGTA      350
   AACATCCTAT TGATTTTGTG GACGCCCCGT A                          381
```

20 2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC 25

35 2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200

TCAAAGAAGA AACTAAAAAA GCTGT 25

50

2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201

AACGTAGGTG TCCTTCTTC

19

5

2) INFORMATION FOR SEQ ID NO: 1202

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202

20 GTGTTGAAAT GTCCGTAAA CA

22

2) INFORMATION FOR SEQ ID NO: 1203

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203

35

GGIGARMGIG GIAAYGARAT G

21

40 2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

55

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

50

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

10

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGHTIG ARTCIGCCA

19

25

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

40 CCITCITCWC CIGGCATYTC

20

2) INFORMATION FOR SEQ ID NO: 1208

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

55

TCAAAAAGTT TTCTAAAAAA TTTAC

25

60 2) INFORMATION FOR SEQ ID NO: 1209

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

ACGGGCGTCC ACAAATCAA TAGGA 25

15 2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG 22

30 2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTAA CAGGCTTTGA TCCC 24

45 2) INFORMATION FOR SEQ ID NO: 1212

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

60 CCICCCIRGIG GIGAIACIGC WCC 23

2) INFORMATION FOR SEQ ID NO: 1213

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

15

AARGGIGGIA CIGCIGCIAT HCCIGG

26

20 2) INFORMATION FOR SEQ ID NO: 1214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

30

GGTAAAACAG GTACCTCTAA CTA

23

35

2) INFORMATION FOR SEQ ID NO: 1215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
(B) STRAIN: D471
(C) ACCESSION NUMBER: X65717

50

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

AACAAAATAA	AAGAACTTAC	CTATTTTCCA	TCCAAAATGT	TTAGCAATCA	50
TCATCTGCAA	GGCAACGTAT	TGCATGGCAT	TGATGTGATG	AGCAACTAAT	100
ATGTCATTAG	AACGTTGCGT	CAAACTAGCA	TCTAAATAAA	GATCGAAATG	150
CAGTTATCAA	AAATGCAAGC	TCCTATCGGC	CCTTGTTTTA	ATTATTACTC	200
ACATTGCCTT	AATGTATTTA	CTTGCTTATT	ATTAAGTTT	TTGCTAAGTT	250
AGTAGCGTCA	GTTATTCATT	GAAAGGACAT	TATTATGAAA	ATTCTTGTA	300
CAGGCTTTGA	TCCCTTTGGC	GGCGAAGCTA	TTAATCCTGC	CCTTGAAGCT	350
ATCAAGAAAT	TGCCAGCAAC	CATTCATGGA	GCAGAAATCA	AATGTATTGA	400

	AGTTCCAACG	GTTTTTCAAA	AATCTGCCGA	TGTGCTCCAG	CAGCATATCG	450
	AAAGCTTTCA	ACCTGATGCA	GTCCTTTGTA	TTGGGCAAGC	TGGTGGCCGG	500
	ACTGGACTAA	CGCCAGAACG	CGTTGCCATT	AATCAAGACG	ATGCTCGCAT	550
	TCCTGATAAC	GAAGGGAATC	AGCCTATTGA	TACACCTATT	CGTGCAGATG	600
5	GTAAAGCAGC	TTATTTTTCA	ACCTTGCCAA	TCAAAGCGAT	GGTTGCTGCC	650
	ATTCATCAGG	CTGGGCTTCC	TGCTTCTGTT	TCTAATACAG	CTGGTACCTT	700
	TGTTTGCAAT	CATTTGATGT	ATCAAGCCCT	TTACTTAGTG	GATAAATATT	750
	GTCCAAATGC	CAAAGCTGGG	TTTATGCATA	TTCCCTTTAT	GATGGAACAG	800
	GTTGTTGATA	AACCTAATAC	AGCTGCCATG	AACCTCGATG	ATATTACAAG	850
10	AGGAATTGAG	GCTGCTATTT	TTGCCATTGT	CGATTTCAAA	GATCGTTCCG	900
	ATTTAAACG	TGTAGGGGGC	GCTACTCACT	GACTGTGACG	CTACTAAACC	950
	TATTTTAAAA	AAACAGAGAT	ATGAATAAC	TCTGTTTTTT	TTGTGCTAAA	1000
	AATGAAAGAC	CTAGGGAAAC	TTTTCATCGG	TCTTTCTCAA	TTGTCATCTT	1050
	AATCTAATAC	TACTTCTAAC	ATCAGCGGGT	ATAGTTTGCC	AGTAATTAAG	1100
15	AAACGTTGTT	GATCTAAATG	AGCAATCCCA	TTCAAAACAT	TAAGGTCAGG	1150
	GTAATGGGAC	TTATCAAGAT	TTAAGGCTTT	TTACAAAGGA	CTAATATCAT	1200
	AGGTGGCTAC	CACCTTTCCA	GAATCAGGT	GGAGTTTGAC	AATAGTATTG	1250
	GTTTGCCAAA	TATTGGCATA	GAGATAACCA	TCTACATACT	CTAATTCGTT	1300
	AAGCATTGAG	ATAGGGACAC	TTTCTATAGC	AACTAGT		1337

2) INFORMATION FOR SEQ ID NO: 1216

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

35 GGTAAGACTG GTACATCAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1217

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217

50 CAAATGCCAT TTCAAGTAAC ACAAC

25

55 2) INFORMATION FOR SEQ ID NO: 1218

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218

CAAACGCCAT TTCAAGTAAC ACAAC

25

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2) INFORMATION FOR SEQ ID NO: 1219

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases.
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219

CAAATGCTAT TTCAAGTAAT ACAAC

25

25

2) INFORMATION FOR SEQ ID NO: 1220

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGCCAT TTCAAGTAAT ACGAC

25

40

2) INFORMATION FOR SEQ ID NO: 1221

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

55 GAYACICCG GICAYGTIGA YTT

23

60

2) INFORMATION FOR SEQ ID NO: 1222

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222
10 ATYGAYACIC CIGGICAYGT IGAYTT 26

15 2) INFORMATION FOR SEQ ID NO: 1223

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223
AYITCIARRT GIARYTCRCC CATICC 26

30 2) INFORMATION FOR SEQ ID NO: 1224

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224
CCIGYIHTIY TIGARCCAT IATG 24

45 2) INFORMATION FOR SEQ ID NO: 1225

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225
60 TAICCRAACA TYTCISMIAR IGGIAC 26

2) INFORMATION FOR SEQ ID NO: 1226

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226
15 GTIRMRTAIC CRAACATYTC 20

2) INFORMATION FOR SEQ ID NO: 1227

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227
30 GTICCIYTIK CIGARATGTT YGGITA 26

35 2) INFORMATION FOR SEQ ID NO: 1228

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228
45 GTICCIYTIK CIGARATGTT YGGITAYGC 29

50 2) INFORMATION FOR SEQ ID NO: 1229

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229
60

TCCATYTGIG CIGCICCI GT IATCAT

26

5 2) INFORMATION FOR SEQ ID NO: 1230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2145 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (D) ACCESSION NUMBER: X00415

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

20 TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT 50
 CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA 100
 CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAA CCATAAAATC 150
 GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA 200
 25 GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG 250
 GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG 300
 GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCCATGC GTGTTCTCGA 350
 TGGTGCGGTA ATGGTTTACT GCGCAGTTGG TGGTGTTCAG CCGCAGTCTG 400
 AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCCGCG CATTGCGTTC 450
 30 GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCCTGAAAG TTGTTAACCA 500
 GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG 550
 GTGCTGAAGA ACATTTACC GGTGTTGTTG ACCTGGTGAA AATGAAAGCT 600
 ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT 650
 CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG 700
 35 AATCCGCAGC TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT 750
 GAAGAAGTGA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT 800
 GAACAACGAA ATCATCCTGG TAACCTGTGG TTCTGCGTTC AAGAACAAAG 850
 GTGTTCAAGC GATGCTGGAT GCGGTAATTG ATTACCTGCC ATCCCCGGTT 900
 GACGTACCTG CGATCAACGG TATCCTGGAC GACGGTAAAG ACACTCCGGC 950
 40 TGAACGTCAC GCAAGTGATG ACGAGCCGTT CTCTGCACTG GCGTTCAAAA 1000
 TCGCTACCGA CCCGTTTGTT GGTAACCTGA CCTTCTTCCG TGTTTACTCC 1050
 GGTGTGGTTA ACTCTGGTGA TACCGTACTG AACTCCGTGA AAGCTGCACG 1100
 TGAGCGTTTC GGTCTGATCG TTCAGATGCA CGCTAACAAA CGTGAAGAGA 1150
 TCAAAGAAGT TCGCGCGGGC GACATCGCTG CTGCTATCGG TCTGAAAGAC 1200
 45 GTAACCACTG GTGACACCCT GTGTGACCCG GATGCGCCGA TCATTCTGGA 1250
 ACGTATGGAA TTCCCTGAGC CGGTAATCTC CATCGCAGTT GAACCGAAAA 1300
 CCAAAGCTGA CCAGGAAAAA ATGGGTCTGG CTCTGGGCCG TCTGGCTAAA 1350
 GAAGACCCGT CTTTCCGTGT ATGGACTGAC GAAGAATCTA ACCAGACCAT 1400
 CATCGCGGGT ATGGGCGAAC TGCACCTCGA CATCATCGTT GACCGTATGA 1450
 50 AGCGTGAATT CAACGTTGAA GCGAACGTAG GTAAACCGCA GGTTGCTTAC 1500
 CGTGAACTA TCCGCCAGAA AGTTACCGAT GTTGAAGGTA AACACGCGAA 1550
 ACAGTCTGGT GGTCTGGTGC AGTATGGTCA TGTTGTTATC GACATGTACC 1600
 CGCTGGAGCC GGGTTCAAAC CCGAAAGGCT ACGAGTTCAT CAACGACATT 1650
 AAAGGTGGTG TAATCCCTGG CGAATACATC CCGGCCGTG ATAAAGGTAT 1700
 55 CCAGGAACAG CTGAAAGCAG GTCCGCTGGC AGGCTACCCG GTAGTAGACA 1750
 TGGGTATTCT TCTGCACTTC GGTTCTTACC ATGACGTTGA CTCCTCTGAA 1800
 CTGGCGTTTA AACTGGCTGC TTCTATCGCC TTAAAGAAG GCTTTAAGAA 1850
 AGCGAAACCA GTTCTGCTTG AGCCGATCAT GAAGGTTGAA GTAGAAACTC 1900
 CGGAAGAGAA CACCGGTGAC GTTATCGGTG AATTGAGCCG TCGTCGTGGT 1950
 60 ATGCTCAAAG GTCAGGAATC TGAAGTTACT GCGGTTAAGA TCCACGCTGA 2000

AGTACCGCTG	TCTGAAATGT	TCGGATACGC	AACTCAGCTG	CGTTCTCTGA	2050
CCAAAGGTCTG	TGCATCATACT	ACTATGGAAT	TCCTGAAGTA	TGATGAAGCG	2100
CCGAGTAACG	TTGCTCAGGC	CGTAATTGAA	GCCCGTGTA	AATAA	2145

5

2) INFORMATION FOR SEQ ID NO: 1231

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

20 GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC 37

2) INFORMATION FOR SEQ ID NO: 1232

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

35 GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC 42

2) INFORMATION FOR SEQ ID NO: 1233

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - 45 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233

50 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

55 2) INFORMATION FOR SEQ ID NO: 1234

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - 60 (C) STRANDEDNESS: Single

664

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234

ACTAAATAAA CGCTCATTCG

20

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2) INFORMATION FOR SEQ ID NO: 1235

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235

GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC

38

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2) INFORMATION FOR SEQ ID NO: 1236

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTGC CGTTGGTGGC TCGC

34

40

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

55 GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

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2) INFORMATION FOR SEQ ID NO: 1238

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238

10 GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC 38

- 15 2) INFORMATION FOR SEQ ID NO: 1239

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: DNA

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239

 GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC 33

- 30 2) INFORMATION FOR SEQ ID NO: 1240

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240

 GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC 38

- 45 2) INFORMATION FOR SEQ ID NO: 1241

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241

60 GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC 35

2) INFORMATION FOR SEQ ID NO: 1242

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 600 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 15 (E) STRAIN: BM4147-1
 (F) ACCESSION NUMBER: U39790

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

20	TTCTTAGAGA CATTGAATAT GCCTTATGTC GGCGCAGGCG TATTGACCAG	50
	TGCATGTGCC ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG	100
	GTGTGCCGCA AGTTCCTTAT GTACCAGTAC TTAAGAATCA ATGGAAAGAA	150
	AATCCTAAAA AAGTATTTGA TCAATGTGAA GGTTCTTTGC TTTATCCGAT	200
	GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT ACAAAGGCAG	250
25	AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT	300
	TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC	350
	TGTATTAGGA AATGAAGATG TTCGGACGAC TTTGCCTGGC GAAGTCGTAA	400
	AAGACGTAGC ATTCTATGAT TATGAAGCCA AATATATCAA TAATAAAATC	450
	GAAATGCAGA TTCCAGCCGA AGTGCCGGA GAAGTTTATC AAAAAGCGCA	500
30	AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC GGATTGAGCC	550
	GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA	600

35 2) INFORMATION FOR SEQ ID NO: 1243

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2275 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecalis*
 (C) ACCESSION NUMBER: M38386

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

50	GGTACCAAAG AAAAAAACGA ACGCCACAAC CAACAGCCTC TAAAGCAACA	50
	CCTGCTTCTG AAATTGAGGG AGATTTAGCA AATGTCAATG AGATTCTTTT	100
	GGTTCACGAT GATCGTGTCTG GGTCAGCAAC GATGGGAATG AAAGTCTTAG	150
	AAGAAATTTT AGATAAAGAG AAAATTTCAA TGCCGATTCG AAAAATTAAT	200
55	ATTAATGAAT TAACTCAACA AACACAGGCT TTAATTGTCA CAAAAGCTGA	250
	ACTAACGGAA CAAGCACGTA AAAAAGCACC GAAAGCGACA CACTTATCAG	300
	TAAAAAGTTA TGGTTAATCC CCAAAAATAT GAAACAGTGG GTTTCGCTCT	350
	TAAAAGAAAG TGCCTAGAGA GGAAGAAAAC AATGGAAAAT CTTACGAATA	400
	TTTCAATTGA ATTAAATCAA CAGTTTAATA CAAAAGAAGA AGCTATTCGC	450
60	TTTTCGGGCC AGAAACTAGT CGAGGCAGCG TGTGTTGAGC CCGCTTATAT	500

	CGAAGCAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCCAT	ATGGGGAATT	550
	TTATTGCCAT	TCCTCATGGA	ACAGAAGAAG	CCAAAAAATT	AGTGAAAAAA	600
	TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCGA	650
	AGAAGATGAA	AAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
5	AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
	GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800
	AAATTTAGCC	ATTGCTTAAA	GGAGAGAATA	AGAATGAACG	CAGTACATTT	850
	TGGAGCAGGA	AATATTGGAC	GCGGCTTTAT	TGGCGAAATT	TTAGCTAAAA	900
	CGGGTTTCAT	ATTACCGTTT	GTGGATGTTA	ATGGAAACCA	TCATCAAGCG	950
10	TTAAAAGAAC	GTAAGGTTA	TACAATTGAA	TTGGCCGATG	CCTCACATCA	1000
	ACAAATTAAC	GTTGAAAATG	TGACCGGGT	AAATAACATG	ACAGAACCGAG	1050
	AAAAAGTAGT	AGAAGCAATT	GCGGAAGCCG	ATTTAGTCAC	GACGGCAATT	1100
	GGTCCTAATA	TTTTACCAAG	AATTGCTGAA	TTAATTGCTC	AAGGAATTGA	1150
	TGCACGTGCC	GAAGCAAATT	GTCAAAACGG	CCCGCTGGAT	ATTATCGCTT	1200
15	GTGAAAATAT	GATTGGTGGT	TCAACCTTTT	TAGCAGAAGA	AGTGGCCATA	1250
	ATATTTGAAA	AACCCAGCTT	ATCTGAACAA	TGGATTGGTT	TTCTTGATGC	1300
	GGCAGTTGAT	CGGATTGTTT	CATTACAAA	ACATAAAGAT	CCACTTTTGT	1350
	TTCAAGTTGA	GCCTTTTTGT	GAATGGGTCA	TTGATGATAC	CAACCGAAAA	1400
	GCCAAAGAGA	TTCAAGTTAGA	AGGCGTCATT	ACTTGTCGAT	TAGAGCCGTA	1450
20	TATTGAACGA	AAATTATTTA	GTGTAACCAG	TGGCCATGCT	ACAGTTGCCT	1500
	ATACAGGGGC	GTTGTTAGGC	TATCAAACCA	TTGACGAAGC	GATGCAGGAC	1550
	GCCTTAGTGG	TAGCGCAACT	CAAATCAGTT	TTGCAGGAAA	CCGGTAAACT	1600
	TTTAGTGGCC	AAATGGAATT	TTGATGAACA	AGAACATGCA	GCCTATATTG	1650
	AAAAAATTAT	CAACCGTTTC	CAAATAAAT	ATATTTTCAGA	TGCTATTACA	1700
25	CGTGTAGCAC	GGACACCAAT	CAGAAAATTA	GGTGCAGCAAG	AACGGTTTAT	1750
	TCGACCAATC	CGTGAATTAC	AGGAACGCAA	TCTAGTGTCG	GCCGCATTTA	1800
	TAGCAATGAT	TGGTATTGTC	TTTAATTATC	ATGATCCAGA	AGATGAACAA	1850
	AGCCGTCAAT	TACAGGAAAT	GCTTGACCAA	GAAAGTGTTG	ATACAGTGGA	1900
	TCGCTGAAGT	AACGGGCATT	GAAGATCCAG	AAACGGTTAA	AAATATTTAA	1950
30	CAAAACGTAG	AACTGCTATG	CGCGACCACA	AGTAGCATAA	TTAACAAAAT	2000
	CCTTCTACCA	AGATACTTCA	CATTTCTTAA	TTAAAGAAAA	AACAACCGCG	2050
	CCTCACCTGA	GCCGACCCCC	AAAAGTTAGA	CCTAGAAATC	TAACTTTTGG	2100
	AGGTTTTTTT	GTATGGCAAA	ATACAGTTTT	GAAATTTTAA	CTTAAACTTG	2150
	TTCATGACTA	CTTATATGGT	CAAGGAGGTC	TAAGGTTTCT	CGCAAAGAAG	2200
35	TATGGGTTTA	AAGATAGTCT	CAAATAAGCA	AATGGATAAA	TGCCTATAAA	2250
	GAACTTGGTG	AAGAAGGGGG	GATCC			2275

40 2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

55	GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
	TTCGCGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
	AATCTCATTA	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
	CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
60	CCAGCCAAAA	CGATATTTTT	ATAATCATTA	CGTGAAAAAG	GTTTCCCTTC	250

ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

2) INFORMATION FOR SEQ ID NO: 1245

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245

GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAGAG 50
CAACGAAAAC GGAACAAGCA TTAACCTAAC ATTTGAAGTT GCACTTCATT 100
TAGGTGATGA CACAGTTCGT ACAGTTGCAA TGTCTTCCAC AGATGGACTT 150
20 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
TGGTGATGCA ACACTTGGTC GTGTATTTAA CGTATTAGGT GATGCAATTG 250
ACTTAGATGG TGAGGTTCTT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
CAAGCACCTG CATTCGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350
TGGTATTAAA GTAGTAGACT TACTTGCTCC TTACATTAAG GGTGGTAAGA 400
25 TCGGTCTATT CGGTGGTGCC GGTGTAGGTA AAACGGTATT AATTCAGGAA 450
TTAATCAATA ACATCGCACA AGAACACGGT GGTATCTCTG TATTCGCTGG 500
TGTAAGTGAG CGTACTCGTG AGGGTAATGA CTTATACCAC GAAATGAGCG 550
ATTCTGGCGT AATTAAGAAA ACTGCGATGG TATTCGGACA AATGAACGAG 600
CCACCTGGAG CACGTCAACG TGTTGCGTTA ACAGGTTTAA CAATGGCTGA 650
30 GCATTTCCGT GATGAGCAAG GACAAGATGT ACTTCTGTTC ATCGATAATA 700
TCTTCCGTTT CACGCAAGCA GGTTCTGAAG TATCTGCCCT TCTTGGCCGT 750
ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA 800
ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTC 845

35

2) INFORMATION FOR SEQ ID NO: 1246

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 656 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
(B) STRAIN: ATCC 11986

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246

TGCACTTCAT TTAGGTGATG ACACAGTTCG TACAGTTGCA ATGTCTTCCA 50

	CAGATGGACT	TGTTTCGTGGC	ACAGAAAGTAG	AAGATACTGG	TAAAGCAATC	100
	TCTGTACCAG	TTGGTGATGT	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	150
	TGATGCAATT	GACTTAGATG	GTGATGTTCC	TGCGGATGTA	CGTCGTGATC	200
	CAATTCACCG	TCAAGCGCCT	GCATTGGAAG	AGTTATCTAC	TAAAGTAGAA	250
5	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	300
	GGGTGGTAAG	ATTGGTCTAT	TCGGTGGTGC	CGGCGTAGGT	AAAACAGTAT	350
	TAATTCAGGA	ATTAATTAAT	AACATCGCAC	AAGAGCACGG	TGGTATCTCT	400
	GTATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAAGGTAACG	ACTTATACCA	450
	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	GTATTCGGAC	500
10	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCATT	AACAGGTTTA	550
	ACAATGGCTG	AACATTTCCG	TGATGAGCAA	GGACAAGACG	TACTATTGTT	600
	CATCGATAAC	ATCTTCCGTT	TCACGCAAGC	GGGTTCTGAA	GTATCTGCCC	650
	TTCTTG					656

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2) INFORMATION FOR SEQ ID NO: 1247

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247

	CGAAAACGGA	AGTATTAACT	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50
	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTTCGT	100
35	GGCACAGAAG	TAGAAGATAC	TGGTAAACCA	ATCTCTGTAC	CAGTTGGTGA	150
	TGTAACACTT	GGTCGCGTAT	TTAACGTATT	AGGTGATGCA	ATTGACTTAG	200
	ATGGTGAGGT	TCCTGCAGAT	GTACATCGTG	ATCCAATTCA	CCGTCAAGCA	250
	CCTGCATTCG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AAACTGGTAT	300
	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC	350
40	TATTCGGTGG	TGCCGGCGTA	GGTAAAACAG	TATTAATTCA	GGAATTAATT	400
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTCG	CTGGTGTAGG	450
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG	500
	GCGTAATCAA	GAAAACTGCG	ATGGTATTCG	GACAAATGAA	CGAGCCACCT	550
	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATTT	600
45	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC	650
	GTTTCACGCA	AGCGGGTTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA	700
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA	750
	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT	A	791

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2) INFORMATION FOR SEQ ID NO: 1248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: BGSC 4AC1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248

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15 ATCTACAATG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGCATGAA      50
   CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
   TTGCGATGTC TTCCACAGAT GGACTTGTTT GTGGCACAGA AGTAGAAGAT      150
   ACTGGTAAAG CAATCTCTGT ACCAGTTGGT GATGCAACAC TTGGACGTGT      200
   ATTCAACGTA TTAGGTGATG CAATTGACTT AGATGGTGAA CTCCTGCGG      250
20 ATGTACACCG TGATCCAATT CACCGTCAAG CACCTGCATT CGAAGAATTA      300
   TCTACTAAAG TAGAAATTCT TGAAACTGGT ATTAAAGTAG TAGACTTACT      350
   TGCTCCTTAC ATTAAGGGTG GTAAGATCGG CCTATTCTGGT GGTGCCGGCG      400
   TAGGTAAAAC AGTATTAATT CAGGAGTTAA TCAATAACAT CGCACAAGAG      450
   CACGGTGGTA TCTCTGTATT CGCTGGTGTA GGTGAGCGTA CTCGTGAGGG      500
25 TAATGACTTA TACCACGAAA TGAGCGATTC TGGCGTAATC AAGAAAAC TG      550
   CGATGGTATT CGGACAAATG AACGAGCCAC CTGGAGCACG TCAACGTGTT      600
   GCATTAACAG GTTTAACAAT GGCTGAGCAT TTCCGTGATG AGCAAGGACA      650
   AGACGTACTT CTGTTTCATCG ATAACATCTT CCGTTTCACG CAAGCGGGTT      700
   CTGAAGTATC TGCCCTTCTT GGTCGTATGC CATCTGCGGT AGGTTACCAA      750
30 CCAACACTTG CAACAGAAAT GGGTCAATTA CAAGAGCGTA TTACATCTAC      800
   AAATAAAGGG TCTATCACGT CTATC      825

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35 2) INFORMATION FOR SEQ ID NO: 1249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249

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50 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGTATTAA      50
   CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
   TTGCGATGTC TTCCACAGAT GGACTTGTTT GTGGCACAGA AGTAGAAGAT      150

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	ACTGGTAAAC	CAATCTCTGT	ACCAGTTGGT	GATGTAACAC	TTGGTCGCGT	200
	ATTTAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAG	GTTCTGTCAG	250
	ATGTACATCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
5	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAAC	AGTATTAATT	CAGGAATTAA	TTAACAACAT	CGCACAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
	TAATGACTTA	TACCACGAAA	TGAGCGATTC	TGGCGTAATC	AAGAAAACCTG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
10	GCATTAACAG	GTTTAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTACTT	CTGTTTCATCG	ATAACATCTT	CCGTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
	CCAACACTTG	CAACAGAAAT	GGGTC			775

15

2) INFORMATION FOR SEQ ID NO: 1250

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10204

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250

	CCAGCAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAGC	50
	GAGCATCAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	GATGACACAG	100
35	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTCTG	TGGCACAGAA	150
	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	ATGTAACACT	200
	TGGTCGCGTA	TTCAACGTAT	TAGGTGATGC	AATTGACTTA	GATGGTGATG	250
	TTCCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	ACCTGCATTC	300
	GAAGAACTAT	CTACAAGAAT	AGAAATTCTT	GAAACTGGTA	TTAAAGTAGT	350
40	AGATTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACG	GTATTAATTC	AGGAATTAAT	TAACAACATC	450
	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	GTGAGCGTAC	500
	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	GGCGTAATTA	550
	AGAAAACCTGC	GATGGTATTT	GGACAAATGA	ACGAGCCACC	TGGAGCACGT	600
45	CAACGTGTTG	CATTAACAGG	TTTAACAATG	GCTGAACATT	TCCGTGATGA	650
	GCAAGGACAA	GACGTACTAT	TGTTTCATCGA	TAACATCTTC	CGTTTCACGC	700
	AAGCAGGTTT	TGAAGTATCT	GCCCTTCTTG	GTCGTATGCC	ATCTGCGGTA	750
	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	AAGAGCGTAT	800
	TACATCTACA	AATAAAGGGT	CTATCACGTC	TA		832

50

2) INFORMATION FOR SEQ ID NO: 1251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251

15 AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100
 AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA GAAGTAGAAG 150
 ATACTGGTAA ACCAATCTCT GTACCAGTTG GTGATGTAAC ACTTGGTCGC 200
 20 GTATTTAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG AGGTTCCTGC 250
 AGATGTACAT CGTGATCCAA TTCACCGTCA AGCACCTGCA TTCGAAGAAT 300
 TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT AGTAGACTTA 350
 CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCATTTCG GTGGTGCCGG 400
 CGTAGGTAAA ACAGTATTAA TTCAGCAATT AATTAACAAC ATCGCAACAAG 450
 25 AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG TACTCGTGAG 500
 GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA TCAAGAAAAC 550
 TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA CGTCAACGTG 600
 TTGCATTAAC AGGTTTAAAC ATGGCTGAGC ATTTCCGTGA TGAGCAAGGA 650
 CAAGACGTAC TTCTGTTTCAT CGATAACATC TTCCGTTTCA CGCAAGCGGG 700
 30 TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG GTAGGTTACC 750
 AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG TATTACATCT 800
 AC 802

35

2) INFORMATION FOR SEQ ID NO: 1252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1410

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252

AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100

	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	GAAGTAGAAG	150
	ATACTGGTAA	ACCAATCTCT	GTACCAGTTG	GTGATGTAAC	ACTTGGTCGC	200
	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	AGGTTCTGC	250
	AGATGTACAT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	TTCGAAGAAT	300
5	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	AGTAGACTTA	350
	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCT	GTGGTGCCGG	400
	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATTAACAAC	ATCGCACAAAG	450
	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	TCAAGAAAAC	550
10	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	CGTCAACGTG	600
	TTGCATTAAC	AGGCTTAACA	ATGGCTGAGC	ATTTCCGTGA	TGAGCAAGGA	650
	CAAGACGTAC	TTCTGTTCAT	CGATAACATC	TTCCGTTTCA	CGCAAGCGGG	700
	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	GTAGGTTACC	750
	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	TATTACATCT	800
15	ACAAATAAAG	GGTCTATCAC	GTC			823

2) INFORMATION FOR SEQ ID NO: 1253

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253

35	CCAGAAATCT	ACAATGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	CATGAACTTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCTGTG	CACAGAAGTA	150
	GAAGATACTG	GTAAAGCAAT	CTCTGTACCA	GTTGGTGATG	CAACACTTGG	200
	ACGTGTATTC	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAAGTTC	250
40	CTGCGGATGT	ACACCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
	CCGGCGTAGG	TAAAACAGTA	TTAATTCAGG	AATTAATCAA	TAACATCGCA	450
	CAAGAGCATG	GTGGTATCTC	TGTATTCGCT	GGTGTAGGTG	AGCGTACTCG	500
45	TGAGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTCGAT	TAACAGGTTT	AACAATGGCT	GAGCATTTC	GTGATGAGCA	650
	AGGACAAGAC	GACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
50	TACCAACCGA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATT	798

2) INFORMATION FOR SEQ ID NO: 1254

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 767 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 7064

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254

CATTGAAGT TGCACTTCAT TTAGGTGATG ACACAGTTCG TACAGTTGCA 50
 ATGTCTTCCA CAGATGGACT TGTTCTGGC ACAGAAAGTAG AAGATACTGG 100
 TAAAGCAATC TCTGTACCAG TTGGTGATGC AACACTTGGT CGTGTATTTA 150
 20 ACGTATTAGG TGATGCAATT GACTTAGATG GTGAGGTTCC TCGGATGTA 200
 CGTCGTGATC CAATTCACCG TCAAGCACCT GCATTCTGAAG AATTATCTAC 250
 TAAAGTAGAA ATTCTTGAAA CTGGTATTAA AGTAGTAGAC TTACTTGCTC 300
 CTTACATTAA GGGTGGTAAG ATCGGTCTAT TCGGTGGTGC CGGTGTAGGT 350
 AAAACGGTAT TAATTCAGGA ATTAATCAAT AACATCGCAC AAGAACACGG 400
 25 TGGTATCTCT GTATTCTGCTG GTGTAGGTGA GCGTACTCGT GAGGGTAATG 450
 ACTTATACCA CGAAATGAGC GATTCTGGCG TAATTAAGAA AACTGCGATG 500
 GTATTCTGAC AAATGAACGA GCCACCTGGA GCACGTCAAC GTGTTGCGTT 550
 AACAGGTTTA ACAATGGCTG AGCATTTCCG TGATGAGCAA GGACAAGACG 600
 TACTTCTGTT CATCGATAAT ATCTTCCGTT TCACGCAAGC AGGTTCTGAA 650
 30 GTATCTGCCC TTCTTGCCG TATGCCATCT GCGGTAGGTT ACCAACCAAC 700
 ACTTGCAACA GAAATGGGTC AATTACAAGA GCGTATTACA TCTACAAATA 750
 AAGGGTCTAT CACGTCT 767

35

2) INFORMATION FOR SEQ ID NO: 1255

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1174 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: C-14

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255

GAAATGCGTG AATCATTTTT AGATTATGCG ATGAGTGTTA TCGTTGCTCG 50
 TGCATTGCCA GATGTTCTGT ACGGTTTAA ACCAGTACAT CGTCGTATAC 100

TATATGGATT AAATGAACAA GGTATGACAC CGGATAAATC ATATAAAAAA 150
 TCAGCACGTA TCGTTGGTGA CGTAATGGGT AAATATCACC CTCATGGTGA 200
 CTTATCTATT TATGAAGCAA TGGTACGTAT GGCTCAAGAT TTCAGTTATC 250
 GTTATCCGCT TGTTGATGGC CAAGGTAAC TGGTTCAAT GGATGGAGAT 300
 5 GGC GCAGCAG CAATGCGTTA TACTGAAGCG CGTATGACTA AAATCACACT 350
 TGA ACTGTTA CGTGATATTA ATAAAGATAC AATAGATTTT ATCGATAACT 400
 ATGATGGTAA TGAAAGAGAG CCGTCAGTCT TACCTGCTCG ATTCCTAAC 450
 TTATTAGCCA ATGGTGCATC AGGTATCGCG GTAGGTATGG CAACGAATAT 500
 TCCACCACAT AACTTAACAG AATTAATCAA TGGTGTACTT AGCTTAAGTA 550
 10 AGAACCCCTGA TATTTCAATT GCTGAGTTAA TGGAGGATAT TGAAGGTCCT 600
 GATTTCCCAA CTGCTGGACT TATTTTAGGT AAGAGTGGTA TTAGACGTGC 650
 ATATGAAACA GGTCTGGTT CAATTCAAAT GCGTTCTCGT GCAGTTATTG 700
 AAGAACGTGG AGNCGGACGT CAACGTATTG TTGTCACTGA AATTCCTTTC 750
 CAAGTGAATA AGGCTCGTAT GATTGAAAAA ATTCAGAGC TCGTTCGTGA 800
 15 CAAGAAAATT GACGGTATCA CTGATTACG TGATGAAACA AGTTTACGTA 850
 CTGGTGTGCG TGTCGTTATT GATGTGCGTA AGGATGCAA TGCTAGTGTC 900
 ATTTTAAATA ACTTATACAA ACAACACCT CTTCAAACAT CATTTGGTGT 950
 GAATATGATT GCACTTGTA ATGGTAGACC GAAGCTTATT AATTTAAAAG 1000
 AAGCGTTGGT ACATTATTTA GAGCATCAA AGACAGTTGT TAGAAGACGT 1050
 20 ACGCAATACA ACTTACGTAA AGCTAAAGAT CGTGCCCA TTTTAGAAGG 1100
 ATTACGTATC GCACTTGACC ATATCGATGA AATTATTTCA ACGATTCGTG 1150
 AGTCAGATAC AGATAAAGTT GCAA 1174

25

2) INFORMATION FOR SEQ ID NO: 1256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10209

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256

ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAGCAAGCAT 50
 TAACTTAACA TTTGAAGTTG CACTTCATTT AGGTGATGAC ACAGTTCGTA 100
 CAGTTGCAAT GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA 150
 45 GATACTGGTA AAGCAATCTC TGTACCAGTT GGTGATGTAA CACTTGGTGC 200
 TGTATTTAAC GTATTAGGTG ATGCAATTGA CTTAGATGGA GATGTTCTTG 250
 CGGATGTACG TCGTGATCCA ATTCACCGTC AAGCGCCTGC ATTCGAAGAG 300
 TTATCTACTA AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT 350
 ACTTGCTCCT TACATTAAGG GTGGTAAGAT CGGTCTATTC GGTGGTGCCG 400
 50 GTGTAGGTAA AACAGTATTA ATTCAGGAAT TAATTAACAA CATCGCACAA 450
 GAGCACGGTG GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA 500
 AGGTAACGAC TTATACCACG AAATGAGCGA TTCTGGCGTA ATTAAGAAAA 550
 CTGCGATGGT ATTCGGACAA ATGAACGAGC CACCTGGAGC ACGTCAACGT 600

GTTGCATTAA	CAGGTTTAAAC	AATGGCTGAA	CATTTCCTGT	ATGAGCAAGG	650
GCAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
GTTCTGAAGT	ATCTGCCCTT	CTTGGTCGTA	TGCCATCTGC	GGTAGGTTAC	750
CAGCCAACAC	TTGCAACAGA	AATGGGTCAA			780

5

2) INFORMATION FOR SEQ ID NO: 1257

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 7700

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257

CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	ACGAAAACGG	50
25	AACAAGCATT	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	100
	CAGTTCGTAC	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	150
	GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	200
	ACTTGGTCGT	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	250
	AGGTTTCCTGC	GGATGTACGT	CGTGATCCAA	TTCACCGTCA	300
30	TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	350
	AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	400
	GTGGTGCCGG	TGTAGGTAAA	ACGGTATTAA	TTCAGGAATT	450
	ATCGCACAAG	AACACGGTGG	TATCTCTGTA	TTCGCTGGTG	500
	TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	550
35	TTAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	600
	CGTCAACGTG	TTGCGTTAAC	AGGTTTAAAC	ATGGCTGAGC	650
	TGAGCAAGGA	CAAGATGTAC	TTCTGTTCAT	CGATAATATC	700
	CGCAAGCAGG	TTCTGAAGTA	TCTGCCCTTC	TTGGCCGTAT	750
	GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	800
40	TATTACATCT	ACAAATA			817

2) INFORMATION FOR SEQ ID NO: 1258

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1404

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258

CCAGAAATCT ACAACGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
 TATTAACCTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
 GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCTGTG CACAGAAGTA 150
 10 GAAGATACTG GTAAACCAAT CTCTGTACCA GTTGGTGATG TAACACTTGG 200
 TCGCGTATTT AACGTATTAG GTGATGCAAT TGAAGTAGAT GGTGAGGTTT 250
 CTGCAGATGT ACATCGTGAT CCAATTCACC GTCAAGCACC TGCATTGCAA 300
 GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350
 CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
 15 CCGGCGTAGG TAAAACAGTA TTAATTCAGG AATTAATTAA CAACATCGCA 450
 CAAGAGCACC GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG 500
 TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
 AACTGCGAT GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
 CGTGTTGCAT TAACAGGTTT AACAAATGGCT GAGCATTTCC GTGATGAGCA 650
 20 AGGACAAGAC GACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT 750
 TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
 ATCTACAAAT AAAGGGTCTA TCACGTCTA 829

25

2) INFORMATION FOR SEQ ID NO: 1259

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

40 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259

TGGCGGAAAG CTACCAGAAA TCTACAACGC CCTTACGGTA AAACAGAGCA 50
 45 ACGAAAACGG TGAACCTAAC TTAACATTTG AAGTTGCACT TCATTTAGGT 100
 GATGATACAG TTCGTACAGT TGCGATGTCT TCCACAGATG GACTTGTTTCG 150
 TGGCACAGAA GTAGAAGATA CTGGTAAAGC AATCTCTGTA CCAGTTGGTG 200
 ATGCAACACT TGGTCGCGTA TTTAACGTAT TAGGTGATGC TATTGACTTA 250
 GATGGTGAGG TTCCTGCGGA TGTACGTCGT GATCCAATTC ACCGTCAAGC 300
 50 ACCTGCATTC GAAGAATTAT CTACTAAAGT AGAAATTCTT GAAACTGGTA 350
 TTAAAGTAGT AGACTTACTT GCTCCTTACA TTAAGGGTGG TAAGATCGGC 400
 CTATTCCGGT GTGCCGGTGT AGGTAAACA GTATTAATTC AGGAGTTAAT 450
 CAACAACATC GCACAAGAGC ACGGTGGTAT CTCTGTATTC GCTGGTGTAG 500

GTGAGCGTAC TCGTGAGGGT AATGACTTAT ACCACGAAAT GAGCGATTCT 550
 GGCCTAATTA AGAAACTGC GATGGTATTC GGACAAATGA ACGAGCCACC 600
 TGGAGCACGT CAACGTGTTG CATTAAACAGG CTTAACAATG GCTGAATATT 650
 TCCGTGATGA GCAAGGACAA GACGTACTTC TGTTTCATCGA TAATATCTTC 700
 5 CGTTTCACGC AAGCAGGTTC TGAAGTATCT GCCCTTCTTG GCCGTATGCC 750
 ATCTGCGGTA GGTTACCAAC CAACACTTGC AACAGAAATG GGTCAATTAC 800
 AAGAGCGTAT TACATCTACA AATAAAGGGT CTATCACGTC TATC 844

10

2) INFORMATION FOR SEQ ID NO: 1260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 49064

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260

AAGCTACCAG AAATCTACAA CGCCCTTACG GTAAACAGAG GCAACGAAAA 50
 CGGAACAAGC ATTAACCTAA CATTTGAAGT TGCACTTCAT TTAGGTGATG 100
 ACACAGTTCG TACAGTTGCA ATGTCTTCCA CAGATGGACT TGTTTCGTGGC 150
 30 ACAGAAGTAG AAGATACTGG TAAAGCAATC TCTGTACCAG TTGGTGATGC 200
 AACACTTGGT CGTGTATTTA ACGTATTAGG TGATGCAATT GACTTAGATG 250
 GTGAGGTTCC TGC GGATGTA CGCCGTGATC CAATTCACCG TCAAGCACCT 300
 GCATTGCAAG AATTATCTAC TAAAGTAGAA ATTCTTGAAA CTGGTATTAA 350
 AGTAGTAGAC TTA CTTGCTC CTTACATTAA GGGTGGTAAG ATCGGTCTAT 400
 35 TCGGTGGTGC CGGTGTAGGT AAAACAGTAT TAATTCAGGA ATTAATCAAC 450
 AACATCGCAC AAGAACACGG TGGTATCTCT GTATTCGCTG GTGTAGGTGA 500
 GCGTACTCGT GAGGGTAATG ACTTATACCA CGAAATGAGC GATTCAGGCG 550
 TAATTAAGAA AACTGCGATG GTATTCGAC AAATGAACGA GCCACCTGGA 600
 GCGCGTCAAC GTGTTGCGTT AACAGGTTTA ACAATGGCTG AGCATTTCCG 650
 40 TGATGAGCAA GGACAAGACG TTCTTCTGTT CATCGATAAT ATCTTCCGTT 700
 TCACGCAAGC AGGTTCTGAA GTATCTGCCC TTCTTGGTCG TATGCCATCT 750
 GCGGTAGGTT ACCAACCAAC ACTTGCAACA GAAATGGGTC AATTACAAGA 800
 GCGTATTACA TCTACAAATA AAGGGTCTAT CACGTCTATC 840

45

2) INFORMATION FOR SEQ ID NO: 1261

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4AZ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261

10	GCGGAAAGCT	ACCAGAAATC	TACAATGCCC	TTACGGTAAA	ACAAAGCAAC	50
	GAAAACGGAA	GCATGAACTT	AACATTTGAA	GTTGCACTTC	ATTTAGGTGA	100
	TGATACAGTT	CGTACAGTTG	CGATGTCTTC	CACAGATGGA	CTTGTTTCGTG	150
	GCACAGAAGT	AGAAGATACT	GGTAAAGCAA	TCTCTGTACC	AGTTGGTGAT	200
	GCAACACTTG	GACGTGTATT	CAACGTATTA	GGTGATGCAA	TTGACTTAGA	250
15	TGGTGAACTT	CCTGCGGATG	TACACCGTGA	TCCAATTCAC	CGTCAAGCAC	300
	CTGCATTCTG	AGAATTATCT	ACTAAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTAGTAG	ACTTACTTGC	TCCTTACATT	AAGGGTGGTA	AGATCGGCCT	400
	ATTCGGTGGT	GCCGGCGTAG	GTAAACAGT	ATTAATTCAG	GAGTTAATCA	450
	ATAACATCGC	ACAAGAGCAC	GGTGGTATCT	CTGTATTCGC	TGGTGTAGGT	500
20	GAGCGTACTC	GTGAGGGTAA	TGACTTATAC	CACGAAATGA	GCGATTCTGG	550
	CGTAATCAAG	AAAAC TGCGA	TGGTATTCGG	ACAAATGAAC	GAGCCACCTG	600
	GAGCACGTCA	ACGTGTTGCA	TTAACAGGTT	TAACAATGGC	TGAGCATTTC	650
	CGTGATGAGC	AAGGACAAGA	CGTACTTCTG	TTCATCGATA	ACATCTTCCG	700
	TTTCACGCAA	GCGGGTTCTG	AAGTATCTGC	CCTTCTTGGT	CGTATGCCAT	750
25	CTGCGGTAGG	TTACCAACCA	ACACTTGCAA	CAGAAATGGG	TCAATTACAA	800
	GAGCGTATTA	CATCTACAAA	TAAAGGGTCT	ATCACGTCT		839

30 2) INFORMATION FOR SEQ ID NO: 1262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4H2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262

45	AAGCTACCAG	AAATCTACAA	TGCCCTTACG	GTAAAACAAA	GCAACGAAAA	50
	CGGAAGCATG	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGATA	100
	CAGTTCGTAC	AGTTGCGATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
	GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
50	ACTTGGACGT	GTATTCAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
	AACTTCCTGC	GGATGTACAC	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
	TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
	AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTTCG	400

GTGGTGCCGG CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATCAATAAC 450
 ATCGCACAAAG AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG 500
 TACTCGTGAG GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA 550
 TCAAGAAAAC TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA 600
 5 CGTCAACGTG TTGCATTAAC AGGTTTAAAC ATGGCTGAGC ATTTCCGTGA 650
 TGAGCAAGGA CAAGACGTAC TTCTGTTCAT CGATAACATC TTCCGTTTCA 700
 CGCAAGCGGG TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG 750
 GTAGGTTACC AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG 800
 TATTACATCT ACAAATAAAG GGTCTATCAC GTC 833
 10

2) INFORMATION FOR SEQ ID NO: 1263

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 25 (B) STRAIN: BGSC 4Q1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263

CGAAACGGGA AGCATGAACT TAACATTTGA AGTTGCACTT CATTTAGGTG 50
 30 ATGATACAGT TCGTACAGTT GCGATGTCTT CCACAGATGG ACTTGTTCTG 100
 GGCACAGAAG TAGAAGATAC TGGTAAAGCA ATTTCTGTAC CAGTTGGTGA 150
 TGTAACACTT GGACGTGTAT TCAACGTATT AGGTGATGCA ATTGACTTAG 200
 ATGGTGAAC TCCGTGCGGAT GTACACCGTG ATCCAATTCA CCGTCAAGCA 250
 CCTGCATTCG AAGAATTATC TACTAAAGTA GAAATTCTTG AACTGGGTAT 300
 35 TAAAGTAGTA GACTTACTTG CTCCTTACAT TAAGGGTGGT AAGATCGGCC 350
 TATTCGGTGG TGCCGGTGTA GGTAAAACAG TATTAATTCA GGAATTAATT 400
 AACAACATCG CACAAGAGCA CGGTGGTATC TCTGTATTCG CTGGTGTAGG 450
 TGAGCGTACT CGTGAGGGTA ATGACTTATA CCACGAAATG AGCGATTCTG 500
 GCGTAATCAA GAAACTGCG ATGGTATTTCG GACAAATGAA CGAGCCACCT 550
 40 GGAGCACGTC AACGTGTTGC ATTAACAGGT TTAACAATGG CTGAGCATTT 600
 CCGTGATGAG CAAGGACAAG ACGTACTTCT GTTCATCGAT AACATCTTCC 650
 GTTTCACGCA AGCGGGTCT GAAGTATCTG CCCTTCTTGG TCGTATGCCA 700
 TCTGCGGTAG GTTACCAACC AACACTTGCA ACAGAAATGG GTCAATTACA 750
 AGAGCGTATT ACATCTACAA ATAAAGGGTC TATCACGTCT 790
 45

2) INFORMATION FOR SEQ ID NO: 1264

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264

10 AGTTGCACTT CATTTAGGTG ATGATACAGT TCGTACAGTT GCGATGTCTT 50
 CCACAGATGG ACTTGTCGT GGCACAGAAG TAGAAGATAC TGGTAAACCA 100
 ATCTCTGTAC CAGTTGGTGA TGTAACACTT GGTCGCGTAT TTAACGTATT 150
 AGGTGATGCA ATTGACTTAG ATGGTGAGGT TCCTGCAGAT GTACATCGTG 200
 15 ATCCAATTCA CCGTCAAGCA CCTGCATTCTG AAGAATTATC TACTAAAGTA 250
 GAAATTCTTG AAAGTGGTAT TAAAGTAGTA GACTTACTTG CTCCTTACAT 300
 TAAGGGTGGT AAGATCGGCC TATTCGGTGG TGCCGGCGTA GGTAAAACAG 350
 TATTAATTCA GGAATTAATT AACACATCG CACAAGAGCA CGGTGGTATC 400
 TCTGTATTCG CTGGTGTAGG TGAGCGTACT CGTGAGGGTA ATGACTTATA 450
 20 CCACGAAATG AGCGATTCTG GCGTAATCAA GAAAGTGGC ATGGTATTCTG 500
 GACAAATGAA CGAGCCACCT GGAGCACGTC AACGTGTTGC ATTAACAGGT 550
 TTAACAATGG CTGAGCATTT CCGTGATGAG CAAGGACAAG ACGTACTTCT 600
 GTTCATCGAT AACATCTTCC GTTTCACGCA AGCGGGTTCT GAAG 644

25

2) INFORMATION FOR SEQ ID NO: 1265

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265

GGCGGAAAGC TACCAGAAAT CTACAACGCC CTTACGGTAA AACAGAGCAA 50
 CGAAAACGGA ACAAGCATTA ACTTAACATT TGAAGTTGCA CTTCATTTAG 100
 45 GTGATGACAC AGTTCGTACA GTTGCAATGT CTTCCACAGA TGGACTTGTT 150
 CGTGGCACAG AAGTAGAAGA TACTGGTAAA GCAATCTCTG TACCAGTTGG 200
 TGATGCAACA CTTGGTCGTG TATTTAACGT ATTAGGTGAT GCAATTGACT 250
 TAGATGGTGA GGTTCCTGCG GATGTACGTC GTGATCCAAT TCACCGTCAA 300
 GCACCTGCAT TCGAAGAATT ATCTACTAAA GTAGAAATTC TTGAAACTGG 350
 50 TATTAAAGTA GTAGACTTAC TTGCTCCTTA CATTAGGGT GGTAAGATCG 400
 GTCTATTCCG TGGTGCCGGT GTAGGTAAAA CGGTATTAAT TCAGGAATTA 450
 ATCAATAACA TCGCACAAGA ACACGGTGGT ATCTCTGTAT TCGCTGGTGT 500
 AGGTGAGCGT ACTCGTGAGG GTAATGACTT ATACCACGAA ATGAGCGATT 550

	CTGGCGTAAT	TAAGAAACT	GCGATGGTAT	TCGGACAAAT	GAACGAGCCA	600
	CCTGGAGCAC	GTCAACGTGT	TGCGTTAACA	GGTTTAACAA	TGGCTGAGCA	650
	TTTCCGTGAT	GAGCAAGGAC	AAGATGTACT	TCTGTTTCATC	GATAATATCT	700
	TCCGTTTAC	GCAAGCAGGT	TCTGAAGTAT	CTGCCCTTCT	TGGCCGTATG	750
5	CCATCTGCGG	TAGGTTACCA	ACCAACACTT	GCAACAGAAA	TGGGTCAATT	800
	ACAAGAGCGT	ATTACATCTA	CAA			823

10 2) INFORMATION FOR SEQ ID NO: 1266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266

25	TGGTCCGAGR	CCCGATTCTMA	TGAAATTATC	AAGGAAACCT	CCAAYTTCAT	50
	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	CCCATTTCTG	100
	GTTTCCAGGG	TGACAACATG	ATCGATSCCT	CTGCCAACTG	CCCATGGTAC	150
	AAGGGCTGGT	ACMAKGAGAC	TGCCGACAGG	CAAGYACTCT	GGCAAGACCC	200
30	TTCTTGAGGC	CATTGACGSC	ATTGAGCCCC	CCAMSCGTCC	TWCCGATAAA	250
	CCTCTCCGTC	TTCCTCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGMAC	300
	TGTTCCCTGTC	GGACGTRTTG	AGACTGGAGT	CATCAAGCCC	GGTATGGTCG	350
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAAATG	400
	CACCACCAGC	AGCTTTCCGA	CGGTAWCCCC	GGTGACAACG	TCGGCTTCAA	450
35	CGTCAAGAAT	GTTTCCGTCA	AAGAAGTCCG	CCGTGGTAAC	GTTGCCTGGT	500
	GACTCTAAGA	ATGATCCCCG	MAWGGGCTGC	GATTCCTTCA	ATGCYCAGGT	550
	CATCGTCTC	AACCACCCTG	GTCAGGTTGG	CGCTGGTTAT	GCCCCAGTCC	600
	TCGAYTGCCA	TACTGCCCCA	ATTGCTTGCA	ARTTCGCTGA	GMTCMAGAG	650
	AAGATTGAYC	GCCGAACCGG	MAAGTCTGTT	GAGAACGCCC	CCAAGTTCAT	700
40	CAAGTCCGGT	GATGC				715

2) INFORMATION FOR SEQ ID NO: 1267

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 (B) STRAIN: ATCC 56220

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267

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GAGTCCTCTT ATTTACTTTT GTCATGACTA CCTTACTAAT CTGTCATAGA      50
TCGTTACAAC GAAATCGTCA AGGAGACTTC CAACTTCATC AAGAAGGTCTG     100
GATACAACCC CAAGAACGTT CCTTTCGTTC CTATCTCCGG TTCAACGGC       150
10 GACAACATGC TTGAGCCCTC CCCCAACTGC CCCTGGTACA AGGGTTGGGA     200
GAAGGAGACC AAGGCCGGTA AGGTCACTGG TAAGACCCTC CTCGAGGCCA       250
TCGACGCCAT TGAGCCCCCT ACCCGTCCCG CCAACAAGGT CAGTACTACC       300
TCAATTACTT GAACTCTCTT CATACGTTCC GATTACTGAC TGCTTCACAG       350
CCCCCTCCGTC TTCCCCCTCCA GGACGTTTAC AAGATCGGTG GTATTGGAAC     400
15 GGTGCCCCGTC GGTTCGTGTTG AGACCGGTAC CATCTCCCCT GGTATGGTCG     450
TTACCTTGTA TGTATCCTGA CCATCCCCCT TGGCAATCAT TACGTACTAA       500
CTCACTCTTC AGCGCTCCCG CCAACGTCAC CACTGAAGTC AAGAGTGTTG       550
AAATGCACCA CCAGCAGCTC GCTGCCGGTC AGCCCGGTGA CAACGTTGGT       600
TTCAACGTGA AGAACGTCTC CGTCAAGGAA ATCCGTCGTG GTAACGTTGC       650
20 TGGTGATAGC AAGAACGACC CCCCTGCCGG TGCTGCTTCC TTCAACGCCC       700
AGGTCATCGT CCTCAACCAC CCCGGTCAGG TCGGTGCTGG TTACGCCCCA       750
GTCCTTGACT GCCACACTGC CCACATTGCT TGCAAGTTCT CTGAACCTCT       800
TGAGAAGATT GACCGTCGTA CCGGAAAGTC TGTTGAGGAC CACCCCAAGT       850
TCATCAAGTC CGGTGACGCT GCCAT
25

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2) INFORMATION FOR SEQ ID NO: 1268

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 40 (B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268

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GTGAGCGTGG TATCACCATC GATATTGCCC TCTGGAAATT CGAGACCCCG      50
45 AAGTACAGTG TCACTGTCAT TGGTGAGTGC TTTTACCCC TCTTAAGCAG     100
ATTTCAACTT CCAGAGTATC TACTCTAACA TATCCGCTTA GATGCTCCCG       150
GCCATCGTGA CTTTCATCAAG AACATGATCA CTGGTACCTC CCAGGCTGAC       200
TGCGCTATCC TCATCATTCG TGCCGGTACT GGTGAGTTCG AGGCTGGTAT       250
CTCCAAGGAT GGCCAGACTC GTGAGCACGC TCTGCTTGCT TTCACCCTTG       300
50 GTGTGAGGCA ACTCATCGTT GCCATCAACA AGATGGACAC CACCAAGTGG       350
TCCGAGTCCC GTTTCAACGA AATCATCAAG GAGGTTTCCA ACTTCATCAA       400
GAAGGTCGGA TATAACCCCA AGGCTGTTCC CTTCGTGCCA ATCTCTGGTT       450
TCGAGGGTGA CAACATGATT GAACCCTCCC CCAACTGCAC CTGGTACAAG       500

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	GGCTGGAACA	AGGAGACTGC	CTCTGGCAAG	TCTTCTGGTA	AAACCCTTCT	550
	CGATGCCATT	GACGCCATTG	AACCCCCAAC	CCGTCCTACC	GATAAGCCTC	600
	TCCGTCTTCC	CCTCCAGGAT	GTTTACAAAA	TCTCTGGTAT	TGGCACTGTT	650
	CCCGTCGGAC	GTGTTGAGAC	TGGTGTCATC	AAGCCCGGTA	TGGTCGTGAC	700
5	TTTCGCTCCC	TCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACCAACAAC	CCAGGCTGGT	TACCCTGGTG	ACAACGTCGG	CTTCAACGTC	800
	AAGAACGTTT	CAGTCAAGGA	AGTCCGCCGT	GGCAACGTTG	CTGGCGACTC	850
	CAAAAATGAT	CCCCCAAGG	GCTGCGAATC	CTTCAATGCC	CAGGTCATCG	900
	TCCTTAACCA	CCCCGGCCAG	GTTGGCGCTG	GTTATGCCCC	AGTCCTCGAC	950
10	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCTGAACTCA	TTGAGAAGAT	1000
	CGACCGCCGT	ACTGGAAAGT	CTGTTGAGAA	CAACCCCAAG	TTCATCAAGT	1050
	CTGGTGATGC	TGCTATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTG	1100
	GAGCCCTTCA	CTGACTATCC	CCCT			1124

15

2) INFORMATION FOR SEQ ID NO: 1269

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1043 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton rubrum*
 (B) STRAIN: WSA-224

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269

	GTGAGCGTGG	TATCACCATC	GATATCGCCC	TCTGGAAGTT	CGAGACCCCC	50
	AAGTACAATG	TCACCGTCAT	TGGTATGTTT	CTTTGCCTTG	TTCCCTCATG	100
35	TGGTTGTACC	ATATCTAACG	AGAGTAGACG	CCCCCGGTCA	CCGTGACTTC	150
	ATCAAGAACA	TGATCACTGG	TACCTCCCAG	GCTGACTGCG	CTATTCTCAT	200
	CATTGCTGCC	GGTACTGGTG	AGTTCGAGGC	TGGTATCTCC	AAGGATGGCC	250
	AGACCCGTGA	GCACGCTCTG	CTCGCCTTCA	CCCTCGGTGT	CAAGCAGCTC	300
	ATCGTTGCCA	TCAACAAGAT	GGACACCACC	GGCTGGTCCG	AGGATCGTTT	350
40	CAAGGAAATT	ATCAAGGAAG	TCACCAACTT	CATCAAGAAG	GTTGGCTACG	400
	ACCCCAAGGG	TGTTCCATTC	GTTCCAATCT	CTGGTTTCAA	CGGTGACAAC	450
	ATGATTGAGG	CCTCCACCAA	CTGCCCATGG	TACAAGGGAT	GGAACAAGGA	500
	GACCAAGGCC	GGTGGTGCCA	AGTCCGGCAA	GACCCTCCTC	GAGGCCATCG	550
	ATGCCATCGA	CATGCCAACC	CGTCCTACCG	ACAAGCCCCT	CCGTCTCCCA	600
45	CTCCAGGATG	TCTACAAGAT	CTCTGGTATC	GGAAGTGTGC	CAGTCGGTGC	650
	TGTTGAGACC	GGTATCATCA	AGCCCGGTAT	GGTCGTCACC	TTNGCCCCCG	700
	CCAACGTCAC	CACTGAAGTC	AAGTCCGTYK	AAATGCACCA	CCAGCAGCTT	750
	CAGCAGGGTG	TCCCCGGTGA	CAACGTCGGC	TTCAATGTCA	AGAACGTTTC	800
	CGTCAAGGAA	GTCCGCCGTG	GTAACGTTGC	CGGTGACTCC	AAGAACGACC	850
50	CACCATCCGG	CTGTGCCTCC	TTCAACGCCC	AGGTCATYGT	CCTCAACCAC	900
	CCCGGCCAGA	TCGGTGCTGG	TTACGSTCCA	GTCCTCGACT	GCCACACTGS	950
	TCACATTGCT	TGCAAGTTCG	CTGAGCTCCT	CGAGAAGATT	GACCGCCGTA	1000
	CCGGTAAATC	CGTCGAAGCC	AACCCCAAGT	TCGTCAAGTC	TGG	1043

2) INFORMATION FOR SEQ ID NO: 1270

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium canis*
 (B) STRAIN: WSA-217

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270

GCTGAGCGTG AGCGTGGTAT CACCATTGAT ATCGCCCTCT GGAAGTTCGA 50
 GACCCCAAG TACATGGTCA CCGTCATCGG TATGCTTTAT CTGTTTCCCA 100
 TTTATAGTTG CGACCAAGTAA CTAACAAAAA GTAGATGCCC CCGGGCACCG 150
 20 TGAATTCATC AAGAACATGA TTACTGGTAC CTCCCAGGCC GACTGCGCTA 200
 TTCTCATCAT TGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG 250
 GATGGCCAGA CTCGTGAGCA CGCCCTGCTC GCTTTCACCC TCGGTGTCAA 300
 GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAC TGGTCTGAGT 350
 CCCGTTTCGG TGAAATCATC AAGGAAGTCA CCAACTTCAT CAAGAAGGTC 400
 25 GGCTACGACC CCAAGGGTGT CCCATTTCGTC CCAATCTCTG GCTTCAACGG 450
 TGACAACATG ATTGAGCCCT CCACCAACTG CCCATGGTAC AAGGGATGGA 500
 ACAAGGAGAC CAAGGCCGGT GGCAAATCCT CTGGTAAGAC CCTCCTTGAG 550
 GCCATCGATG CCATTGACAT GCCCACTCGT CCCACCGACA AGCCTCTCCG 600
 TCTCCCCTC CAGGATGTCT ACAAGATCTC TGGTATCGGA ACAGTACCAG 650
 30 TCGGTCGTGT TGAGACTGGT ATCATCAAGC CTGGTATGGT TGTCACCTTY 700
 GCCCCCGCCA ACGTCACCAC TGAAGTCAAG TCCGTCGAAA TGCACCACCA 750
 GCAGCTYGTG CAGGGTGTTT CCGGTGACAA CGTTGGCTTC AACGTCAAGA 800
 ACGTYTCTGT CAAGGAAGTC CGCCGTGGTA ACGTTGCCGG TGATTCCAAG 850
 AACGACCCAC CAGCTGGCTG CGCCTCTTTC AAGGCCCAGG TCATCGTCTT 900
 35 CAACCAACCC GGCCAGATCG GTGCTGGTTA CGCCCCAGTC CTTGACTGCC 950
 AACTGCCCCA CATTGCTTGC AAGTTCTCTG AGCTTCTTGA GAAGATTGAC 1000
 CGCCGTACTG GTAAATCCGT CGAAACCAGC CCTAAGTTCG TCAAGTCTGG 1050
 TGATGCCGCT ATTGCCACCA TGGTTCCATC CAAGCCCATG TGC GTTGAGG 1100
 CTTTC 1105

40

2) INFORMATION FOR SEQ ID NO: 1271

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus versicolor*

(B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271

5
 GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA AGTTCCAGAC 50
 CCCTAAGTAT GAGGTCACCG TCATTGGTAT GTTGTCTTTC TTGTGTTACC 100
 ATCGAAACAT ATCTAACCTA CAACTGCAGA CGCCCCCGGT CACCGTGA CT 150
 TCATCAAGAA CATGATCACT GGTACCTCCC AGGCCGACTG CGCTATTCTC 200
 10 ATCATTGCTT CCGGTACTGG TGAATTCGAG GCTGGTATCT CCAAGGATGG 250
 CCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTCGGT GTCCGTCAGC 300
 TCATCGTTGC CCTCAACAAG ATGGACACTG CTGGCTGGGC TGAGGCTCGT 350
 TACAACGAAA TCGTCAAGGA AACTTCCGGT TTCATCAAGA AGGTCGGCTA 400
 CAACCCCAAG TCGGTTCCCT TCGTCCCAT CTCCGGTTTC AACGGTGACA 450
 15 ACATGCTTGA GCCCTCCTCC AACTGCCCCCT GGTACAAGGG TTGGGAGAAG 500
 GAGACCAAGG CTGGTAAGGC CACTGGTAAG ACCCTCCTCG AGGCCATCGA 550
 CGCCATTGAG CCTCCCGTCC GTCCCTCCAA CAAGCCTCTC CGTCTTCCCC 600
 TCCAGGATGT CTACAAGATC TCTGGTATTG GAACTGTCCC CGTCGGCCGT 650
 GTCGAGACCG GTACCATCGT CCCC GGATG GTCGTCACCT TCGTCCCCGC 700
 20 CAACGTCACC ACTGAAGTCA AGTCCGTTGA GATGCACCAC CAGCAGCTCA 750
 AGGAGGGTGT TCCCGGKAC AACGTTGGTT TCAACGTGAA GAACGTTTCC 800
 GTCAAGGAAG TCCGCCGTGG TAACGTCGCT GGTGACTCCA AGAACGACCC 850
 CCCTGCCGGT GCTGCCTCTT TCACCGCCCA GGTCATCGTC CTCAACCACC 900
 CCGGTCAGGT CGGCGCTGGT TACGCTCCCG TCCTCGACTG CCACACCGCT 950
 25 CACATTGCCT GCAAGTTCG TGAGCTCCAG GAGAAGATCG ACCGCCGTAC 1000
 CGGAAAGTCT GTCGAATYTG CCCCCAAGTT CATCAAGTCT GGTGACGCCG 1050
 CTATCGTCAA GATGATTCCC TCCAAGCCCA TGTGTGTCGA GTCTTTTCACT 1100
 GACTACCCTC CTYTCGGCCG TTTCGCCGTC CGTGACGTAA GTTCTTTCCC 1150
 CAGCTTTTCG ATGCTACCCT TCTMTGAATC ACGTGTCTATG TCTTGGCACC 1200
 30 CGCCCATCAC ATGACCACGC AACCCCTATAC CCCGCCACAC CCTT 1244

2) INFORMATION FOR SEQ ID NO: 1272

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Exophiala moniliae*
 (B) STRAIN: WSA-219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272

50 GCTGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT GGAAGTTCGA 50
 GACCCCAAG TACTATGTCA CCGTCATCGA CGCCCCCGGT CATCGTGA CT 100
 TCATCAAGAA CATGATCACT GGTACTTCCC AAGCTGACTG CGCCATTCTC 150
 ATCATTGCTG CCGGTACTGG TGAATTCGAA GCCGGTATCT CCAAGGATGG 200

	TCAGACCCGT	GAGCACGCTC	TGCTTGCCTA	CACCCTGGGT	GTCAAGCAGC	250
	TCATTGTGCG	CATCAACAAG	ATGGACACTA	CCAAGTGGTC	TGAGGACCGT	300
	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	AGGTCGGCTA	350
	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	AACGGTGACA	400
5	ACATGATCGA	CGTCTCCACC	AACTGCCCCT	GGTACAAGGG	CTGGGAGAAG	450
	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTTG	AGGCCATCGA	500
	CGCCATTGAC	CCCCCTCTC	GTCCCAACGA	CAAGCCTYTC	CGTCTCCCTC	550
	TCCAGGATGT	GTACAAGATC	TCTGGTATCG	GAACGGTGCC	CGTCGGTCGT	600
	GTCGAGACTG	GTATCATCAA	GGCCGGTATG	GTCGTTACCT	TCGCTCCTGC	650
10	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	GAACAGCTCG	700
	CCGAGGGTGT	TCCAGGTGAC	AACGTCGGTT	TCAACGTCAA	GAACGTYTCC	750
	GTCAAGGAGG	TTCGTCGTGG	AAACGTTTGC	GGTGACTCCA	AGAACGACCC	800
	ACCCAAGGGC	GCTGATTCTT	TCAACGCCCA	GGTCATCGTC	TTGAACCACC	850
	CTGGTCAAGT	TGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	CCACACTGCC	900
15	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATCG	ATCGTCGKAC	950
	CGGAAAGTCG	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	GGTGACGCTG	1000
	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TG		1032

20

2) INFORMATION FOR SEQ ID NO: 1273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hortaea werneckii*
 (B) STRAIN: ATCC 34944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273

	TAACAGCCCG	TGCGACCGTC	TCGTCCAATA	ACTAATGATT	CGCAGGTACT	50
	ATGTCGTGAG	TATCCGGTCC	TTTTTTGTTA	ATTTACCAGA	AATGACGAAA	100
	TTTTTGACTA	ATTAACACAC	TCAGACCGTC	ATTGACGCCC	CGGGTCACCG	150
40	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCAGGCC	GACTGCGCTG	200
	TCCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTCGCCATCA	ATAAGATGGA	CACCACCAAG	TGGTCCGAGG	350
	AGCGTTACGG	CGAGATCATC	AAGGAGACCT	CTGCCTTCAT	CAAGAAGGTC	400
45	GGTTTCAACC	CGAAGCACGT	CCCGTTCGTC	CCGATCTCCG	GTTTCAACGG	450
	TGACAACATG	ATCGAGGCCT	YCACCAACTG	CCCGTGGTAC	AAGGGCTGGG	500
	AGAAGGAGAC	CAAGGCCAAG	GTCACCGGCA	AGACCCTYCT	TGAGGCCATT	550
	GACAACATCG	ACCCGCCGAG	CCGTCTTCC	GACAAGCCGC	TCCGTCTTCC	600
	CCTCCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGGACAGTC	CCAGTCGGCC	650
50	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTTAC	CTTCGCTCCG	700
	GCTGGTGTCA	CCACTGAAGT	GAAGTCCGTT	GARATGCACC	ACGAGCAGCT	750
	CGCTGAGGGT	YTGCCGGGTG	ACAACGTCGG	CTTCAACGTC	AAGAACGTTT	800
	CCGTCAAGGA	GATCCGTCGT	GGCAACGTTG	CTGGTGACAG	CAAGGCTGAC	850

	CCGCCGAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	TCCTGAACCA	900
	CCCTGGCCAG	GTCGGTGCTG	GTTACGCTCC	AGTCCTGGAC	TGCCACACTG	950
	CCCACATTGC	CTGCAAGTTC	GGCGAGCTCC	TCGAGAAGAT	CGACCGTCGC	1000
	TYTGGCAAGT	CCATTGAAGC	CTYGCCTAAG	TACATCAAGT	CTGGTGACGC	1050
5	TGCCATYGTC	AAGATGATTC	CGTCCAAGCC	GATGTGCGTT	GAGCCATTCA	1100
	CTGAGT					1106

10 2) INFORMATION FOR SEQ ID NO: 1274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
 (B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274

25	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
	GTTTCGAGACT	CCCCGCTACT	ATGTCACCGT	CATTGGTATG	TTGCTGTCAC	100
	CTCTCTCACA	CATGTCTCAC	CACTAACAAAT	CAACAGACGC	CCCCGGCCAC	150
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGACTGCGC	200
30	CATTCTCATC	ATTGCCGCCG	GTA CTGGTGA	GTTTCGAGGCT	GGTATCTCCA	250
	AGGATGGCCA	GACCCGTGAG	CACGCCCTGC	TCGCCTACAC	CCTCGGTGTC	300
	AAGAACCTCA	TTGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	350
	GTCCCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCA ACTTC	ATCAAGAAGG	400
	TCGGCTACAA	CCCCAAGGCT	GTCGCTTTTCG	TCCCCATCTC	CGGTTTCAAC	450
35	GGCGACAACA	TGCTTACTCC	CTCCACCAAC	TGCCCCCTGGT	ACAAGGGCTG	500
	GGAGCGTGAG	ATCAAGTCCG	GCAAGCTCAC	TGGCAAGACC	CTCCTCGAGG	550
	CCATTGACTC	CATCGAGCCC	CCCAAGCGTC	CCGTCGACAA	GCCCCCTYCGA	600
	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATTGGCA	CGGTTCCCGT	650
	CGGCCGTATC	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTMG	700
40	CCCCCTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	750
	CAGCTCTYTG	AGGGTCTTCC	CGGTGACAAC	GTCGGCTTCA	ACGTGAAGAA	800
	CGTYTCCGTC	AAGGAGATCC	GACGTGGCAA	CGTCGCTGGT	GACTCCAAGA	850
	ACGACCCCCC	TYTGGGTGCC	GCCTCTTTCA	CCGCCCAGGT	CATTGTCCTC	900
	AACCACCTTG	GCCAGGTCGG	TGCCGGTTAC	GCCCCCGTTY	TGGACTGCCA	950
45	CACTGCCCAC	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	1000
	GCCGA ACTGG	TAAGGCTGTT	GAGTCCGCC	CCAAGTTCAT	CAAGTCTGGT	1050
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1100
	TTTCACTGAC	TACCCCCCT				1119

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2) INFORMATION FOR SEQ ID NO: 1275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Aureobasidium pullulans*
(B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275

```
15 CTGAAGTCTG AGCGTGAGCG TGGTATCACT ATCGATATCG CCCTCTGGAA      50
   GTTCGAGACC CCCAAGTACA TGGTCACCGT CATCGATGCC CCCGGTCACC      100
   GTGATTTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC TGA CTGCGCC      150
   ATTCTCATCA TTGCTGCCGG TACTGGTGAG TTCGAGGCTG GTATCTCCAA      200
   GGATGGCCAG ACTCGTGAGC ACGCTCTCCT CGCCTACACC CTTGGTGTCA      250
20 AGCAGCTCAT CGTTGCCATC AACAAAGATGG ACACCACCAA GTGGTCTGAG      300
   GCCCGTTACC AGGAGATCAT CAAGGAGACC TCCGGTTTCA TCAAGAAGGT      350
   CGGCTACAAC CCCAAGCACG TTCCCTTCGT CCCCATCTCC GGCTTCAACG      400
   GAGACAACAT GATCGAGGTC AGCTCCAAC T GCCCTTGGTA CAAGGGTTGG      450
   GAGAAGGAGA CCAAGGCCAA GGCCACTGGC AAGACCCTCC TCGAGGCCAT      500
25 TGACGCCATC GACCCTCCTT CCCGTCCTAC CGACAAGCCC CTCCGTCTTC      550
   CCCTCCAGGA TGTCTACAAG ATCGGTGGTA TTGGCACGGT GCCCGTCGGT      600
   CGTGTTGAGA CCGGTAAGAT CATGGGTGGT ATGGTTGTCA CCTTCGCCCC      650
   CGCTGGTGTC ACCACCGAGG TCAAGTCCGT CGAGATGCAC CACGAGCAGC      700
   TCACCGAGGG TCTTCCCGGT GACAACGTCG GCTTCAACGT CAAGAACGTY      750
30 TCCGTCAAGG AGATCCGTCG TGGCAACGTT GCCGGTGA CT CCAAGAACGA      800
   CCCCCCAAG GGTGTGACT CCTTCAACGC CCAGGTCATC GTCCTGAACC      850
   ACCCTGGTCA GGTCCGTGCT GGTTACGCAC CCGTCCTCGA CTGCCACACT      900
   GCCCACATTG CTTGCAAGTT YTCCGAGCTT GTTGAGAAGA TTGACCGCAG      950
   AACCGGCAAG TCCGTTGAGG CTGCCCCCAA GTTCATCAAG TCTGGTGACG      1000
35 CCGCCATCGT CAAGATGGTT CCCTCCAAGC CCATGTGTGT TGAGGCTTTC      1050
   ACCGACTACC CTCCTYTCGG TCGTTTCGCC GTCCGGTATG TTTTCTTCT      1100
   TCAATCATTC TTC                                     1113
```

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2) INFORMATION FOR SEQ ID NO: 1276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
(B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276

	GGTCTGAGAC	CCGTTTCAAC	GAAATTATCA	AGGAAGTCAG	CAACTTCATC	50
5	AAGAAGGTCG	GATACAACCC	CAAGTCTGTT	CCCTTCGTGC	CAATCTCCGG	100
	TTTCGAGGGT	GACAACATGA	TTGAGCCTTC	CCCCAACTGC	CCTTGGTACA	150
	AGGGCTGGAA	CAAGGAGACT	GCTGCTGGCA	AGGCCGCCGG	TAAGACTCTT	200
	CTCGATGCCA	TTGACGCCAT	CGACCCCCCC	GTCCGTCCTA	CCGAGAAGCC	250
	TCTCCGTCTT	CCCCTCCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	300
10	TTCCCGTTGG	ACGTGTCGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTG	350
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TTGAAATGCA	400
	CCACCAGCAG	CTCCAGGCTG	GTTACCCTGG	TGACAACGTC	GGCTTCAACG	450
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCGGTGAC	500
	TCCAAGAACG	ACCCCCCCAA	GGGCTGCGAG	TCCTTCAACG	CCCAGGTCAT	550
15	CGTCCTCAAC	CACCCCGGCC	AGGTTGGCGC	TGGTTATGCC	CCAGTCCTCG	600
	ACTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCTGAGCT	CATCGAGAAG	650
	ATTGACCGCC	GTACCGGAAA	GTCTGTTGAG	GACAACCCCA	AGTTCATCAA	700
	GTCCGGTGAT	GCTGCTATCG	TCAAGATGAT	T		731

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2) INFORMATION FOR SEQ ID NO: 1277

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 1046 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Exophiala dermatitidis</i>
	(B) STRAIN: ATCC 76088

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277

	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCCCTCTG	GAAGTTCGAG	50
	ACCCCCAAGT	ACTATGTCAC	CGTCATCGAC	GCCCCGGGTC	ATCGTGACTT	100
40	TATCAAGAAC	ATGATCACTG	GTACCTCGCA	GGCCGACTGC	GCCATCTTGA	150
	TCATTGCCGC	CGGTACCGGT	GAATTCGAAG	CCGGTATCTC	CAAGGATGGT	200
	CAGACCCGTG	AGCACGCTCT	GCTCGCCTAC	ACCTTGGGTG	TCAAGCAGCT	250
	CATCGTCGCC	ATCAACAAGA	TGGACACCAC	CAAGTGGTCC	GAGGAGCGTT	300
	TCAACGAAAT	CATCAAGGAG	ACTTCCAAC	TCATCAAGAA	GGTCGGCTAC	350
45	AACCCCCAAG	CCGTTCCCTT	CGTCCCCATC	TCCGGCTTCA	ACGGTGACAA	400
	CATGATTGAG	GTCTCCACCA	ACTGCCCGTG	GTACAAGGGA	TGGGAGAAGG	450
	AGTCCAAGGC	TGGCAAGGCC	ACCGGCAAGA	CCCTCCTCGA	GGCCATTGAC	500
	GCCATCGACC	CACCCACCCG	TCCCACCGAC	AAGCCTCTCC	GTCTCCCTCT	550
	CCAGGATGTC	TACAAGATCT	CTGGTATCGG	AACGGTTCCT	GTCGGTCGTG	600
50	TCGAGACCGG	TACCATCAAG	GCCGGTATGG	TCGTCACCTT	CGCTCCGGCC	650
	AACGTCACCA	CTGAAGTCAA	GTCCGTCGAA	ATGCACCACG	AGCAGCTCGC	700
	CGAGGGTYTG	CCAGGTGACA	ACGTTGGCTT	CAACGTCAAG	AACGTYTCCG	750
	TCAAGGAGGT	TCGTCGTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCG	800

	CCCAAGGGTG	CCGAGTCCTT	CAACGCCCAG	GTCATTGTCC	TCAACCACCC	850
	TGGTCAGATC	GGTGCCGGCT	ACGCTCCAGT	CTTGGATTGC	CACACTGCCC	900
	ACATTGCTTG	CAAGTTCGCC	GAGTTGCTCG	AGAAGATCGA	CCGTCGTACC	950
	GGAAAGTCCA	TCGAGAACAA	CCCCAAGTTC	ATCAAGTCTG	GTGATGCTGC	1000
5	CATCGTCAAG	ATGATTCCCA	GCAAGCCCAT	GTGTGTCGAG	GCTTTC	1046

2) INFORMATION FOR SEQ ID NO: 1278

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278

25	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	TCGAGACTCC	50
	TCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GTCGCTCATA	CCTCATCCTA	100
	CTTCCTCATA	CTAACACATC	ATTGAGACGC	TCCCGGTCAC	CGTGATTTC	150
	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGATTGCGC	CATTCTCATC	200
	ATTGCCGCCG	GTAATGGTGA	GTTGAGAGCT	GGTATCTCCA	AGGATGGCCA	250
30	GACCCGTGAG	CACGCTCTTC	TTGCCTACAC	CCTTGGTGTC	AAGAACCTCA	300
	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCTGA	GGCCCGTTAC	350
	CAGGAGATCA	TCAAGGAGAC	CTCCTCTTTC	ATCAAGAAGG	TCGGCTACAA	400
	CCCCAAGGCT	GTCGCTTTCG	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	450
	TGCTTACCCC	CTCCACCAAC	TGCCCCCTGGT	ACAAGGGTTG	GGAGCGTGAG	500
35	ATCAAGTCCG	GCAAGCTCTC	CGGCAAGACC	CTCCTCGAGG	CCATTGACTC	550
	CATCGAGCCT	CCCAAGCGTC	CCGTTGACAA	GCCCCCTCCG	CTTCCCCTCC	600
	AGGATGTCTA	CAAGATCGGT	GGTATTGGAA	CGGTTCCCGT	CGGCCGTATT	650
	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTCG	CTCCCTCCAA	700
	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	CAGYTCAGTK	750
40	AGGGCCAGCC	CGGTGACAAC	GTTGGTTTCA	ACGTGAAGAA	CGTTTCCGTC	800
	AAGGACATCC	GACGTGGTAA	CGTCGCTGGT	GACTCCAAGA	ACGACCCCCC	850
	CCAGGGTGCC	GCTTCTTTCA	CCGCCCAGGT	CATCGTCCTC	AACCACCCCG	900
	GCCAGGTCGG	TGCTGGTTAC	GCTCCTGTCC	TCGATTGCCA	CACTGCCCCAC	950
	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	GCCGAACCGG	1000
45	TAAGGCTACT	GAGGCCGCTC	CCAAGTTCAT	CAAGTCTGGT	GACTCCGCCA	1050
	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GTGTCGAGGC	TTTCACTGAC	1100
	TACCCTCCT					1109

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2) INFORMATION FOR SEQ ID NO: 1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus terreus*
 (B) STRAIN: WSA-174

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279

15 CCTGCAAGTG GTCTGAGGAC CGTTACAACG AAATCGTGAA GGAGACCTCC 50
 AACTTCATCA AGAAGGTCGG CTACAACCCC AAGGCCGTTC CCTTCGTCCC 100
 CATCTCCGGT TTCAACGGTG ACAACATGCT TGAGCCTTCC CCCAACTGCC 150
 CCTGGTACAA GGGTTGGGAG AAGGAGGGCA AGTCCGGCAA GGTCACCGGT 200
 AAGACTCTCC TCGAGGCCAT CGATGCCATC GAGCCCCCGG TCCGTCCTGC 250
 CAACAAGCCT CTCCGTCTTC CCCTCCAGGA TGTGTACAAG ATCTCTGGTA 300
 20 TCGGAAGTGT CCCCCTCGGC CGTGTGCGAGA CTGGTGTCAT CACCCCCGGC 350
 ATGGTTGTTA CCTTCGCTCC TTCCAACGTC ACCACTGAAG TGAAGTCCGT 400
 TGAGATGCAC CACCAGCAGC TCAAGGAGGG TCTCCCCGGT GACAACGTTG 450
 GTTTC AACGT CAAGAACGTC TCCGTCAAGG AGGTCCGTCG TGGTAAACGTC 500
 GCTGGTGA CT CCAAGAACGA CCCCCCTGCT GCGCTGCCT CCTTCACCGC 550
 25 CCAGGTCATC GTTCTCAACC ACCCCGGTCA GGTGCGCGCT GGCTACGCCC 600
 CCGTCCTCGA CTGCCACACT GCCCACATTG CCTGCAAGTT CGCTGAGCTC 650
 CAGGAGAAGA TTGACCGCCG TACCGGAAAG TCTGTTGAGT CTTCTCCCAA 700
 GTTCATCAAG TCTGGTGATG CTGCCATCGT CAAGATGATC CCTYCAAAGC 750
 CCATGTGCGT CGAAG 765

30

2) INFORMATION FOR SEQ ID NO: 1280

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280

50 GCGTGGTATC ACCATCGACA TTGCCCTCTG GAAGTCCAG ACTCCCAAGT 50
 ATGAGGTCAC TGTCATCGGT AAGCTCGACT CGCCCCGATA TGTTTTGGTG 100
 CTGTAGCTAA CACGATCTGA AGATGCCCCC GGTCACCGTG ACTTCATCAA 150
 GAACATGATC ACTGGTACCT CCCAGGCTGA CTGCGCTATC CTCATCAT TG 200
 CCTCCGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACC 250

	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	GGTGTCAAGC	AGCTCATCGT	300
	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	GTCCGAGGAT	CGTTACAACG	350
	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	400
	AAGGCCGTTC	CCTTCGTMCC	CATCKCTGGC	TTCAACGGTG	ACAACATGCT	450
5	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	GGGATGGGAG	AAGGAGACCA	500
	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	TCGAGGCCAT	YGACGCCATT	550
	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	CTYCGTCTTC	CCCTCCAGGA	600
	TGTYTACAAG	ATCTCTGGTA	TCGGAACGGT	CCCTGTCGGC	CGTGTCGAGA	650
	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	CCTTTGCCCC	CGCCAACGTC	700
10	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	CACCAGCAGC	TCCAGGAGGG	750
	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	CAAGAACGTT	TCCGTCAAGG	800
	AAGTCCSCCG	TGGTAACGTT	TGCGGTGACT	CCAAGAACGA	TCCCCCTCAG	850
	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	GTCTTCAACC	ACCCCGGTCA	900
	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	CTGCCACACT	GCCACATTG	950
15	CTTGCAAGTT	CTYTGAGCTG	CTTGAGAAGA	TTGACCGCCG	TACCGGCAAG	1000
	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	TCCGGTGAWG	CCGCCATCGT	1050
	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	CGAGTCCTTC	ACTGACTACC	1100
	CCCCT					1105

20

2) INFORMATION FOR SEQ ID NO: 1281

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 1343 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus laurentii*
(B) STRAIN: ATCC 44096
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281

	GCCGAGCGAG	AGCGAGGTAT	CACCATCGAC	ATTGCTCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACAACGTCA	CCGTCAATGA	CGCCCCCGGA	CACCGAGACT	100
40	TCATCAAGAA	CATGATCACC	GGTACCTCCC	AGGCCGACTG	CGCCATCCTT	150
	ATCATTGCCA	CCGGTATCGG	AGAGTTCGAG	GCCGGTATCT	CTAAGGACGG	200
	TCAGACCCGA	GAGCACGCTT	TGCTCGCCTT	CACCCTCGGT	GTCAGGCAGC	250
	TCATCGTTGC	TTGCAACAAG	ATGGACACCT	GCAAGTGGTC	CGAGGACCGA	300
	TTCAACGAGA	TCGTCAAGGA	GACCAACGGT	TTCATCAAGA	AGGTTCGATA	350
45	CAACCCCAAG	GCTGTTCCCT	TCGTCCCCAT	CTCTGGATGG	CACGGAGACA	400
	AGTGAGTGCC	GTTCTTTGCG	TTGAGCCCTC	TTTGTCGCTC	CCCCTCCCTC	450
	TCAAGTGGCG	GCGGCGGTCT	CCACCCACAA	ATCGGGTGGC	GAATCCGCCA	500
	CACCCACCAC	TTCTCGCCAC	CGAGTGTGGC	ACTTCTTCCA	ACTCCTCTTT	550
	CCACTCCTCC	TCGTCTCGTC	TCTTTTTTTC	TCCGTTGTCT	TTGACAAGGG	600
50	GAGTGTGCTG	ATAGTAAAGC	ATGCTTGAGG	AGACCACCAA	CATGCCGTGG	650
	TACAAGGGAT	GGACCAAGGA	GACCAAGTCC	GGTGTCGTTA	AGGGTAAGAC	700
	CCTCCTCGAC	GCCATCGACG	CCATCGAGCC	TCCTCAACGA	CCCACCGACA	750
	AGCCCTCCG	ACTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATCGGT	800

	ACGGTGCCCG	TCGGCCGAGT	CGAGACCGGT	GTCATCAAGG	CCGGGTAAGT	850
	CACGGGAGCC	TGACGGCTGT	TGTTGCCACA	CCCAACTTAT	ATCCAGTATG	900
	GTCGTCACCT	TCGCTCCTAC	CAACGTCACC	ACTGAGGTTA	AGTCCGTTGA	950
	GATGCACCAC	GAGCAGATCC	CTGAGGGTCT	TCCCGGAGAC	AACGTTGGTT	1000
5	TCAACGTGAA	GAACGTTTCC	ATCAAGGACA	TCCGACGAGG	AAACGTYTGC	1050
	TCCGACTCCA	AGAACGACCC	CGCTAAGGAG	GCCGCTTCTT	TCAACGCCCA	1100
	GGTCATTGTC	CTCAACCACC	CTGGACAGAT	TGGTGCCGGT	TACACCCCCG	1150
	TCCTCGACTG	CCACACCGCC	CACATTGCCT	GCAAGTTCGC	CGAGCTCATC	1200
	GAGAAGATCG	ACCGACGAAC	TGGTAAGACC	ATGGAGGCCG	CCCCCAAGTT	1250
10	CGTCAAGTCC	GGAGACGCCG	CCATTGTCAA	GCTCGTTGCC	CAGAAGCCCA	1300
	TCTGTGTCGA	GTCTTACTCT	GACTACCCTC	CCCTTGACG	ATT	1343

15 2) INFORMATION FOR SEQ ID NO: 1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282

30	TGGTCCGAGG	CTCGTTTCAA	CGAAATCATC	AAGGAAGTCA	CCAAC TTCAT	50
	CAAGAAGGTC	GGATACAACC	CCAAGTCTGT	TCCCTTCGTG	CCAATCTCTG	100
	GTTTCGAGGG	TGATAACATG	ATTGAGCCCT	CCACCAACTG	CCCCTGGTAC	150
	AAGGGCTGGA	CCAAGGAGAC	CGCTGCCGGC	AAGTCAACCG	GTAAGACTCT	200
35	TCTTGACGCC	ATTGATGCCA	TCGATCAACC	CTCCCGTCCT	ACCGACAAGC	250
	CCCTCCGTCT	TCCCCTCCAG	GATGTGTACA	AGATCTCCGG	TATTGGCACT	300
	GTTCCC GTTG	GACGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTCG	350
	GACCTTCGCT	CCCTCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	400
	ACCACCAACA	GCTCTTGGCT	GGTAACCCCG	GTGACAACGT	CGGTTTCAAC	450
40	GTCAAGAACG	TTTCCGTCAA	GGAAGTCCGC	CGTGGCAACG	TTGCTGGTGA	500
	CTCAAAGAAC	GACCCCCCCA	AGGGCTGCGA	CTCCTTCAAC	GCCCAGGTCA	550
	TCGTCCCTCA	TCACCCCGGT	CAAGTTGGCG	CTGGTTATGC	CCCAGTCCTC	600
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TCCTCGAGAA	650
	GATTGACCGC	CGTACCGGAA	AGTCCACTGA	GAACAACCCC	AAGTTCATCA	700
45	AGTCTGGTGA	CGCCGCTATC	GTCAAGATGG	TTCC		734

2) INFORMATION FOR SEQ ID NO: 1283

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*

(B) STRAIN: ATCC 62877

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283

```

CGTGAGCGTG GTATCACCAT CGACATTGCC CTCTGGAAGT TCGAGACTCC      50
CCGCTACTAT GTCACCGTCA TTGGTATGTT GCTGTCACCT CTCTCACACA      100
TGTCTCACCA CTAACAATCA ACAGACGCCC' CCGGCCACCG TGACTTCATC      150
15 AAGAACATGA TCACTGGTAC TTCCCAGGCC GACTGCGCCA TTCTCATCAT      200
TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      250
CCCGTGAGCA CGCCCTGCTC GCCTACACCC TCGGTGTCAA GAACCTCATT      300
GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGT CCCGTTACCA      350
GGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC      400
20 CCAAGGCTGT CGCTTTCGTC CCCATCTCCG GTTTC AACGG CGACAACATG      450
CTTACTCCCT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGCGTGAGAT      500
CAAGTCCGGC AAGCTCACTG GCAAGACCCT CCTCGAGGCC ATTGACTCCA      550
TCGAGCCCCC CAAGCGTCCC GTCGACAAGC CCCTCCGACT TCCCCTCCAG      600
GATGTCTACA AGATCGGTGG TATTGGCAGG GTTCCCGTCG GCCGTATCGA      650
25 GACTGGTGTC ATCAAGCCCG GTATGGTCGT TACCTTCGCC CCCTCCAACG      700
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCTYTGAG      750
GGTCTTCCCG GTGACAACGT CGGCTTCAAC GTKAAGAAGC TYTCCGTCAA      800
GGAGATCCGA CGTGGCAACG TCGCTGGTGA CTCCAAGAAC GACCCCCCTY      850
TGGGTGCCGC CTCTTTCACC GCCCAGGTCA TTGTCTCTCAA CCACCCTGGC      900
30 CAGGTCGGTG CCGGTTACGC CCCCCTTYTG GACTGCCACA CTGCCCACAT      950
TGCCTGCAAG TTCGCCGAGA TCCAGGAGAA GATCGACCGC CGAACTGGTA      1000
AGGCTGTTGA GTCCGCCCCC AAGTTCATCA AGTCTGGTGA CTCCGCCATC      1050
GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGACTA      1100
CCCCCTT                                     1107

```

35

2) INFORMATION FOR SEQ ID NO: 1284

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*

50

(B) STRAIN: ATCC 14285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284

	GCTCAAGGCC	GAGCGTGAGC	GCGGTATCAC	CATCGATATT	GCTCTGTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TACGTCACCG	TCATTGACGC	CCCCGGTCAT	100
	CGCGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTCGAGGCT	GGTATCTCCA	200
5	AGGATGGCCA	GACTCGTGAG	CACGCTCTGC	TCGCCTACAC	CCTGGGTGTG	250
	CGGCAGCTGA	TCGTCGCCAT	CAACAAGATG	GACACGGCCA	AGTGGGCTGA	300
	GGCTCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAACCTC	ATCAAGAAGG	350
	TCGGCTACAA	CCCCAAGACT	GTTGCCTTCG	TCCCCATCTC	GGGCTTCCAC	400
	GGCGACAACA	TGCTTACTCC	CTCGACCAAC	TGCCCCCTGGT	ACAAGGGCTG	450
10	GGAGAAGGAG	GGCAAGAGCG	GCAAGGTTAC	CGGTAAGACT	CTGCTGGACG	500
	CCATTGACGC	CGTCGAGCCC	CCCAAGCGCC	CCACGGACAA	GCCCCTGCGT	550
	CTGCCCTCC	AGGATGTCTA	CAAGATCGGC	GGTATCGGCA	CTGTCCCTGT	600
	CGGCCGTATC	GAGACTGGTG	TCCTGAAGCC	CGGCATGGTC	GTCACCTTTG	650
	CCCCGTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
15	CAGCTTGTTG	AGGGTGTTCC	CGGCGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
	CGTYTCCGTC	AAGGAGATCC	GTGTGGCAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCCCC	CTCGGGCGCC	GCCACCTTCA	ACGCCCAGGT	CATTGTCCTG	850
	AACCACCCCG	GCCAGGTCGG	CAACGGCTAC	GCCCCGGTTY	TGGACTGCCA	900
	CACCGCCAC	ATTGCCTGCA	AGTTCACCGA	GATCCTTGAG	AAGATCGACC	950
20	GCCGTACCGG	CAAGTCGGTT	GAGAACAACC	CCAAGTTCAT	CAAGTCGGGT	1000
	GACGCCGCCA	TTGTCAAGCT	GACGCCCTYG	AAGCCCATGT	GCGTT	1045

25 2) INFORMATION FOR SEQ ID NO: 1285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285

40	TTGCCAGTGG	TCCGAGGCC	GTTACAACGA	AATCGTCAAG	GAGACTTCCG	50
	GTTTCATCAA	GAAGGTCGGA	TACAACCCCA	AGTCCGTTGC	CTTCGTCCCC	100
	ATCTCCGGTT	TCAACGGTGA	CAACATGCTC	GAGGCCTCTA	CCAACTGCCC	150
	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	GGCCGGTAAG	GCCACTGGTA	200
45	AGACCCTCCT	TGAGGCCATC	GACGCCATTG	AGCCCCCCAC	CCGTCCCTCC	250
	AACAAGCCCC	TCCGTCTTCC	CCTCCAGGAT	GTCTACAAGA	TCTCCGGTAT	300
	TGGAACGTGC	CCCGTCGGCC	GTGTCGAGAC	TGGTGTTATC	ACCCCCGGCA	350
	TGGTCGTAC	CTTCGCTCCT	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTT	400
	GAGATGCACC	ACCAGCAGCT	CAAGGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
50	TTTCAACGTC	AAGAACGTTT	CCGTCAAGGA	AATCCGTCGT	GGTAACGTTG	500
	CCTCCGACTC	CAAGAACGAC	CCCGCCTCCG	GCGCTGCCTC	TTTCAACGCC	550
	CAGGTCATCG	TTCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	600
	CGTCCTCGAC	TGCCACACCG	CCCACATTGC	TTGCAAGTTC	TCTGAGCTTC	650

TTCAGAAAGAT	TGACCGCCGT	ACCGGAAAGG	CTGTTGAAAC	CAGCCCCAAG	700
TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	CTTCCAAGCC	750
CATGTGCGKT	CCGA				764

5

2) INFORMATION FOR SEQ ID NO: 1286

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 971 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cladophialophora carrionii*
- (B) STRAIN: ATCC 16264

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286

ACCATCGATA	TCGCGCTCTG	GAAGTTCGAG	ACTCCCAAGT	ACTTCGTCAC	50
CGTCATCGAT	GCCCCTGGTC	ATCGTGACTT	CATCAAGAAC	ATGATCACTG	100
25 GTACCTCCCA	GGCTGATTGT	GCTATTCTCA	TCATTGCCGC	TGGTACTGGT	150
GAGTTCGAGG	CCGGTATCTC	CAAGGATGGC	CAGACCCGTG	AGCATGCTCT	200
GCTCGCCTAC	ACCCTGGGCG	TGAAGCAGCT	TATCGTCGCC	ATCAACAAGA	250
TGGACACCAC	CAAATGGTCT	GAGGATCGTT	TCAACGAAAT	CATCAAGGAG	300
ACTTCCAACT	TCATCAAGAA	GGTCGGATAC	AACCCCAAGT	CCGTTCCATT	350
30 CGTGCCCATC	TCCGGCTTCA	ACGGTGACAA	CATGATCGAC	GTCTCCACCA	400
ATGCCCCCTG	GTACAAGGGC	TGGGAAAAGG	AGTCCAAGGC	TGGCAAGGCC	450
ACCGGCAAGA	CCCTCCTTGA	GGCTATCGAC	TCCATCGACC	CTCCTGCTCG	500
TCCCACCGAC	AAGCCTCTCC	GTCTCCCACT	CCAGGATGTC	TACAAGATTT	550
CTGGTATCGG	CACGGTGCCC	GTCGGTCGTG	TTGAGACTGG	TACCATCAAG	600
35 GCCGGTATGG	TCGTCACTT	TGCCCCCGCC	AACGTCACCA	CTGAAGTCAA	650
GTCCGTCGAA	ATGCACCACG	AACAGCTYGC	CGAGGGCGTT	CCGGGTGACA	700
ACGTCGGCTT	CAACGTCAAG	AACGTYTCCG	TGAAGGAGGT	TCGTCGTGGA	750
AACGTTGCTG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTG	CCGACTCCTT	800
CAACGCCCAG	GTCATCGTCC	TCAACCACCC	TGGTCAGGTC	GGTGCTGGCT	850
40 ACGCCCCGGT	CTTGGATTGC	CACACTGCCC	ACATTGCCTG	CAAGTTCTYT	900
GAGCTCCTCG	AGAAGATCGA	TCGTCGKACC	GGCAAGTCCA	TGAAAACAA	950
CCCCAAGTTC	ATCAAGTCTG	G			971

45

2) INFORMATION FOR SEQ ID NO: 1287

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 732 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Exserohilum rostratum*
(B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287

```
10 GGTCTGAGGA CCGTTACCAG GAGATCATCA AGGAGACCTC CAACTTCATC 50
    AAGAAGGTCG GCTACAACCC CAAGCACGTT CCCTTCGTCC CCATCTCCGG 100
    TTTCAACGGA GACAACATGA TCGAGGCCTC CAGCAACTGC CCCTGGTACA 150
    AGGGTTGGGA GAAGGAGACC AAGGCCAAGG CCACTGGTAA GACCCTCCTT 200
    GAGGCCATTG ACGCCATCGA CCCTCCCAGC CGTCCTACCG ACAAGCCCCT 250
    CCGTCTTCCC CTCCAGGATG TCTACAAGAT TGGTGGTATT GGCACGGTTC 300
15 CCGTCGGTCG TGTCGAGACC GGTATCATCA AGGCCGGTAT GGTCGTCACC 350
    TTCGCCCCCG CTGGTGTAC CACTGAAGTC AAGTCCGTCG AGATGCACCA 400
    CGAGCAGCTT ACCGAGGGTG TCCCCGGTGA CAACGTCGGC TTCAACGTCA 450
    AGAACGTCTC CGTCAAGGAG ATCCGTCGTG GTAACGTTGC CGGTGACTCC 500
    AAGAACGACC CCCCCAAGGG CTGCGAGTCT TTCAACGCTC AGGTCATTGT 550
20 CCTCAACCAC CCTGGTCAGG TCGGTGCCGG TTACGCGCCA GTCCTCGACT 600
    GCCACACCGC CCACATTGCC TGCAAGTTCT CTGAGCTCCT CGAGAAGATT 650
    GACCGCCGTA CCGGAAAGTC TGTCGAAGCC TCTCCCAAGT TCATCAAGTC 700
    TGGTGACGCG GCCATCGTCA AGATGGTTCC CT 732
```

25

2) INFORMATION FOR SEQ ID NO: 1288

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 337 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288

```
45 AATGGATCCT GTATACGCAC AAAAATTAGG CGTTAACATA GATGAATTTC 50
    TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA 100
    CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC 150
    TCTTGTACCG AAAGCAGAGA TTGAAGGCGA TATGGGTGAC TCACACGTAG 200
    GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA 250
    ATCAACAAAT CARRARCAAT WGAATCTTT ATTAACCAAA TTCGWGAAAA 300
    AGTTGGGGTT ATGTTTCGGAA ACCCAGAAAC AACTCCA 337
```

50

2) INFORMATION FOR SEQ ID NO: 1289

700

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289

15 AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTRC 50
TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA 100
CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC 150
TCTTGTACCG AAAGCAGAGA TTGAAGGCGA TATGGGTGAC TCACACGTAG 200
20 GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA 250
ATCAACAAAT CARAARCAAT TGCAATCTTT ATTAACCAA TTCGTGAAAA 300
AGTTGGGGTT ATGTTTCGGAA ACCCAGAAAC AACTCC 336

25 2) INFORMATION FOR SEQ ID NO: 1290

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
30 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290

GAYTAYGCIA TGISIGTIAT HGT 23

40 2) INFORMATION FOR SEQ ID NO: 1291

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291

GCIYTICIG AYGTIMGIGA YGG

23

5 2) INFORMATION FOR SEQ ID NO: 1292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292

ARISCYTCIA RIATRTGIGC

20

20

2) INFORMATION FOR SEQ ID NO: 1293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293

ATGGCTGAAT TACCTCAATC

20

35

2) INFORMATION FOR SEQ ID NO: 1294

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294

ATGATTGTTG TATATCTTCT TCAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1295

702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295
- CAGAAAGTTT GAAGCGTTGT 20
- 15 2) INFORMATION FOR SEQ ID NO: 1296
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296
- AACGATTCGT GAGTCAGATA 20
- 30 2) INFORMATION FOR SEQ ID NO: 1297
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297
- CGGTCAACAT TGAGGAAGAG CT 22
- 45 2) INFORMATION FOR SEQ ID NO: 1298
- (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298

ACGAAATCGA CCGTCTCTTT TTC

23

10

2) INFORMATION FOR SEQ ID NO: 1299

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 2711 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: 601055
(C) ACCESSION NUMBER: X71437

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299

	ATGGCTGAAT	TACCTCAATC	AAGAATAAAT	GAACGAAATA	TTACCAGTGA	50
	AATGCGTGAA	TCATTTT TAG	ATTATGCGAT	GAGTGTTATC	GTTGCTCGTG	100
30	CATTGCCAGA	TGTTCTGTGAC	GGTTTAAAC	CAGTACATCG	TCGTATACTA	150
	TATGGATTAA	ATGAACAAGG	TATGACACCG	GATAAATCAT	ATAAAAAATC	200
	AGCACGTATC	GTTGGTGACG	TAATGGGTAA	ATATCACCCCT	CATGGTGACT	250
	CATCTATTTA	TGAAGCAATG	GTACGTATGG	CTCAAGATTT	CAGTTATCGT	300
	TATCCGCTTG	TTGATGGCCA	AGGTAAC TTT	GGTTCAATGG	ATGGAGATGG	350
35	CGCAGCAGCA	ATGCGTTATA	CTGAAGCGCG	TATGACTAAA	ATCACACTTG	400
	AACTGTTACG	TGATATTAAT	AAAGATACAA	TAGATTTTAT	CGATAACTAT	450
	GATGGTAATG	AAAGAGAGCC	GTCAGTCTTA	CCTGCTCGAT	TCCCTAATTT	500
	ATTAGCCAAT	GGTGCATCAG	GTATCGCGGT	AGGTATGGCA	ACGAATATTC	550
	CACCACATAA	CTTAACAGAA	TTAATCAATG	GTGTACTTAG	CTTAAGTAAG	600
40	AACCCTGATA	TTTCAATTGC	TGAGTTAATG	GAAGATATTG	AAGGTCCTGA	650
	TTTCCCAACT	GCTGGACTTA	TTTTAGGTAA	GAGTGGTATT	AGACGTGCAT	700
	ATGAAACAGG	TCGTGGTTCA	ATTCAAATGC	GTTCTCGTGC	AGTTATTGAA	750
	GAACGTGGAG	GCGGACGTCA	ACGTATTGTT	GTCACTGAAA	TTCCTTTCCA	800
	AGTGAATAAG	GCTCGTATGA	TTGAAAAAAT	TGCAGAGCTC	GTTTCGTGACA	850
45	AGAAAATTGA	CGGTATCACT	GATTTACGTG	ATGAAACAAG	TTTACGTACT	900
	GGTGTGCGTG	TCGTTATTGA	TGTGCGTAAG	GATGCAAATG	CTAGTGTCAT	950
	TTTAAATAAC	TTATACAAAC	AAACACCTCT	TCAAACATCA	TTTGGTGTGA	1000
	ATATGATTGC	ACTTGTAAT	GGTAGACCGA	AGCTTATTAA	TTTAAAAGAA	1050
	GCGTTGGTAC	ATTATTTAGA	GCATCAAAAG	ACAGTTGTTA	GAAGACGTAC	1100
50	GCAATATAAC	TTACGTAAAG	CTAAAGATCG	TGCCCATATT	TTAGAAGGGT	1150
	TACGTATCGC	ACTTGACCAT	ATCGATGAAA	TTATTTCAAC	GATTCGTGAG	1200
	TCAGATACAG	ATAAAGTTGC	AATGGAAAGC	TTGCAACAAC	GCTTCAAAC T	1250
	TTCTGAAAAA	CAAGCTCAAG	CTATTTTAGA	CATGCGTTTA	AGACGTCTAA	1300

	CAGGTTTAGA	GAGAAACAAA	ATTGAAGCTG	AATATAATGA	GTTATTAAAT	1350
	TATATTAGTG	AATTAGAAGC	CATCTTAGCT	GATGAAGAAG	TGTTATTACA	1400
	GTTAGTTAGA	GATGAATTGA	CTGAAATTAG	AGATCGTTTC	GGTGATGAGC	1450
	GTCGTACAGA	AATTCAATTA	GGTGGATTG	AAGACTTAGA	GGACGAAGAC	1500
5	TTAATTCCAG	AAGAACAAAT	AGTAATTACT	TTGAGCCATA	ATAACTACAT	1550
	TAAACGTTTG	CCGGTATCTA	CATATCGTGC	TCAAAACCGT	GGTGGTCGTG	1600
	GTGTTCAAGG	TATGAATACA	TTGGAAGAAG	ATTTTGTGAG	TCAATTGGTA	1650
	ACTTTAAGTA	CACATGACCA	TGTATTGTTT	TTTACTAACA	AAGGTCGTGT	1700
	ATACAAACTA	AAAGGTTATG	AAGTGCCTGA	GTTATCAAGA	CAGTCTAAAG	1750
10	GTATTCCCTGT	AGTGAATGCT	ATTGAACTTG	GAAATGATGA	AGTCATTAGT	1800
	ACAATGATTG	CTGTTAAAGA	CCTTGAAAGT	GAAGACAACT	TCTTAGTGTT	1850
	TGCAACTAAA	CGTGGTGTTG	TTAAACGTTT	AGCATTAAGT	AACTTCTCAA	1900
	GAATAAATAG	AAATGGTAAG	ATTGCGATTT	CGTTCAGAGA	AGATGATGAG	1950
	TTAATTGCAG	TTCGTTTAAC	AAGTGGTCAA	GAAGATATCT	TGATTGGTAC	2000
15	ATCACATGCA	TCATTAATTC	GATTCCCTGA	ATCAACATTA	CGTCCTTTAG	2050
	GCCGTACAGC	AACGGGTGTG	AAAGGTATTA	CACTTCGTGA	AGGTGACGAA	2100
	GTTGTAGGGC	TTGATGTAGC	TCATGCAAAC	AGTGTTGATG	AAGTATTAGT	2150
	AGTTACTGAA	AATGGTTATG	GTAAACGTAC	GCCAGTTAAT	GACTATCGTT	2200
	TATCAAATCG	TGGTGGTAAA	GGTATTAAAA	CAGCTACGAT	TACTGAGCGT	2250
20	AATGGTAATG	TTGTATGTAT	CACTACAGTA	ACTGGTGAAG	AAGATTTAAT	2300
	GATTGTTACT	AATGCCGGTG	TCATTATTTCG	ACTAGATGTT	GCAGATATTT	2350
	CTCAAAATGG	TCGTGCAGCA	CAAGGTGTTT	GCTTAATTTCG	CTTAGGCGAT	2400
	GATCAATTTG	TTTCAACGGT	TGCTAAAGTA	AAAGAGGATG	CAGATGAAGT	2450
	AAATGAAGAT	GAACAATCTA	CTGTATCTGA	AGATGGTACT	GAACAACAAC	2500
25	GTGAAGCGGT	TGTAAATGAT	GAAACACCAG	GAAATGCAAT	TCATACTGAA	2550
	GTGATTGATT	CAGAAGAAAA	TGATGAAGAT	GGACGTATTG	AAGTAAGACA	2600
	AGATTTTCATG	GATCGTGTTG	AAGAAGATAT	ACAACAATCA	TCAGATGAAG	2650
	ATGAAGAATA	A				2711

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2) INFORMATION FOR SEQ ID NO: 1300

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2628 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: K12
 45 (C) ACCESSION NUMBER: X57174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300

	ATGAGCGACC	TTGCGAGAGA	AATTACACCG	GTCAACATTG	AGGAAGAGCT	50
50	GAAGAGCTCC	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	100
	TGCCAGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	150
	GCCATGAACG	TACTAGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCTGC	200
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCATCCCCAT	GGTGACTCGG	250

	CGGTCTATGA	CACGATCGTC	CGCATGGCGC	AGCCATTCTC	GCTGCGTTAT	300
	ATGCTGGTAG	ACGGTCAGGG	TAACCTCGGT	TCTATCGACG	GCGACTCTGC	350
	GGCGGCAATG	CGTTATACGG	AAATCCGTCT	GGCGAAAATT	GCCCATGAAC	400
	TGATGGCCGA	TCTCGAAAAA	GAGACGGTCG	ATTTCTGTTGA	TAACATATGAC	450
5	GGCACGGA	AAATTCCGGA	CGTCATGCCA	ACCAAAATTC	CTAACCTGCT	500
	GGTGAACGGT	TCTTCCGGTA	TCGCCGTAGG	TATGGCAACC	AACATCCCGC	550
	CGCACAACCT	GACGGAAGTC	ATCAACGGTT	GTCTGGCGTA	TATTGATGAT	600
	GAAGACATCA	GCATTGAAGG	GCTGATGGAA	CACATCCCGG	AGCCGGACTT	650
	CCCGACGGCG	GCAATCATTA	ACGGTCGTCT	CGGTATTGAA	GAAGCTTACC	700
10	GTACCGGTCT	CGGCAAGGTG	TATATCCGCG	CTCGCGCAGA	AGTGGAAGTT	750
	GACGCCAAAA	CCGGTCGTGA	AACCATTATC	GTCCACGAAA	TTCCGTATCA	800
	GGTAAACAAA	GCGCGCCTGA	TCGAGAAGAT	TGCGGAACTG	GTAAAAGAAA	850
	AACGCGTGGA	AGGCATCAGC	GCGCTGCGTG	ACGAGTCTGA	CAAAGACGGT	900
	ATGCGCATCG	TGATTGAAGT	GAAACGCGAT	GCGGTCGGTG	AAGTTGTGCT	950
15	CAACAACCTC	TACTCCCAGA	CCCAGTTGCA	GGTTTCTTTC	GGTATCAACA	1000
	TGGTGGCATT	GCACCATGGT	CAGCCGAAGA	TCATGAACCT	GAAAGACATC	1050
	ATCGCGGCGT	TTGTTTCGTCA	CCGCCGTGAA	GTGGTGACCC	GTCGTACTAT	1100
	TTTCGAACCTG	CGTAAAGCTC	GCGATCGTGC	TCATATCCTT	GAAGCATTAG	1150
	CCGTGGCGCT	GGCGAACATC	GACCCGATCA	TCGAACTGAT	CCGTCATGCG	1200
20	CCGACGCCTG	CAGAAGCGAA	AACTGCGCTG	GTTGCTAATC	CGTGGCAGCT	1250
	GGGCAACGTT	GCCGCGATGC	TCAACGTCG	TGGCGACGAT	GCTGCGCGTC	1300
	CGGAATGGCT	GGAGCCAGAG	TTCGGCGTGC	GTGATGGTCT	GTACTACCTG	1350
	ACCGAACAGC	AAGCTCAGGC	GATTCTGGAT	CTGCGTTTGC	AGAAACTGAC	1400
	CGGTCTTGAG	CACGAAAAAC	TGCTCGACGA	ATACAAAGAG	CTGCTGGATC	1450
25	AGATCGCGGA	ACTGTTGCGT	ATTCTTGGA	GCGCCGATCG	TCTGATGGAA	1500
	GTGATCCGTG	AAGAGCTGGA	GCTGGTTCGT	GAACAGTTCG	GTGACAAACG	1550
	TCGTACTGAA	ATCACCGCCA	ACAGCGCAGA	CATCAACCTG	GAAGATCTGA	1600
	TCACCCAGGA	AGATGTGGTC	GTGACGCTCT	CTCACCAGGG	CTACGTTAAG	1650
	TATCAGCCGC	TTTCTGAATA	CGAAGCGCAG	CGTCGTGGCG	GGAAAGGTAA	1700
30	ATCTGCCGCA	CGTATTAAAG	AAGAAGACTT	TATCGACCGA	CTGCTGGTGG	1750
	CGAACACTCA	CGACCATATT	CTGTGCTTCT	CCAGCCGTGG	TCGCGTCTAT	1800
	TCGATGAAAG	TTTATCAGTT	GCCGGAAGCC	ACTCGTGGCG	CGCGCGGTCT	1850
	TCCGATCGTC	AACCTGCTGC	CGCTGGAGCA	GGACGAACGT	ATCACTGCCA	1900
	TCCTGCCAGT	GACCGAGTTT	GAAGAAGGCG	TGAAAGTCTT	CATGGCGACC	1950
35	GCTAACGGTA	CCGTGAAGAA	AACTGTCCCT	ACCGAGTTCA	ACCGTCTGCG	2000
	TACCGCCGGT	AAAGTGGCGA	TCAAACCTGGT	TGACGGCGAT	GAGCTGATCG	2050
	GCGTTGACCT	GACCAGCGGC	GAAGACGAAG	TAATGCTGTT	CTCCGCTGAA	2100
	GGTAAAGTGG	TGCGCTTTAA	AGAGTCTTCT	GTCCGTGCGA	TGGGCTGCAA	2150
	CACCACCGGT	GTTTCGCGTA	TTCGCTTAGG	TGAAGGCGAT	AAAGTCGTCT	2200
40	CTCTGATCGT	GCCTCGTGGC	GATGGCGCAA	TCCTCACC GC	AACGCAAAAC	2250
	GGTTACGGTA	AACGTACCGC	AGTGGCGGAA	TACCCAACCA	AGTCGCGTGC	2300
	GACGAAAGGG	GTTATCTCCA	TCAAGGTAC	CGAACGTAAC	GGTTTAGTTG	2350
	TTGGCGCGGT	ACAGGTAGAT	GACTGCGACC	AGATCATGAT	GATCACCAGT	2400
	GCCGGTACGC	TGGTACGTAC	TCGCGTTTCG	GAAATCAGCA	TCGTGGGCCG	2450
45	TAACACCCAG	GGCGTGATCC	TCATCCGTAC	TGCGGAAGAT	GAAAACGTAG	2500
	TGGGTCTGCA	ACGTGTTGCT	GAACCGGTTG	ACGAGGAAGA	TCTGGATACC	2550
	ATCGACGGCA	GTGCCGCGGA	AGGGGACGAT	GAAATCGCTC	CGGAAGTGGA	2600
	CGTTGACGAC	GAGCCAGAAG	AAGAATAA			2628

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2) INFORMATION FOR SEQ ID NO: 1301

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301

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GTIMGIAWIM GICCIGSIAT GTA

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- 15 2) INFORMATION FOR SEQ ID NO: 1302

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302

TAIADIGGIG GIKKIGCIAT RTA

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- 2) INFORMATION FOR SEQ ID NO: 1303

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303

GGIGAIGAID YIMGIGARGG

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- 2) INFORMATION FOR SEQ ID NO: 1304

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1304

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CIARYTTIKY ITTIGTYTG

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10 2) INFORMATION FOR SEQ ID NO: 1305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305

ATGGTGACTG CATTGTCAGA TG

22

25

2) INFORMATION FOR SEQ ID NO: 1306

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306

GTCTACGGTT TTCTACAACG TC

22

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2) INFORMATION FOR SEQ ID NO: 1307

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1923 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: M86227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307

5	ATGGTGACTG	CATTGTCAGA	TGTAAACAAC	ACGGATAATT	ATGGTGCTGG	50
	GCAAATACAA	GTATTAGAAG	GTTTAGAAGC	AGTACGTAAA	AGACCAGGTA	100
	TGTATATAGG	ATCGACTCAG	AGAGAGTTGC	ACATTAGTGT	GGAAATTGTC	150
	GATAATAGTA	TCGATGAAGC	ATTAGCTGGT	TATGCAAATA	AAATTGAAGT	200
	TGTTATTGAA	AAAGATAACT	GGATTAAAGT	AACGGATAAC	GGACGTGGTA	250
10	TCCCAGTTGA	TATTCAAGAA	AAAATGGGAC	GTCCAGCTGT	CGAAGTTATT	300
	TTAACTGTTT	TACATGCTGG	TGGTAAATTC	GGCGGTGGCG	GATACAAAGT	350
	ATCTGGTGGT	TTACATGGTG	TTGGTTCATC	AGTTGTAAAC	GCATTGTCAC	400
	AAGACTTAGA	AGTATATGTA	CACAGAAATG	AGACTATATA	TCATCAAGCA	450
	TATAAAAAAG	GTGTACCTCA	ATTTGACTTA	AAAGAAGTTG	GCACAACTGA	500
15	TAAGACAGGT	ACTGTCATTC	GTTTTAAAGC	AGATGGAGAA	ATCTTCACAG	550
	AGACAACGTG	ATACAACCTAT	GAAACATTAC	AGCAGCGTAT	TAGAGAGCTT	600
	GCTTTCTTAA	ACAAAGGAAT	TCAAATCACA	TTAAGAGATG	AACGTGATGA	650
	AGAAAACGTT	AGAGAAGACT	CCTATCACTA	TGAGGGCGGT	ATTAAATCGT	700
	ACGTTGAGTT	ATTGAACGAA	AATAAAGAAC	CTATTCATGA	TGAGCCAATT	750
20	TATATTCATC	AATCTAAAGA	TGATATTGAA	GTAGAAATTG	CGATTCAATA	800
	TAAGTCAGGA	TATGCCACAA	ATCTTTTAA	TTACGCAAAT	AACATTCATA	850
	CGTACGAAGG	TGGTACGCAT	GAAGACGGAT	TCAAACGTGC	ATTAACGCGT	900
	GTCTTAAATA	GTTATGGTTT	AAGTAGCAGA	TATGAAGAAG	AAAAGATAGC	950
	TTCTGGTGAA	GATACACGAG	AAGGTATGAC	AGCAATTATA	TCTATCAAAC	1000
25	ATGGTGATCC	TCAATTCGAA	GGTCAAACGA	AGACAAAATT	AGGTAATTCT	1050
	GAAGTGCCTC	AAGTTGTAGA	TAAATTATTC	TCAGAGCACT	TTGAACGATT	1100
	TTTATATGAA	AATCCACAAG	TCGCACGTAC	AGTGGTTGAA	AAAGGTATTA	1150
	TGGCGGCACG	TGCACGTGTT	GCTGCGAAAA	AAGCGCGTGA	AGTAACACGT	1200
	CGTAAATCAG	CGTTAGATGT	AGCAAGTCTT	CCAGGTAAAT	TAGCCGATTG	1250
30	CTCTAGTCAA	AGTCCTGAAG	AATGTGAGAT	TTTCTTAGTC	GAAGGGGACT	1300
	CTGCCGGAGG	GTCTACAAAA	TCTGGTCGTG	ACTCTAGAAC	GCAGGCGATT	1350
	TTACCATTAC	GAGGTAAGAT	ATTAAATGTT	GAAAAAGCAC	GATTAGATAG	1400
	AATTTTGAAT	AACAATGAAA	TTCGTCAAAT	GATCACAGCA	TTTGGTACAG	1450
	GAATCGGTGG	CGACTTTGAT	CTAGCGAAAG	CAAGATATCA	CAAAATCGTC	1500
35	ATTATGACTG	ATGCCGATGT	GGATGGAGCG	CATATTAGAA	CATTGTTATT	1550
	AATATTCTTC	TATCGATTTA	TGAGACCGTT	AATTGAAGCA	GGCTATGTGT	1600
	ATATTGCACA	GCCACCGTTG	TATAAACTGA	CACAAGGTAA	ACAAAAGTAT	1650
	TATGTATACA	ATGATAGGGA	ACTTGATAAA	CTTAAATCTG	AATTGAATCC	1700
	AACACCAAAA	TGGTCTATTG	CGCTATACAA	AGGTCTTGGA	GAAATGAATG	1750
40	CAGATCAATT	ATGGGAAACA	ACAATGAACC	CTGAGCACCG	CGCTCTTTTA	1800
	CAAGTAAAAC	TTGAAGATGC	GATTGAAGCG	GACCAAACAT	TTGAAATGTT	1850
	AATGGGTGAC	GTTGTAGAAA	ACCGTAGACA	ATTTATAGAA	GATAATGCAG	1900
	TTTATGCAAA	CTTAGACTTC	TAA			1923

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2) INFORMATION FOR SEQ ID NO: 1308

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308

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ATGTAYGTIA TIATGGAYMG IGC

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10 2) INFORMATION FOR SEQ ID NO: 1309

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309

ATIATYTTRT TICCYTTICC YTT

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2) INFORMATION FOR SEQ ID NO: 1310

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310

ATIATITSIA TIACYTCRTC

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2) INFORMATION FOR SEQ ID NO: 1311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311

GARATGAARA TIMGIGGIGA RCA

23

5 2) INFORMATION FOR SEQ ID NO: 1312

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312

AARTAYATIA TICARGARMG IGC

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2) INFORMATION FOR SEQ ID NO: 1313

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313

AMIAYICKRT GIGGITTITT YTT

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2) INFORMATION FOR SEQ ID NO: 1314

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314

TAIGAITYA CIGAISMICA RGC

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2) INFORMATION FOR SEQ ID NO: 1315

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315
- ACIATIGCIT CIGCYTGIKS YTC 23
- 15 2) INFORMATION FOR SEQ ID NO: 1316
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316
- GTGAGTGAAA TAATTCAAGA TT 22
- 30 2) INFORMATION FOR SEQ ID NO: 1317
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317
- CACCAAAATC ATCTGTATCT AC 22
- 45 2) INFORMATION FOR SEQ ID NO: 1318
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318

ACCTAYTCSA TGTACGTRAT CATGGA

26

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2) INFORMATION FOR SEQ ID NO: 1319

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319

AGRTCCTCIA CCATCGGYAG YTT

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2) INFORMATION FOR SEQ ID NO: 1320

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2259 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Escherichia coli*
(B) STRAIN: K-12 MG1655
(C) ACCESSION NUMBER: AE000384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320

	ATGAGCGATA	TGGCAGAGCG	CCTTGCGCTA	CATGAATTTA	CGGAAAACGC	50
45	CTACTTAAAC	TACTCCATGT	ACGTGATCAT	GGACCGTGCG	TTGCCGTTTA	100
	TTGGTGATGG	TCTGAAACCT	GTTGAGCGCC	GCATTGTGTA	TGCGATGTCT	150
	GAACTGGGCC	TGAATGCCAG	CGCCAAATTT	AAAAAATCGG	CCCGTACCGT	200
	CGGTGACGTA	CTGGGTAAAT	ACCATCCGCA	CGGCGATAGC	GCCTGTTATG	250
	AAGCGATGGT	CCTGATGGCG	CAACCGTTCT	CTTACCGTTA	TCCGCTGGTT	300
50	GATGGTCAGG	GGAAGTGGGG	CGCGCCGGAC	GATCCGAAAT	CGTTCGCGGC	350
	AATGCGTTAC	ACCGAATCCC	GGTTGTCGAA	ATATTCCGAG	CTGCTATTGA	400
	GCGAGCTGGG	GCAGGGGACG	GCTGACTGGG	TGCCAAACTT	CGACGGCACT	450
	TTGCAGGAGC	CGAAAATGCT	ACCTGCCCCG	CTGCCAAACA	TTTTGCTTAA	500

	CGGCACCACC	GGTATTGCCG	TCGGCATGGC	GACCGATATT	CCACCGCATA	550
	ACCTGCGTGA	AGTGGCTCAG	GCGGCAATCG	CATTAATCGA	CCAGCCGAAA	600
	ACCACGCTCG	ATCAGCTGCT	GGATATCGTG	CAGGGGCCGG	ATTATCCGAC	650
	TGAAGCGGAA	ATTATCACTT	CGCGCGCCGA	GATCCGTAAA	ATCTACGAGA	700
5	ACGGACGTGG	TTCAGTGCGT	ATGCGCGCGG	TGTGGAAGAA	AGAAGATGGC	750
	GCGGTGGTTA	TCAGCGCATT	GCCGCATCAG	GTTTCAGGTG	CGCGCGTACT	800
	GGAGCAAATT	GCTGCGCAAA	TGCGCAACAA	AAAGCTGCCG	ATGGTTGACG	850
	ATCTGCGCGA	TGAATCTGAC	CACGAGAACC	CGACCCGCCT	GGTGATTGTG	900
	CCGCGTTCCA	ACCGCGTGGA	TATGGATCAG	GTGATGAACC	ACCTCTTCGC	950
10	TACCACCGAT	CTGGAAAAGA	GCTATCGTAT	TAACCTTAAT	ATGATCGGTC	1000
	TGGATGGTCG	TCCGGCGGTG	AAAAACCTGC	TGGAAATCCT	CTCCGAATGG	1050
	CTGGTGTTCC	GCCGCGATAC	CGTGCGCCGC	CGACTGAACT	ATCGTCTGGA	1100
	GAAAGTCCTC	AAGCGCCTGC	ATATCCTCGA	AGGTTTGCTG	GTGGCGTTTC	1150
	TCAATATCGA	CGAAGTGATT	GAGATCATTC	GTAATGAAGA	TGAACCGAAA	1200
15	CCGGCGCTGA	TGTCGCGGTT	TGGCCTTACG	GAAACCCAGG	CGGAAGCGAT	1250
	CCTCGAACTG	AAACTGCGTC	ATCTTGCCAA	ACTGGAAGAG	ATGAAGATTC	1300
	GCGGTGAGCA	GAGTGAAC TG	GAAAAAGAGC	GCGACCA GTT	GCAGGGCATT	1350
	TTGGCTTCCG	AGCGTAAAAT	GAATAACCTG	CTGAAGAAAG	AACTGCAGGC	1400
	AGACGCGCAA	GCCTACGGTG	ACGATCGTCG	TTCGCCGTTG	CAGGAACGCG	1450
20	AAGAAGCGAA	AGCGATGAGC	GAGCACGACA	TGCTGCCGTC	TGAACCTGTC	1500
	ACCATTTGTG	TGTCGCAGAT	GGGCTGGGTA	CGCAGCGCTA	AAGGCCATGA	1550
	TATCGACGCG	CCGGGCCTGA	ATTATAAAGC	GGGTGATAGC	TTCAAAGCGG	1600
	CGGTGAAAGG	TAAGAGCAAC	CAACCGGTAG	TGTTTGTTGA	TTCCACCGGT	1650
	CGTAGCTATG	CCATTGACCC	GATTACGCTG	CCGTCGGCGC	GTGGTCAGGG	1700
25	CGAGCCGCTC	ACCGGCAAAT	TAACGTTGCC	GCCTGGGGCG	ACCGTTGACC	1750
	ATATGCTGAT	GGAAAGCGAC	GATCAGAAAC	TGCTGATGGC	TTCCGATGCG	1800
	GGTTACGGTT	TCGTCTGCAC	CTTTAACGAT	CTGGTGGCGC	GTAACCGTGC	1850
	AGGTAAGGCT	TTGATCACCT	TACCGGAAAA	TGCCCATGTT	ATGCCGCCGG	1900
	TGGTGATTGA	AGATGCTTCC	GATATGCTGC	TGGCAATCAC	TCAGGCAGGC	1950
30	CGTATGTTGA	TGTTCCCGGT	AAGTGATCTG	CCGCAGCTGT	CGAAGGGCAA	2000
	AGGCAACAAG	ATTATCAACA	TTCCATCGGC	AGAAGCCGCG	CGTGGAGAAG	2050
	ATGGTCTGGC	GCAATTGTAC	GTTCTGCCGC	CGCAAAGCAC	GCTGACCATT	2100
	CATGTTGGGA	AACGCAAAAT	TAAACTGCGC	CCGGAAGAGT	TACAGAAAGT	2150
	CACTGGCGAA	CGTGGACGCC	GCGGTACGTT	GATGCGCGGT	TTGCAGCGTA	2200
35	TCGATCGTGT	TGAGATCGAC	TCTCCTCGCC	GTGCCAGCAG	CGGTGATAGC	2250
	GAAGAGTAA					2259

40 2) INFORMATION FOR SEQ ID NO: 1321

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 2403 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: KMP9
 (C) ACCESSION NUMBER: D67074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321

	GTGAGTGAAA	TAATTCAAGA	TTTATCACTT	GAAGATGTTT	TAGGTGATCG	50
5	CTTTGGAAGA	TATAGTAAAT	ATATTATTCA	AGAGCGTGCA	TTGCCAGATG	100
	TTCGTGATGG	TTTAAAACCA	GTACAACGTC	GTATTTTATA	TGCAATGTAT	150
	TCAAGTG GTA	ATACACACGA	TAAAAATTTT	CGTAAAAGTG	CGAAAACAGT	200
	CGGTGATGTT	ATTGGTCAAT	ATCATCCACA	TGGAGACTTC	TCAGTGTACA	250
	AAGCAATGGT	CCGTTTAAGT	CAAGACTGGA	AGTTACGACA	TGTCTTAATA	300
10	GAAATGCATG	GTAATAATGG	TAGTATCGAT	AATGATCCGC	CAGCGGCAAT	350
	GCGTTACACT	GAAGCTAAGT	TAAGCTTACT	AGCTGAAGAG	TTATTACGTG	400
	ATATTAATAA	AGAGACAGTT	TCTTTCATTC	CAAACATGA	TGATACGACA	450
	CTCGAACCAA	TGGTATTGCC	ATCAAGATTT	CCTAACTTAC	TAGTGAATGG	500
	TTCTACAGGT	ATATCTGCAG	GTTACGCGAC	AGATATACCA	CCACATAATT	550
15	TAGCTGAAGT	GATTCAAGCA	ACACTTAAAT	ATATTGATAA	TCCGGATATT	600
	ACAGTCAATC	AATTAATGAA	ATATATTAAA	GGTCCTGATT	TTCCAAC TGG	650
	TGGTATTATT	CAAGGTATTG	ATGGTATTAA	AAAAGCTTAT	GAATCAGGTA	700
	AAGGTAGAAT	TATAGTTCGT	TCTAAAGTTG	AAGAAGAAAC	TTTACGCAAT	750
	GGACGTAAAC	AGTTAATTAT	TACTGAAATT	CCATATGAAG	TGAACAAAAG	800
20	TAGCTTAGTA	AAACGTATCG	ATGAATTACG	TGCTGACAAA	AAAGTCGATG	850
	GTATCGTTGA	AGTACGTGAT	GAAACTGATA	GAAC TGGTTT	ACGAATAGCA	900
	ATTGAATTGA	AAAAAGATGT	GAACAGTGAA	TCAATCAAAA	ATTATCTTTA	950
	TAAAAACTCT	GATTTACAGA	TTTCATATAA	TTTCAACATG	GTCGCTATTA	1000
	GTGATGGTCG	TCCAAAATTG	ATGGGTATTTC	GTCAAATTAT	AGATAGTTAT	1050
25	TTGAATCATC	AAATTGAGGT	TGTTGCAAAT	AGAACGAAGT	TTGAATTAGA	1100
	TAATGCTGAA	AAACGTATGC	ATATCGTTGA	AGGTTTGATT	AAAGCGTTGT	1150
	CAATTTTAGA	TAAAGTAATT	GAATTGATTC	GTAGCTCTAA	AAACAAGCGT	1200
	GACGCTAAAG	AAAACCTTAT	CGAAGTATTC	GAGTTCACAG	AAGAACAGGC	1250
	TGAAGCAATT	GTAATGTTAC	AGTTATATCG	TTTAACAAAC	ACTGACATAG	1300
30	TTGCGCTTGA	AGGTGAACAT	AAAGAACTTG	AAGCATTAAT	CAAACAATTA	1350
	CGTCATATTTC	TTGATAACCA	TGATGCATTA	TTGAATGTCA	TAAAAGAAGA	1400
	ATTGAATGAA	ATTAAAAAGA	AATTCAAATC	TGAACGACTG	TCTTTAATTG	1450
	AAGCAGAAAT	TGAAGAAATT	AAAATTGACA	AAGAAGTTAT	GGTGCCTAGT	1500
	GAAGAAGTTA	TTTTAAGTAT	GACACGTCAT	GGATATATTA	AACGTACTTC	1550
35	TATTCGTAGC	TTTAATGCTA	GCGGTGTTGA	GGATATTGGT	TTAAAAGATG	1600
	GTGACAGTTT	ACTTAAACAT	CAAGAAGTAA	ATACGCAAGA	TACCGTACTA	1650
	GTATTTACAA	ATAAAGGTCG	TTATCTATTT	ATACCGGTTT	ATAAATTAGC	1700
	AGATATTTCGT	TGGAAAAGAAT	TGGGGCAACA	TGTATCACAA	ATAGTTCCTA	1750
	TCGAAGAAGA	TGAAGTG GTT	ATTAATGTCT	TTAATGAAAA	GGACTTTAAT	1800
40	ACAGATGCAT	TTTATGTTTT	TGCGACTCAA	AATGGCATGA	TTAAGAAAAG	1850
	TACAGTGCCT	CTATTTAAAA	CAACGCGTTT	TAATAAACCT	TTAATTGCTA	1900
	CTAAAGTTAA	AGAAAATGAT	GATTTGATTA	GTGTTATGCG	CTTTGAAAAA	1950
	GATCAATTAA	TTACCGTCAT	TACTAATAAA	GGTATGTCAT	TAACGTATAA	2000
	TACAAGTGAA	CTATCAGATA	CCGGATTAAAG	GGCAGCTGGT	GTTAAATCAA	2050
45	TAAATCTTAA	AGCTGAAGAT	TTCGTTGTTA	TGACAGAAGG	TGTTTCTGAA	2100
	AATGATACTA	TATTGATGGC	CACACAACGC	GGCTCGTTAA	AACGTATTAG	2150
	TTTTAAATC	TTACAAGTTG	CTAAAAGAGC	ACAACGTGGA	ATAACTTTAT	2200
	TAAAAGAATT	AAAGAAAAAT	CCACATCGTA	TTGTAGCTGC	ACATGTAGTG	2250
	ACAGGTGAAC	ATAGTCAATA	TACATTATAT	TCAAAATCAA	ATGAAGAACA	2300
50	TGGTTTAATT	AATGATATTC	ATAAATCTGA	ACAATATACA	AATGGCTCAT	2350
	TCATTGTAGA	TACAGATGAT	TTTGGTGAAG	TAATAGACAT	GTATATTAGC	2400
	TAA					2403

2) INFORMATION FOR SEQ ID NO: 1322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322

RTIGAIAAYI SIGTIGAYGA RG

22

2) INFORMATION FOR SEQ ID NO: 1323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323

ACIAWRSAIG GIGGIACICA YG

22

2) INFORMATION FOR SEQ ID NO: 1324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324

CCICCGICIS WRTCICCYTC

20

2) INFORMATION FOR SEQ ID NO: 1325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325

RTTCATYTCI CCIARICCYT T

21

10

2) INFORMATION FOR SEQ ID NO: 1326

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326

TGATTCAATA CAGGTTTTAG AG

22

25

2) INFORMATION FOR SEQ ID NO: 1327

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327

40 CTAGATTTCC TCCTCATCAA AT

22

2) INFORMATION FOR SEQ ID NO: 1328

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1992 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: RN4220

(C) ACCESSION NUMBER: D67075

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328

	ATGAATAAAC	AAAATAATTA	TTCAGATGAT	TCAATACAGG	TTTTAGAGGG	50
	GTTAGAAGCA	GTTCGTAAAA	GACCTGGTAT	GTATATTGGA	TCAACTGATA	100
10	AACGGGGATT	ACATCATCTA	GTATATGAAA	TTGTCGATAA	CTCCGTCGAT	150
	GAAGTATTGA	ATGGTTACGG	TAACGAAATA	GATGTAACAA	TTAATAAAGA	200
	TGGTAGTATT	TCTATAGAAG	ATAATGGACG	TGGTATGCCA	ACAGGTATAC	250
	ATAAATCAGG	TAAACCGACA	GTCGAAGTTA	TCTTTACTGT	TTTACATGCA	300
	GGAGGTAAAT	TTGGACAAGG	CGGCTATAAA	ACTTCAGGTG	GTCTTCACGG	350
15	TGTTGGTGCT	TCAGTTGTAA	ATGCATTGAG	TGAATGGCTT	GAAGTTGAAA	400
	TCCATCGAGA	TGGTAATATA	TATCATCAAA	GTTTTAAAAA	CGGTGGTTTCG	450
	CCATCTTCTG	GTTTAGTGAA	AAAAGGTAAA	ACTAAGAAAA	CAGGTACCAA	500
	AGTAACATTT	AAACCTGATG	ACACAATTTT	TAAAGCATCT	ACATCATTTA	550
	ATTTTGATGT	TTTAAGTGAA	CGACTACAAG	AGTCTGCGTT	CTTATTGAAA	600
20	AATTTAAAAA	TAACGCTTAA	TGATTTACGC	AGTGGTAAAG	AGCGTCAAGA	650
	GCATTACCAT	TATGAAGAAG	GAATCAAAGA	GTTTGTTAGT	TATGTCAATG	700
	AAGGAAAAGA	AGTTTTGTCAT	GACGTGGCTA	CATTTTCAGG	TGAAGCAAAT	750
	GGTATAGAGG	TAGACGTAGC	TTTCCAATAT	AATGATCAAT	ATTCAGAAAG	800
	TATTTTAAGT	TTTGTAATA	ATGTACGTAC	TAAAGATGGT	GGTACACATG	850
25	AAGTTGGTTT	TAAAACAGCA	ATGACACGTG	TATTTAATGA	TTATGCACGT	900
	CGTATTAATG	AACTTAAAAC	AAAAGATAAA	AACTTAGATG	GTAATGATAT	950
	TCGTGAAGGT	TTAACAGCTG	TTGTGTCTGT	TCGTATTCCA	GAAGAATTAT	1000
	TGCAATTTGA	AGGACAAACG	AAATCTAAAT	TGGGTACTTC	TGAAGCTAGA	1050
	AGTGCTGTTG	ATTGAGTTGT	TGCAGACAAA	TTGCCATTCT	ATTTAGAAGA	1100
30	AAAAGGACAA	TTGTCTAAAT	CACCTGTGAA	AAAAGCGATT	AAAGCACAAAC	1150
	AAGCAAGGGA	AGCTGCACGT	AAAGCTCGTG	AAGATGCTCG	TTCAGGTAAG	1200
	AAAAACAAGC	GTAAAGACAC	TTTGCTATCT	GGTAAATTAA	CACCTGCACA	1250
	AAGTAAAAAC	ACTGAAAAAA	ATGAATTGTA	TTTAGTCGAA	GGTGATTCTG	1300
	CGGGAGGTTT	AGCAAAACTT	GGACGAGACC	GCAAATTCCA	AGCGATATTA	1350
35	CCATTACGTG	GTAAGGTAAT	TAATACAGAG	AAAGCACGTC	TAGAAGATAT	1400
	TTTTAAAAAT	GAAGAAATTA	ATACAATTAT	CCACACAATC	GGGGCAGGCG	1450
	TTGGTACTGA	CTTTAAATTT	GAAGATAGTA	ATTATAATCG	TGTAATTATT	1500
	ATGACTGATG	CTGATACTGA	TGGTGCGCAT	ATTCAAGTGC	TATTGTTAAC	1550
	ATTCTTCTTC	AAATATATGA	AACCGCTTGT	TCAAGCAGGT	CGTGTATTTA	1600
40	TTGCTTTACC	TCCACTTTAT	AAATTGGAAA	AAGGTAAAGG	CAAAACAAAG	1650
	CGAGTTGAAT	ACGCTTGGAC	AGACGAAGAG	CTTAATAAAT	TGCAAAAAGA	1700
	ACTTGGTAAA	GGCTTCACGT	TACAACGTTA	CAAAGGTTTG	GGTGAAATGA	1750
	ACCCTGAGCA	ATTATGGGAA	ACGACGATGA	ACCCAGAAAC	ACGAACTTTA	1800
	ATTCGTGTAC	AAGTTGAAGA	TGAAGTGCCT	TCATCTAAAC	GTGTAACAAC	1850
45	ATTAATGGGT	GACAAAGTAC	AACCTAGACG	TGAATGGATT	GAAAAGCATG	1900
	TTGAGTTTGG	TATGCAAGAG	GACCAAAGTA	TTTTAGATAA	TTCTGAAGTA	1950
	CAAGTGCTTG	AAAATGATCA	ATTTGATGAG	GAGGAAATCT	AG	1992

50

2) INFORMATION FOR SEQ ID NO: 1329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329

10 TGTAGAGCGC GGTATCATCA AAGTA

25

2) INFORMATION FOR SEQ ID NO: 1330

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330

25

AGATTCTGAAC TTGGTGTGCG GG

22

30 2) INFORMATION FOR SEQ ID NO: 1331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331

40

GCCCTTGAGG TACAGAATGG TAATGAAGTT

30

45

2) INFORMATION FOR SEQ ID NO: 1332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332

5 GACCGCGGCG CAGACCATCA

20

2) INFORMATION FOR SEQ ID NO: 1333

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333

20

TCATGGTGAC TTATCTATTT ATG

23

25 2) INFORMATION FOR SEQ ID NO: 1334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334

CATCTATTTA TAAAGCAATG GTA

23

40

2) INFORMATION FOR SEQ ID NO: 1335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335

CTATTTATGG AGCAATGGT

19

2) INFORMATION FOR SEQ ID NO: 1336

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336

TGGAGACTAC TCAGTGT

17

15

2) INFORMATION FOR SEQ ID NO: 1337

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337

TGGAGACTTC TCAGTGT

17

30

2) INFORMATION FOR SEQ ID NO: 1338

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338

45 GTGTACGGAG CAATG

15

2) INFORMATION FOR SEQ ID NO: 1339

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339

CCAGCGGAAA TCGGT

15

10

2) INFORMATION FOR SEQ ID NO: 1340

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340

GAACAAGGTA TGACACCGGA TAAAT

25

25

2) INFORMATION FOR SEQ ID NO: 1341

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341

GATAACTGAA ATCCTGAGCC ATACG

25

40

2) INFORMATION FOR SEQ ID NO: 1342

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342

GATGTTATTG GTCAATATCA TCCA

24

5

2) INFORMATION FOR SEQ ID NO: 1343

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343

AAGAAACTGT CTCTTTATTA ATATCACGT

29

20

2) INFORMATION FOR SEQ ID NO: 1344

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344

35 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1345

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345

50

CCCGCCGAGC ATTTCAACTA TTG

23

2) INFORMATION FOR SEQ ID NO: 1346

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346

GATGTTACGC AGCAGGGCAG TC

22

15

2) INFORMATION FOR SEQ ID NO: 1347

- (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347

ACCAAGCAGG TTCGCAGTCA AGTA

24

30

2) INFORMATION FOR SEQ ID NO: 1348

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
40 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Unidentified bacterium
45 (C) ACCESSION NUMBER: X04555
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348

ATGCGCTCAC GCAACTGGTC CAGAACCTTG ACCGAACGCA GCGGTGGTAA 50
50 CGGCGCAGTG GCGGTTTTCA TGGCTTGTTA TGA CTGTTTT TTTGTACAGT 100
CTATGCCTCG GGCATCCAAG CAGCAAGCGC GTTACGCCGT GGGTCGATGT 150
TTGATGTTAT GGAGCAGCAA CGATGTTACG CAGCAGGGCA GTCGCCCTAA 200
AACAAAGTTA GGCCGCATGG ACACAACGCA GGTACATTG ATACACAAAA 250

TTCTAGCTGC GGCAGATGAG CGAAATCTGC CGCTCTGGAT CGGTGGGGGC 300
TGGGCGATCG ATGCACGGCT AGGGCGTGTA ACACGCAAGC ACGATGATAT 350
TGATCTGACG TTTCCCGGCG AGAGGCGCGG CGAGCTCGAG GCAATAGTTG 400
AAATGCTCGG CGGGCGCGTC ATGGAGGAGT TGGACTATGG ATTCTTAGCG 450
5 GAGATCGGGG ATGAGTTACT TGA CTGCGCAA CCTGCTTGGT GGGCAGACGA 500
AGCGTATGAA ATCGCGGAGG CTCCGCAGGG CTCGTGCCCCA GAGGCGGCTG 550
AGGGCGTCAT CGCCGGGCGG CCAGTCCGTT GTAACAGCTG GGAGGCGATC 600
ATCTGGGATT ACTTTTACTA TGCCGATGAA GTACCACCAG TGGACTGGCC 650
TACAAAGCAC ATAGAGTCCT ACAGGCTCGC ATGCACCTCA CTCGGGGCGG 700
10 AAAAGGTTGA GGTCTTGCGT GCCGCTTTCA GGTGCGGATA TGCGGCCTAA 750

2) INFORMATION FOR SEQ ID NO: 1349

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349

25

CAGCCGACCA ATGAGTATCT TGCC

24

30 2) INFORMATION FOR SEQ ID NO: 1350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350

TAATCAGGGC AGTTGCGACT CCTA

24

45

2) INFORMATION FOR SEQ ID NO: 1351

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: Stone 130
(C) ACCESSION NUMBER: L06157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351

```
10 ATGTTATGGA GCAGCAACGA TGTTACGCAG CAGGGCAGTC GCCCTAAAC 50
   AAAGTTAGGT GGCTCAATGA GCATCATTGC AACCGTCAAG ATCGGCCCTG 100
   ACCAAATTC AGCCATGAGG GCTGTGCTCG ATCTCTTCGG CAAAGAGTTT 150
   GAGGACATTC CAACCTACTC TGATCGCCAG CCGACCAATG AGTATCTTGC 200
   CAATCTTCTG CACAGCGAGA CGTTCATCGC GCTCGCTGCT TTTGACCGCG 250
15 GAACAGCAAT AGGTGGGCTC GCCGCCTACG TTCTACCAA GTTCGAGCAA 300
   GCGCGAAGCG AGATCTACAT TTATGACTTG GCAGTCGCTT CCAGCCATCG 350
   AAGGCTAGGA GTCGCAACTG CCCTGATTAG CCACCTGAAG CGTGTGGCGG 400
   TTGAAGTTGG CGCGTATGTA ATCTATGTGC AAGCAGACTA CCGTGACGAT 450
   CCGGCAGTCG CTCTCTACAC AAAGCTTGA GTTCGGAAG ACGTCATGCA 500
20 CTTGCACATT GATCCAAGAA CCGCCACCTA A 531
```

2) INFORMATION FOR SEQ ID NO: 1352

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352

35

CCACGCTGAC AGAGCCGCAC CG

22

40 2) INFORMATION FOR SEQ ID NO: 1353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353

GGCCAGCTCC CATCGGACCC TG

22

2) INFORMATION FOR SEQ ID NO: 1354

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354

CACGCTGACA GAGCCGCACC G

21

15

2) INFORMATION FOR SEQ ID NO: 1355

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355

ATGCCGTTGC TGTCGAAATC CTCG

24

30

2) INFORMATION FOR SEQ ID NO: 1356

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M97172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356

ATGAACACGA TCGAATCGAT CACGGCGGAC CTGCACGGAC TGGGCGTCCG 50
 50 GCCCGGCGAC CTGATCATGG TCCATGCATC GCTGAAAGCC GTCGGCCCCG 100
 TCGAGGGAGG TGCGGCCTCG GTGGTGTCGG CCCTTCGCGC CGCGGTCCGG 150
 TCCGCAGGGA CCCTGATGGG TTATGCCTCA TGGGACCGCT CGCCCTATGA 200
 GGAGACGCTG AACGGCGCGC GGATGGACGA AGAACTGCGC CGCCGGTGGC 250

CACCCTTCGA TCTGGCCACA TCCGGTACCT ATCCCGGCTT CGGCCTGCTC 300
 AACCGGTTTC TGCTTGAGGC GCGCGACGCA CGGCGCAGCG CGCATCCCGA 350
 CGCCTCCATG GTCGCGGTCG GCGCCCTTGC CGCCACGCTG ACAGAGCCGC 400
 ACCGGCTTGG GCAGGCGCTG GCGGAAGGCT CGCCGCTGGA GCGCTTCGTC 450
 5 GGGCATGGCG GAAAGGTCCT GCTTCTGGGA GCGCCGCTCG ACTCCGTCAC 500
 CGTGCTGCAT TACGCCGAGG CCATCGCCCC CATCCCGAAC AAACGCCGCG 550
 TGACCTATGA AATGCCGATG CTCGGCCCCG ATGGCAGGGT CCGATGGGAG 600
 CTGGCCGAGG ATTTGACAG CAACGGCATT CTCGATTGCT TCGCGGTCGA 650
 TGGGAAGCCG GATGCCGTCG AGACGATCGC CAAGGCTTAT GTCGAACTGG 700
 10 GCCGGCATCG GGAAGGCATC GTCGGTCGCG CACCCTCCTA TCTGTTTGAA 750
 GCGCAGGATA TCGTCTCGTT CGGCGTCACC TATCTCGAAC AGCATTTTCGG 800
 CGCGCCCTGA 810

15

2) INFORMATION FOR SEQ ID NO: 1357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357

GCCCATCCAT TTGCCTTTGC

20

30

2) INFORMATION FOR SEQ ID NO: 1358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358

GCGTACCAAC TTGCCATCCT GAAG

24

45

2) INFORMATION FOR SEQ ID NO: 1359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359

TGCCCCTGCC ACCTCACTC

19

10

2) INFORMATION FOR SEQ ID NO: 1360

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360

CGTACCAACT TGCCATCCTG AAGA

24

25

2) INFORMATION FOR SEQ ID NO: 1361

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 786 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X01385

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361

	GTGCAATACG AATGGCGAAA AGCCGAGCTC ATCGGTCAGC TTCTCAACCT	50
	TGGGGTTACC CCCGGCGGTG TGCTGCTGGT CCACAGCTCC TTCCGTAGCG	100
45	TCCGGCCCCCT CGAAGATGGG CCACTTGACG TGATCGAGGC CCTGCGTGCT	150
	GCGCTGGGTC CGGGAGGGAC GCTCGTCATG CCCTCGTGGT CAGGTCTGGA	200
	CGACGAGCCG TTCGATCCTG CCACGTCGCC CGTTACACCG GACCTTGAG	250
	TTGTCTCTGA CACATTCTGG CGCCTGCCAA ATGTAAAGCG CAGCGCCCAT	300
	CCATTTGCCT TTGCGGCAGC GGGGCCACAG GCAGAGCAGA TCATCTCTGA	350
50	TCCATTGCCC CTGCCACCTC ACTCGCCTGC AAGCCCGGTC GCCCGTGTCC	400
	ATGAAGTCGA TGGGCAGGTA CTTCTCCTCG GCGTGGGACA CGATGCCAAC	450
	ACGACGCTGC ATCTTGCCGA GTTGATGGCA AAGGTTCCCT ATGGGGTGCC	500
	GAGACACTGC ACCATTCTTC AGGATGGCAA GTTGGTACGC GTCGATTATC	550

	TCGAGAATGA	CCACTGCTGT	GAGCGCTTTG	CCTTGCGGGA	CAGGTGGCTC	600
	AAGGAGAAGA	GCCTTCAGAA	GGAAGGTCCA	GTCGGTCATG	CCTTTGCTCG	650
	GTTGATCCGC	TCCCGCGACA	TTGTGGCGAC	AGCCCTGGGT	CAACTGGGCC	700
	GAGATCCGTT	GATCTTCCTG	CATCCGCCAG	AGGGCGGGAT	GCGAAGAATG	750
5	CGATGCCGCT	CGCCAGTCGA	TTGGCTGAGC	TCATGA		786

2) INFORMATION FOR SEQ ID NO: 1362

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362

20

CGCCGCCATC GCCCAAAGCT GG

22

25 2) INFORMATION FOR SEQ ID NO: 1363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363

35

CGGCATAATG GAGCGCGGTG ACTG

24

40

2) INFORMATION FOR SEQ ID NO: 1364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364

50

TTTCTCGCCC ACGCAGGAAA AATC

24

2) INFORMATION FOR SEQ ID NO: 1365

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365

CATCCTCGAC GAATATGCCG CG

22

15

2) INFORMATION FOR SEQ ID NO: 1366

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 900 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (C) ACCESSION NUMBER: M88012

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366

	ATGACTGATC	CCCGCAAAAA	CGGCGATTG	CACGAACCCG	CGACGGCACC	50
	CGCGACGCCC	TGGTCCAAAA	GCGAGCTGGT	CCGGCAATTG	CGCGACCTCG	100
35	GCGTGCGCTC	AGGCGATATG	GTGATGCCGC	ATGTGTCGTT	GCGCGCCGTC	150
	GGGCCGCTGG	CGGACGGACC	GCAGACACTT	GTCGATGCGC	TGATCGAGGC	200
	CGTCGGCCCC	ACCGGGAATA	TTCTCGCCTT	CGTCTCGTGG	CGCGATTTCG	250
	CCTATGAACA	GACGCTGGGT	CATGATGCGC	CGCCCGCCGC	CATCGCCCAA	300
	AGCTGGCCTG	CGTTCGACCC	CGACCATGCG	CCCGCCTACC	CCGGCTTTGG	350
40	CGCGATCAAC	GAATTTATCC	GAACCTATCC	GGGGTGTCGG	CGCACGGCCC	400
	ATCCCGACGC	ATCGATGGCG	GCGATCGGGC	CCGATGCGGC	GTGGCTGGTG	450
	GCGCCGCACG	AGATGGGCGC	CGCTTATGGC	CCCCGCTCGC	CGATCGCGCG	500
	TTTTCTCGCC	CACGCAGGAA	AAATCCTGTC	GATCGGCGCC	GGGCCCAGAT	550
	CAGTCAACGC	GCTCCATTAT	GCCGAAGCGG	TGGCGCGGAT	CGAGGGCAAG	600
45	CGCCGCGTCA	CTTATTCGAT	GCCCTTACTG	CGCGAAGGCA	AGCGCGTCTG	650
	GGTCACCACG	TCCGACTGGG	ATTGCAACGG	CATCCTCGAC	GAATATGCCG	700
	CGCCCGACGG	CCCCGACGCG	GTCGAACGGA	TCGCCCAGCA	CTATCTCGCC	750
	CGCACCAGGG	TTGCGCAAGG	CCCGGTCGGC	GGCGCGCAAT	CCCGGCTGAT	800
	CGACGCGGCC	GATATCGTTT	CCTTCGGCAT	CGAATGGCTC	GAGGCGCGCC	850
50	ACGCCGCGCC	AGCGGCGGCA	GCGCTGAAGC	CGAAACAACG	CCGCGACTGA	900

2) INFORMATION FOR SEQ ID NO: 1367

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367

CAAATATACT AACAGAAGCG TTCA

24

2) INFORMATION FOR SEQ ID NO: 1368

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368

AGGATCTTGC CAATACCTTT AT

22

2) INFORMATION FOR SEQ ID NO: 1369

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369

AAACCTTTGT TTCGGTCTGC TAAT

24

2) INFORMATION FOR SEQ ID NO: 1370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370

AAGCGATTCC AATAATACCT TGCT

24

10

2) INFORMATION FOR SEQ ID NO: 1371

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 558 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter diversus*
- (C) ACCESSION NUMBER: M18967

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371

	ATGAATTATC AAATTGTGAA TATTGCGGAA TGCAGCAATT ATCAGTTAGA	50
	AGCAGCAAAT ATACTAACAG AAGCGTTCAA TGATCTTGGT AACAAATTCAT	100
30	GGCCAGATAT GACGAGTGCA ACAAAGAAG TAAAAGAATG TATTGAGAGT	150
	CCAAACCTTT GTTTCGGTCT GCTAATAAAT AACTCCTTAG TTGGCTGGAT	200
	AGGCTTAAGG CCAATGTACA AGGAAACCTG GGAATTGCAT CCATTGGTTG	250
	TCAGACCAGA TTATCAAAAT AAAGGTATTG GCAAGATCCT GCTTAAGGAA	300
	TTAGAAAACA GAGCTAGAGA GCAAGGTATT ATTGGAATCG CTTTAGGAAC	350
35	AGATGATGAA TACTATAGAA CAAGTCTCTC TTTAATAACT ATAACAGAAG	400
	ATAATATATT TGATTCAATA AAAAATATTA AAAATATTAA TAAACATCCA	450
	TATGAGTTT ATCAGAAGAA TGGTTATTAT ATTGTTGGAA TAATTCCAAA	500
	TGCCAATGGT AAAAACAAAC CAGATATTTG GATGTGGAAA AGTTTAATCA	550
	AAGAGTAA	558

40

2) INFORMATION FOR SEQ ID NO: 1372

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372

GCTTTCGTTG CCTTTGCCGA GGTC

24

5

2) INFORMATION FOR SEQ ID NO: 1373

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373

CACCCCTGTT GCTTCGCCCA CTC

23

20

2) INFORMATION FOR SEQ ID NO: 1374

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374

AGATATTGGC TTCGCCGCAC CACA

24

35

2) INFORMATION FOR SEQ ID NO: 1375

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375

50 CCCTGTTGCT TCGCCCACTC CTG

23

2) INFORMATION FOR SEQ ID NO: 1376

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia marcescens*
(C) ACCESSION NUMBER: M94066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376

ATGATCGTCA	TCTGCGACCA	CGACAACCTC	GACGCCTGGC	TGGCGCTGCG	50
CACCGCGCTG	TGGCCCTCCG	GCTCGCCTGA	AGATCACCGC	GCGGAAATGC	100
GCGAGATATT	GGCTTCGCCG	CACCACACCG	CGTTTATGGC	GCGGGGGCTG	150
GACGGCGCTT	TCGTTGCCTT	TGCCGAGGTC	GCGCTGCGCT	ACGATTACGT	200
CAACGGCTGC	GAATCGTCGC	CGGTGGCGTT	TTTGAAGGA	ATTATACCG	250
CCGAACGCGC	CCGCCGCCAG	GGCTGGGCCG	CGCGCCTGAT	CGCGCAGGTG	300
CAGGAGTGGG	CGAAGCAACA	GGGGTGCAGC	GAGCTGGCGT	CGGATACCGA	350
TATCGCCAAT	CTGGACTCCC	AGCGCCTGCA	TGCGGCGCTG	GGCTTTGCCG	400
AAACGGAGCG	AGTAGTGTTT	TACCGCAAAA	CGCTGGGCTG	A	441

2) INFORMATION FOR SEQ ID NO: 1377

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377

GCCGTGGGTC GATGTTTGAT GTTA

24

2) INFORMATION FOR SEQ ID NO: 1378

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378

GCTCGATGAC GCCAACTACC TCTG

24

5

2) INFORMATION FOR SEQ ID NO: 1379

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379

20 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1380

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380

35

CGCTCGATGA CGCCAACTAC CTCT

24

40 2) INFORMATION FOR SEQ ID NO: 1381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X02340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381

```

5  GTGGTAACGG CGCAGTGGCG GTTTTTCATGG CTTCTTGTTA TGACATGTTT 50
   TTTTGGGGTA CAGTCTATGC CTCGGGCATC CAAGCAGCAA GCGCGTTACG 100
   CCGTGGGTCG ATGTTTGATG TTATGGAGCA GCAACGATGT TACGCAGCAG 150
   GGCAGTCGCC CTAAACAAA GTTAAACATC ATGAGGGAAG CGGTGATCGC 200
   CGAAGTATCG ACTCAACTAT CAGAGGTAAGT TGGCGTCATC GAGCGCCATC 250
   TCGAACCGAC GTTGCTGGCC GTACATTTGT ACGGCTCCGC AGTGGATGGC 300
   GGCCTGAAGC CACACAGTGA TATTGATTG CTGGTTACGG TGACCGTAAG 350
10 GCTTGATGAA ACAACGCGGC GAGCTTTGAT CAACGACCTT TTGGAAACTT 400
   CGGCTTCCCC TGGAGAGAGC GAGATTCTCC GCGCTGTAGA AGTCACCATT 450
   GTTGTGCACG ACGACATCAT TCCGTGGCGT TATCCAGCTA AGCGCGAACT 500
   GCAATTTGGA GAATGGCAGC GCAATGACAT TCTTGCAGGT ATCTTCGAGC 550
   CAGCCACGAT CGACATTGAT CTGGCTATCT TGCTGACAAA AGCAAGAGAA 600
15 CATAGCGTTG CCTTGGTAGG TCCAGCGGCG GAGGAACTCT TTGATCCGGT 650
   TCCTGAACAG GATCTATTTG AGGCGCTAAA TGAAACCTTA ACGCTATGGA 700
   ACTCGCCGCC CGACTGGGCT GGCATGAGC GAAATGTAGT GCTTACGTTG 750
   TCCCGCATTT GGTACAGCGC AGTAACCGGC AAAATCGCGC CGAAGGATGT 800
   CGCTGCCGAC TGGGCAATGG AGCGCCTGCC GGCCCAGTAT CAGCCCCTCA 850
20 TACTTGAAGC TAGACAGGCT TATCTTGAC AAGAAGAAGA TCGCTTGGCC 900
   TCGCGCGCAG ATCAGTTGGA AGAATTTGTC CACTACGTGA AAGGCGAGAT 950
   CACCAAGGTA GTCGGCAAAT AA 972

```

25

2) INFORMATION FOR SEQ ID NO: 1382

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382

TAGATATGAT AGGCGGTAAA AAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1383

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383

CCCAAATTCG AGTAAGAGGT ATT

23

5 2) INFORMATION FOR SEQ ID NO: 1384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384

GATATGATAG GCGGTAAAAA GC

22

20

2) INFORMATION FOR SEQ ID NO: 1385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385

TCCCAAATTC GAGTAAGAGG TA

22

35

2) INFORMATION FOR SEQ ID NO: 1386

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 477 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01282

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386

ATGAAAGAAA GATATGGAAC AGTATATAAA GGCTCTCAGA GGCTCATAGA

50

CGAGGAAAAGT GGAGAAGTAA TAGAGGTAGA TAAGCTATAC CGTAAACAAA 100
 CGTCTGGTAA CTTTGTA AAA GCGTATATCG TCCAATTAAT AAGTATGTTA 150
 GATATGATAG GCGGTAAAA GCTCAAGATT GTTAATTATA TATTAGATAA 200
 TGTACATCTA AGTAATAACA CAATGATAGC AACTGTTAGA GAAATAGCAG 250
 5 AAGGAACAAA TACAAGCACG AAAACCGTAA ATACAACGCT TAAAATCTTA 300
 GAAGAAGGAA ATATCATTAA AAGAAGAACT GGAGCATTAA TGCTAAACCC 350
 AGAGCTACTC ATGAGAGGCG ATGACCAAAA ACAAAAATAC CTCTTACTCG 400
 AATTTGGGAA CTTTGAGCAA GAGGACGACC AAAAGCAAGA AAATGCTTTA 450
 TCAGAATATT ATTCTTTCAA GGAGTAG 477
 10

2) INFORMATION FOR SEQ ID NO: 1387

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387

25 TTATGCCTCT TCCGACCATC AAGC 24

2) INFORMATION FOR SEQ ID NO: 1388

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 35 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388

40 TACGCTCGTC ATCAAAATCA CTCG 24

45 2) INFORMATION FOR SEQ ID NO: 1389

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389

GAATAACGGT TTGGTTGATG CGAG

24

5

2) INFORMATION FOR SEQ ID NO: 1390

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390

20 ATGGCAAGAT CCTGGTATCG GTCT

24

2) INFORMATION FOR SEQ ID NO: 1391

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: J01839

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391

40	ATGAGCCATA TTCAACGGGA AACGTCTTGC TCGAGGCCGC GATTAAATTC	50
	CAACATGGAT GCTGATTTAT ATGGGTATAA ATGGGCTCGC GATAATGTCG	100
	GGCAATCAGG TGCACAAATC TATCGATTGT ATGGGAAGCC CGATGCGCCA	150
	GAGTTGTTTC TGAAACATGG CAAAGGTAGC GTTGCCAATG ATGTTACAGA	200
	TGAGATGGTC AGACTAAACT GGCTGACGGA ATTTATGCCT CTTCGACCA	250
45	TCAAGCATTT TATCCGTACT CCTGATGATG CATGGTTACT CACCACTGCG	300
	ATCCCCGGA AAACAGCATT CCAGGTATTA GAAGAATATC CTGATTCAGG	350
	TGAAAATATT GTTGATGCGC TGGCAGTGTT CCTGCGCCGG TTGCATTCGA	400
	TTCCTGTTTG TAATTGTCCT TTAAACAGCG ATCGCGTATT TCGTCTCGCT	450
	CAGGCGCAAT CACGAATGAA TAACGGTTTG GTTGATGCGA GTGATTTTGA	500
50	TGACGAGCGT AATGGCTGGC CTGTTGAACA AGTCTGGAAA GAAATGCATA	550
	AGCTTTTGCC ATTCTCACCG GATTCACTCG TCACTCATGG TGATTTCTCA	600
	CTTGATAACC TTATTTTGA CGAGGGGAAA TTAATAGGTT GTATTGATGT	650
	TGGACGAGTC GGAATCGCAG ACCGATACCA GGATCTTGCC ATCCTATGGA	700

ACTGCCTCGG TGAGTTTCT CCTTCATTAC AGAAACGGCT TTTTCAAAAA 750
TATGGTATTG ATAATCCTGA TATGAATAAA TTGCAGTTTC ATTTGATGCT 800
CGATGAGTTT TTCTAA 816

5

2) INFORMATION FOR SEQ ID NO: 1392

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392

20 TGGGTGGAGA GGCTATTCGG CTAT 24

2) INFORMATION FOR SEQ ID NO: 1393

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393

35 CAGTCCCTTC CCGCTTCAGT GAC 23

2) INFORMATION FOR SEQ ID NO: 1394

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394

50 GACGTTGTCA CTGAAGCGGG AAGG 24

2) INFORMATION FOR SEQ ID NO: 1395

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1395

CTTGGTGGTC GAATGGGCAG GTAG

24

15

2) INFORMATION FOR SEQ ID NO: 1396

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: V00618

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396

ATGATTGAAC AAGATGGATT GCACGCAGGT TCTCCGGCCG CTTGGGTGGA 50
GAGGCTATTC GGCTATGACT GGGCACAACA GACAATCGGC TGCTCTGATG 100
35 CCGCCGTGTT CCGGCTGTCA GCGCAGGGGC GCCCGGTTCT TTTTGTCAAG 150
ACCGACCTGT CCGGTGCCCT GAATGAACTG CAGGACGAGG CAGCGCGGCT 200
ATCGTGGCTG GCCACGACGG GCGTTCCTTG CGCAGCTGTG CTCGACGTTG 250
TCACTGAAGC GGAAGGGAC TGGCTGCTAT TGGGCGAAGT GCCGGGGCAG 300
GATCTCCTGT CATCTCACCT TGCTCCTGCC GAGAAAGTAT CCATCATGGC 350
40 TGATGCAATG CGGCGGCTGC ATACGCTTGA TCCGGCTACC TGCCCATTCG 400
ACCACCAAGC GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC 450
GGTCTTGTCG ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC 500
AGCCGAACTG TTCGCCAGGC TCAAGGCGCG CATGCCCGAC GGCGAGGATC 550
TCGTCGTGAC CCATGGCGAT GCCTGCTTGC CGAATATCAT GGTGGAAAAT 600
45 GGCCGCTTTT CTGGATTCAT CGACTGTGGC CGGCTGGGTG TGGCGGACCG 650
CTATCAGGAC ATAGCGTTGG CTACCCGTGA TATTGCTGAA GAGCTTGCGC 700
GCGAATGGGC TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT 750
TCGCAGCGCA TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGA 795

50

2) INFORMATION FOR SEQ ID NO: 1397

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397
10 GTGGGAGAAA ATGAAAACCT AT 22
- 15 2) INFORMATION FOR SEQ ID NO: 1398
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398
 ATGGAGTGAA AGAGCCTGAT 20
- 30 2) INFORMATION FOR SEQ ID NO: 1399
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399
 ACCTATGATG TGGAACGGGA AAAG 24
- 45 2) INFORMATION FOR SEQ ID NO: 1400
- (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400

5

CGATGGAGTG AAAGAGCCTG ATG

23

10 2) INFORMATION FOR SEQ ID NO: 1401

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(C) ACCESSION NUMBER: V01547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401

25

ATGGCTAAAA	TGAGAATATC	ACCGGAATTG	AAAAAACTGA	TCGAAAAATA	50
CCGCTGCGTA	AAAGATACGG	AAGGAATGTC	TCCTGCTAAG	GTATATAAGC	100
TGGTGGGAGA	AAATGAAAAC	CTATATTTAA	AAATGACGGA	CAGCCGGTAT	150
AAAGGGACCA	CCTATGATGT	GGAACGGGAA	AAGGACATGA	TGCTATGGCT	200
30 GGAAGGAAAG	CTGCCTGTTC	CAAAGTCTCT	GCACTTTGAA	CGGCATGATG	250
GCTGGAGCAA	TCTGCTCATG	AGTGAGGCCG	ATGGCGTCCT	TTGCTCGGAA	300
GAGTATGAAG	ATGAACAAAG	CCCTGAAAAG	ATTATCGAGC	TGTATGCGGA	350
GTGCATCAGG	CTCTTTCACT	CCATCGACAT	ATCGGATTGT	CCCTATACGA	400
ATAGCTTAGA	CAGCCGCTTA	GCCGAATTGG	ATTACTTACT	GAATAACGAT	450
35 CTGGCCGATG	TGGATTGCGA	AAACTGGGAA	GAAGACACTC	CATTTAAAGA	500
TCCGCGCGAG	CTGTATGATT	TTTTAAAGAC	GGAAAAGCCC	GAAGAGGAAC	550
TTGTCTTTTC	CCACGGCGAC	CTGGGAGACA	GCAACATCTT	TGTGAAAGAT	600
GGCAAAGTAA	GTGGCTTTAT	TGATCTTGGG	AGAAGCGGCA	GGGCGGACAA	650
GTGGTATGAC	ATTGCCTTCT	GCGTCCGGTC	GATCAGGGAG	GATATCGGGG	700
40 AAGAACAGTA	TGTCGAGCTA	TTTTTTGACT	TACTGGGGAT	CAAGCCTGAT	750
TGGGAGAAAA	TAAAATATTA	TATTTTACTG	GATGAATTGT	TTTAG	795

45 2) INFORMATION FOR SEQ ID NO: 1402

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402

TATTCAACAA TTTATCGGAA ACAG

24

5

2) INFORMATION FOR SEQ ID NO: 1403

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403

20 TCAGAGAGCC AACTCAACAT TTT

23

2) INFORMATION FOR SEQ ID NO: 1404

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404

35

AAACAGCGTT TTAGAGCCAA ATAA

24

40 2) INFORMATION FOR SEQ ID NO: 1405

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405

TTCTCAGAGA GCCAACTCAA CATT

24

2) INFORMATION FOR SEQ ID NO: 1406

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 780 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: BM2580
(C) ACCESSION NUMBER: X07753

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406

ATGGAATTGC CCAATATTAT TCAACAATTT ATCGGAAACA GCGTTTTAGA 50
GCCAAATAAA ATTGGTCAGT CGCCATCGGA TGTTTATTCT TTTAATCGAA 100
20 ATAATGAAAC TTTTTTCTT AAGCGATCTA GCACTTTATA TACAGAGACC 150
ACATACAGTG TCTCTCGTGA AGCGAAAATG TTGAGTTGGC TCTCTGAGAA 200
ATTAAAGGTG CCTGAACTCA TCATGACTTT TCAGGATGAG CAGTTTGAAT 250
TCATGATCAC TAAAGCGATC AATGCAAAAC CAATTCAGC GCTTTTTTTA 300
ACAGACCAAG AATTGCTTGC TATCTATAAG GAGGCACTCA ATCTGTTAAA 350
25 TTCAATTGCT ATTATTGATT GTCCATTTAT TTCAAACATT GATCATCGGT 400
TAAAAGAGTC AAAATTTTTT ATTGATAACC AACTCCTTGA CGATATAGAT 450
CAAGATGATT TTGACACTGA ATTATGGGGA GACCATAAAA CTTACCTAAG 500
TCTATGGAAT GAGTTAACCG AGACTCGTGT TGAAGAAAGA TTGGTTTTTT 550
CTCATGGCGA TATCACGGAT AGTAATATTT TTATAGATAA ATTCAATGAA 600
30 ATTTATTTTT TAGATCTTGG TCGTGCTGGG TTAGCAGATG AATTTGTAGA 650
TATATCCTTT GTTGAACGTT GCCTAAGAGA GGATGCATCG GAGGAAACTG 700
CGAAATATT TTAAAGCAT TTAATAAATG ATAGACCTGA CAAAAGGAAT 750
TATTTTTTAA AACTTGATGA ATTGAATTGA 780

35

2) INFORMATION FOR SEQ ID NO: 1407

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407

CCCTGTAATA GAAAAGCAAG TAGG

50

24

2) INFORMATION FOR SEQ ID NO: 1408

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408
- TTGTCGTATC CCTCAAATCA CC 22
- 15 2) INFORMATION FOR SEQ ID NO: 1409
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409
- TGGGATTACA ATGGCAATCA GCG 23
- 30 2) INFORMATION FOR SEQ ID NO: 1410
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410
- GGGGAATAGG TCACAAGATC TGCTT 25
- 45 2) INFORMATION FOR SEQ ID NO: 1411
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 912 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(C) ACCESSION NUMBER: S46063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411

10 ATGCTTTTAT ATAAATGTG TGACAATCAA AATTATGGGG TTACTTACAT 50
 GAAGTTTTTA TTGGCATTTT CGCTTTTAAT ACCATCCGTG GTTTTTGCAA 100
 GTAGTTCAAA GTTTCAGCAA GTTGAACAAG ACGTTAAGGC AATTGAAGTT 150
 TCTCTTTCTG CTCGTATAGG TGTTTCCGTT CTTGATACTC AAAATGGAGA 200
 15 ATATTGGGAT TACAATGGCA ATCAGCGCTT CCCGTTAACA AGTACTTTTA 250
 AAACAATAGC TTGCGCTAAA TTACTATATG ATGCTGAGCA AGGAAAAGTT 300
 AATCCCAATA GTACAGTCGA GATTAAGAAA GCAGATCTTG TGACCTATTC 350
 CCCTGTAATA GAAAAGCAAG TAGGGCAGGC AATCACACTC GATGATGCGT 400
 GCTTCGCAAC TATGACTACA AGTGATAATA CTGCGGCAA TATCATCCTA 450
 20 AGTGCTGTAG GTGGCCCCAA AGGCGTTACT GATTTTTTAA GACAAATTGG 500
 GGACAAAGAG ACTCGTCTAG ACCGTATTGA GCCTGATTTA AATGAAGGTA 550
 AGCTCGGTGA TTTGAGGGAT ACGACAACCT CTAAGGCAAT AGCCAGTACT 600
 TTGAATAAAC TTTTATTTGG TTCCGCGCTA TCTGAAATGA ACCAGAAAAA 650
 ATTAGAGTCT TGGATGCTGA ACAATCAAGT CACTGGTAAT TTACTACGTT 700
 25 CAGTATTGCC GGCGGGATGG AACATTGCGG ATCGCTCAGG TGCTGGCGGA 750
 TTTGGTGCTC GGAGTATTAC AGCAGTTGTG TGGAGTGAGC ATCAAGCCCC 800
 AATTATTGTG AGCATCTATC TAGCTCAAAC ACAGGCTTCA ATGGCAGAGC 850
 GAAATGATGC GATTGTAAAT ATTGGTCATT CAATTTTGA CGTTTATACA 900
 TCACAGTCGC GC 912

30

2) INFORMATION FOR SEQ ID NO: 1412

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412

45 GAGAAAACGC TCCAGCAGGG C

21

2) INFORMATION FOR SEQ ID NO: 1413

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413

CATGAGGCTT TCACTGCGGG G

21

10

2) INFORMATION FOR SEQ ID NO: 1414

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414

TATCGTTAAT CGCACCATCA C

21

25

2) INFORMATION FOR SEQ ID NO: 1415

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415

ATGCAGTAAT GCGGCTTTAT C

21

40

2) INFORMATION FOR SEQ ID NO: 1416

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
(B) STRAIN: HEL-1
(C) ACCESSION NUMBER: X91840

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416

	ATGATGAAAA	AATCGTTATG	CTGCGCTCTG	CTGCTGACAG	CCTCTTTCTC	50
	CACATTTGCT	GCCGCAAAAA	CAGAACAACA	GATTGCCGAT	ATCGTTAATC	100
10	GCACCATCAC	CCCGTTGATG	CAGGAGCAGG	CTATTCCGGG	TATGGCCGTT	150
	GCCGTTATCT	ACCAGGGAAA	ACCCTATTAT	TTCACCTGGG	GTAAAGCCGA	200
	TATCGCCAAT	AACCACCCAG	TCACGCAGCA	AACGCTGTTT	GAGCTAGGAT	250
	CGGTTAGTAA	GACGTTTAAC	GGCGTGTTGG	GCGGCGATGC	TATCGCCCGC	300
	GGCGAAATTA	AGCTCAGCGA	TCCGGTCACG	AAATACTGGC	CAGAACTGAC	350
15	AGGCAAACAG	TGGCAGGGTA	TCCGCTTGCT	GCACTTAGCC	ACCTATACGG	400
	CAGGCGGCCT	ACCGCTGCAG	ATCCCCGATG	ACGTTAGGGA	TAAAGCCGCA	450
	TTACTGCATT	TTTATCAAAA	CTGGCAGCCG	CAATGGACTC	CGGGCGCTAA	500
	GCGACTTTAC	GCTAACTCCA	GCATTGGTCT	GTTTGGCGCG	CTGGCGGTGA	550
	AACCCTCAGG	AATGAGTTAC	GAAGAGGCAA	TGACCAGACG	CGTCCTGCAA	600
20	CCATTAAAAC	TGGCGCATAC	CTGGATTACG	GTTCCGCAGA	ACGAACAAAA	650
	AGATTATGCC	TGGGGCTATC	GCGAAGGGAA	GCCCCGTACAC	GTTTCTCCGG	700
	GACAACTTGA	CGCCGAAGCC	TATGGCGTGA	AATCCAGCGT	TATTGATATG	750
	GCCCCGTGGG	TTCAGGCCAA	CATGGATGCC	AGCCACGTC	AGGAGAAAAC	800
	GCTCCAGCAG	GGCATTGCGC	TTGCGCAGTC	TCGCTACTGG	CGTATTGGCG	850
25	ATATGTACCA	GGGATTAGGC	TGGGAGATGC	TGAACTGGCC	GCTGAAAGCT	900
	GATTCGATCA	TCAACGGCAG	CGACAGCAAA	GTGGCATTGG	CAGCGCTTCC	950
	CGCCGTTGAG	GTAAACCCGC	CCGCCCCCGC	AGTGAAAGCC	TCATGGGTGC	1000
	ATAAAACGGG	CTCCACTGGT	GGATTTGGCA	GCTACGTAGC	CTTCGTTCCA	1050
	GAAAAAAACC	TTGGCATCGT	GATGCTGGCA	AACAAAAGCT	ATCCTAACCC	1100
30	TGTCCGTGTC	GAGGCGGCCT	GGCGCATTCT	TGAAAAGCTG	CAATAA	1146

2) INFORMATION FOR SEQ ID NO: 1417

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417

45

TGGTTAACTA YAATCCSATT GCGGA

25

50 2) INFORMATION FOR SEQ ID NO: 1418

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418

ATGCTTTACC CAGCGTCAGA TT

22

10

2) INFORMATION FOR SEQ ID NO: 1419

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419

25 CGATGAATAA GCTGATTCT CACG

24

2) INFORMATION FOR SEQ ID NO: 1420

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420

40

TGCTTTACCC AGCGTCAGAT TACG

24

2) INFORMATION FOR SEQ ID NO: 1421

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421

AATTAGAGCG GCAGTCGGGA GGAA

24

5

2) INFORMATION FOR SEQ ID NO: 1422

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422

20 GAAATCAGCT TATTCATCGC CACG

24

2) INFORMATION FOR SEQ ID NO: 1423

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: GRI-1
- (C) ACCESSION NUMBER: X92506

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423

40

ATGGTTAAAA	AATCACTGCG	TCAGTTCACG	CTGATGGCGA	CGGCAACCGT	50
CACGCTGTTG	TTAGGAAGTG	TGCCGCTGTA	TGCGCAAACG	GCGGACGTAC	100
AGCAAAAAC	TGCCGAATTA	GAGCGGCAGT	CGGGAGGAAG	ACTGGGTGTG	150
GCATTGATTA	ACACAGCAGA	TAATTTCGCA	ATACTTTATC	GTGCTGATGA	200
45	GCGCTTTGCG	ATGTGCAGCA	CCAGTAAAGT	GATGGCCGTG	250
TGAAGAAAAG	TGAAAGCGAA	CCGAATCTGT	TAAATCAGCG	AGTTGAGATC	300
AAAAAATCTG	ACTTGGTAA	CTATAATCCG	ATTGCGGAAA	AGCACGTCTGA	350
TGGGACGATG	TCCTGGCTG	AGCTTAGCGC	GGCCGCGCTA	CAGTACAGCG	400
ATAACGTGGC	GATGAATAAG	CTGATTTCTC	ACGTTGGCGG	CCCGGCTAGC	450
50	GTCACCGCGT	TCGCCCCACA	GCTGGGAGAC	GAAACGTTCC	500
TACCGAGCCG	ACGTTAAACA	CCGCCATTCC	GGGCGATCCG	CGTGATACCA	550
CTTCACCTCG	GGCAATGGCG	CAAACCTCTG	GTAATCTGAC	GCTGGGTAAA	600
GCATTGGGTG	ACAGCCAACG	GGCGCAGCTG	GTGACATGGA	TGAAAGGCAA	650

TACCACCGGT GCAGCGAGCA TTCAGGCTGG ACTGCCTGCT TCCTGGGTTG 700
 TGGGGGATAA AACCGGCAGC GGTGACTATG GCACCACCAA CGATATCGCG 750
 GTGATCTGGC CAAAAGATCG TGCGCCGCTG ATTCTGGTCA CTTACTTCAC 800
 CCAGCCTCAA CCTAAGGCAG AAAGCCGTCG CGATGTATTA GCGTCGGCGG 850
 5 CTAAATCGT CACCAACGGT TTGTAA 876

2) INFORMATION FOR SEQ ID NO: 1424

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424

20

GTTAACGGTG ATGGCGACGC TAC

23

25 2) INFORMATION FOR SEQ ID NO: 1425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425

35

GAATTATCGG CGGTGTTAAT CAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426

50

CACGCTCAAT ACCGCCATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1427

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427

TTATCGCCCA CTACCCATGA TTTC

24

15

2) INFORMATION FOR SEQ ID NO: 1428

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 876 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: CAS-5
 30 (C) ACCESSION NUMBER: X92507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428

	ATGATGACTC AGAGCATTCG CCGCTCAATG TTAACGGTGA TGGCGACGCT	50
35	ACCCCTGCTA TTTAGCAGCG CAACGCTGCA TGCGCAGGCG AACAGCGTGC	100
	AACAGCAGCT GGAAGCCCTG GAGAAAAGTT CGGGAGGTCG GCTTGCGCTT	150
	GCGCTGATTA ACACCGCCGA TAATTCGCAG ATTCTCTACC GTGCCGATGA	200
	ACGTTTTTGC ATGTGCAGTA CCAGTAAGGT GATGGCGGCC GCGGCGGTGC	250
	TTAAACAGAG CGAGAGCGAT AAGCACCTGC TAAATCAGCG CGTTGAAATC	300
40	AAGAAGAGCG ACCTGGTTAA CTACAATCCC ATTGCGGAGA AACACGTTAA	350
	CGGCACGATG ACGCTGGCTG AGCTTGGCGC AGCGGCGCTG CAGTATAGCG	400
	ACAATACTGC CATGAATAAG CTGATTGCCC ATCTGGGTGG TCCCGATAAA	450
	GTGACGGCGT TTGCTCGCTC GTTGGGTGAT GAGACCTTCC GTCTGGACAG	500
	AACCGAGCCC ACGCTCAATA CCGCCATTCC AGGCGACCCG CGTGATACCA	550
45	CCACGCCGCT CGCGATGGCG CAGACCCTGA AAAATCTGAC GCTGGGTAAA	600
	GCGCTGGCGG AAATCAGCG GGCACAGTTG GTGACGTGGC TTAAGGGCAA	650
	TACTACCGGT AGCGCGAGCA TTCGGGCGGG TCTGCCGAAA TCATGGGTAG	700
	TGGGCGATAA AACCGGCAGC GGAGATTATG GCACCACCAA CGATATCGCG	750
	GTTATCTGGC CGGAAAACCA CGCACCCTG GTTCTGGTGA CCTACTTTAC	800
50	CCAACGGGAG CAGAAGGCGG AAAGCCGTCG GGATATTCTG GCTGCGGCGG	850
	CGAAAATCGT AACCCACGGT TTCTGA	876

2) INFORMATION FOR SEQ ID NO: 1429

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429

TTTACGGCTA AAGATACTGA AAAGT

25

15

2) INFORMATION FOR SEQ ID NO: 1430

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430

GTTTAATAAAA ACAACCACCG AATAAT

26

30

2) INFORMATION FOR SEQ ID NO: 1431

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431

45 TAATTGACAC TCCATTTACG GCTAA

25

2) INFORMATION FOR SEQ ID NO: 1432

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432

ACCGAATAAT ATTTTCCTTT CAGGCA

26

10

2) INFORMATION FOR SEQ ID NO: 1433

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 741 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: AJ223604

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433

	ATGAGCAAGT	TATCTGTATT	CTTTATATTT	TTGTTTTGCA	GCATTGCTAC	50
	CGCAGCAGAG	TCTTTGCCAG	ATTTAAAAAT	TGAAAAGCTT	GATGAAGGCG	100
30	TTTATGTTCA	TACTTCGTTT	GAAGAAGTTA	ACGGGTGGGG	CGTTGTTCCCT	150
	AAACATGGTT	TGGTGGTTCT	TGTAAATGCT	GAGGCTTACC	TAATTGACAC	200
	TCCATTTACG	GCTAAAGATA	CTGAAAAGTT	AGTCACTTGG	TTTGTGGAGC	250
	GTGGCTATAA	AATAAAAGGC	AGCATTTCCCT	CTCATTTTCA	TAGCGACAGC	300
	ACGGGCGGAA	TAGAGTGGCT	TAATTCTCGA	TCTATCCCCA	CGTATGCATC	350
35	TGAATTAACA	AATGAACTGC	TTAAAAAAGA	CGGTAAGGTT	CAAGCCACAA	400
	ATTCATTTAG	CGGAGTTAAC	TATTGGCTAG	TTAAAAATAA	AATTGAAGTT	450
	TTTTATCCAG	GCCCCGGGACA	CACTCCAGAT	AACGTAGTGG	TTTGGTTGCC	500
	TGAAAGGAAA	ATATTATTCT	GTGGTTGTTT	TATTAAACCG	TACGGTTTAG	550
	GCAATTTGGG	TGACGCAAT	ATAGAAGCTT	GGCCAAAGTC	CGCCAAATTA	600
40	TTAAAGTCCA	AATATGGTAA	GGCAAACTG	GTTGTTCCAA	GTCACAGTGA	650
	AGTTGGAGAC	GCATCACTCT	TGAAACTTAC	ATTAGAGCAG	GCGGTTAAAG	700
	GGTTAAACGA	AAGTAAAAAA	CCATCAAAC	CAAGCAACTA	A	741

45

2) INFORMATION FOR SEQ ID NO: 1434

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434

5 CACAATCAAG ACCAAGATTT GCGAT

25

2) INFORMATION FOR SEQ ID NO: 1435

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435

20

GAAAGGGCAG CTCGTTACGA TAGAG

25

25 2) INFORMATION FOR SEQ ID NO: 1436

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436

CAGCATCAAC ATTTAAGATC CCCA

24

40

2) INFORMATION FOR SEQ ID NO: 1437

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437

CTCCACTTGA TTAAGTGC GG AAATTC

26

2) INFORMATION FOR SEQ ID NO: 1438

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: X06046

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438

ATGGCAATCC GAATCTTCGC GATACTTTTC TCCATTTTTT CTCTTGCCAC 50
 TTTCGCGCAT GCGCAAGAAG GCACGCTAGA ACGTTCTGAC TGGAGGAAGT 100
 TTTTCAGCGA ATTTCAAGCC AAAGGCACGA TAGTTGTGGC AGACGAACGC 150
 20 CAAGCGGATC GTGCCATGTT GGTTTTGTGAT CCTGTGCGAT CGAAGAAACG 200
 CTAATCGCCT GCATCGACAT TCAAGATACC TCATACACTT TTTGCACTTG 250
 ATGCAGGCGC TGTTCGTGAT GAGTTCAGAG TTTTTCGATG GGACGGCGTT 300
 AACAGGGGCT TTGCAGGCCA CAATCAAGAC CAAGATTTGC GATCAGCAAT 350
 GCGGAATTCT ACTGTTTGGG TGTATGAGCT ATTTGCAAAG GAAATTGGTG 400
 25 ATGACAAAGC TCGGCGCTAT TTGAAGAAA TCGACTATGG CAACGCCGAT 450
 CCTTCGACAA GTAATGGCGA TTACTGGATA GAAGGCAGCC TTGCAATCTC 500
 GGCGCAGGAG CAAATTGCAT TTCTCAGGAA GCTCTATCGT AACGAGCTGC 550
 CCTTTCGGGT AGAACATCAG CGCTTGGTCA AGGATCTCAT GATTGTGGAA 600
 GCCGGTCGCA ACTGGATACT GCGTGCAAAG ACGGGCTGGG AAGGCCGTAT 650
 30 GGGTTGGTGG GTAGGATGGG TTGAGTGGCC GACTGGCTCC GTATTCTTCG 700
 CACTGAATAT TGATACGCCA AACAGAATGG ATGATCTTTT CAAGAGGGAG 750
 GCAATCGTGC GGGCAATCCT TCGCTCTATT GAAGCGTTAC CGCCCAACCC 800
 GGCAGTCAAC TCGGACGCTG CGCGATAA 828

35

2) INFORMATION FOR SEQ ID NO: 1439

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: J03427

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439

ATGAAAACAT TTGCCGCATA TGTAATTATC GCGTGTCTTT CGAGTACGGC 50

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ATTAGCTGGT TCAATTACAG AAAATACGTC TTGGAACAAA GAGTTCTCTG      100
CCGAAGCCGT CAATGGTGTC TTCGTGCTTT GTAAAAGTAG CAGTAAATCC      150
TGCGCTACCA ATGACTTAGC TCGTGCATCA AAGGAATATC TTCCAGCATC      200
AACATTTAAG ATCCCCAACG CAATTATCGG CCTAGAAACT GGTGTCATAA      250
5  AGAATGAGCA TCAGGTTTTT AAATGGGACG GAAAGCCAAG AGCCATGAAG      300
CAATGGGAAA GAGACTTGAC CTTAAGAGGG GCAATACAAG TTTCAGCTGT      350
TCCCGTATTT CAACAAATCG CCAGAGAAGT TGGCGAAGTA AGAATGCAGA      400
AATACCTTAA AAAATTTTCC TATGGCAACC AGAATATCAG TGGTGGCATT      450
GACAAATTCT GGTGGAAGG CCAGCTTAGA ATTTCCGCAG TTAATCAAGT      500
10 GGAGTTTCTA GAGTCTCTAT ATTTAAATAA ATTGTCAGCA TCTAAAGAAA      550
ACCAGCTAAT AGTAAAAGAG GCTTTGGTAA CGGAGGCGGC ACCTGAATAT      600
CTAGTGCATT CAAAAACTGG TTTTCTGGT GTGGGAACTG AGTCAAATCC      650
TGGTGTGCGA TGGTGGGTG GGTGGGTGA GAAGGAGACA GAGGTTTACT      700
TTTTCGCCTT TAACATGGAT ATAGACAACG AAAGTAAGTT GCCGCTAAGA      750
15 AAATCCATTC CCACCAAAT CATGGAAAGT GAGGGCATCA TTGGTGGCTA      800
A                                                                801

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20 2) INFORMATION FOR SEQ ID NO: 1440

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440

AGACCGTTAT CGTAAACAGG GCTAAG

26

35

2) INFORMATION FOR SEQ ID NO: 1441

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441

TTTTTTGCTC AACTTTTTTC AGGATC

26

50

2) INFORMATION FOR SEQ ID NO: 1442

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: RNL-1
 (C) ACCESSION NUMBER: Z21957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442

```

15  ATGAATGTCA TTATAAAAGC TGTAAGTTACT GCCTCGACGC TACTGATGGT      50
    ATCTTTTAGT TCATTCGAAA CCTCAGCGCA ATCCCCACTG TTAAAAGAGC      100
    AAATTGAATC CATAGTCATT GGAAAAAAG CCACTGTAGG CGTTGCAGTG      150
    TGGGGGCGCTG ACGATCTGGA ACCTTTACTG ATTAATCCTT TTGAAAAATT      200
20  CCCAATGCAA AGTGTATTTA AATTGCATTT AGCTATGTTG GTACTGCATC      250
    AGGTTGATCA GGGAAAAGTTG GATTTAAATC AGACCGTTAT CGTAAACAGG      300
    GCTAAGGTTT TACAGAATAC CTGGGCTCCG ATAATGAAAG CGTATCAGGG      350
    AGACGAGTTT AGTGTTCCAG TGCAGCAACT GCTGCAATAC TCGGTCTCGC      400
    ACAGCGATAA CGTGGCCTGT GATTGTATAT TTGAACTGGT TGGTGGACCA      450
25  GCTGCTTTGC ATGACTATAT CCAGTCTATG GGTATAAAGG AGACCGCTGT      500
    GGTGCGAAAT GAAGCGCAGA TGCACGCCGA TGATCAGGTG CAGTATCAAA      550
    ACTGGACCTC GATGAAAGGT GCTGCAGAGA TCCTGAAAAA GTTTGAGCAA      600
    AAAACACAGC TGTCTGAAAC CTCGCAGGCT TTGTTATGGA AGTGGATGGT      650
    CGAAACCACC ACAGGACCAG AGCGGTTAAA AGGTTTGTTA CCAGCTGGTA      700
30  CTGTGGTCGC ACATAAAACT GGTACTTCGG GTATCAAAGC CGGAAAAACT      750
    GCGGCCACTA ATGATTTAGG TATCATTCTG TTGCCTGATG GACGGCCCTT      800
    GCTGGTTGCT GTTTTGTGA AAGACTCAGC CGAGTCAAGC CGAACCAATG      850
    AAGCTATCAT TGCGCAGGTT GCTCAGACTG CGTATCAATT TGAATTGAAA      900
    AAGCTTTCTG CCCTAAGCCC AAATTAA      927
35

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2) INFORMATION FOR SEQ ID NO: 1443

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443

```

50  CTTCTGCTCT GCTGATGCTT GGC

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23

2) INFORMATION FOR SEQ ID NO: 1444

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444

GGCGACCAGG TATTTTGTAA TACTGC

26

15

2) INFORMATION FOR SEQ ID NO: 1445

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 927 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: JMC
 30 (C) ACCESSION NUMBER: X93314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445

	ATGAATGTCA TCACAAAATG TGTTTTACC GCTTCTGCTC TGCTGATGCT	50
35	TGGCTTAAGT TCATTTGTAG TATCAGCCCA ATCCCCTTTG TTAAAAGAGC	100
	AGATTGAAAC CATAGTGACG GGTA AAAAGG CCACTGTAGG TGTAGCAGTG	150
	TGGGGGCGCTG ACGATCTGGA ACCTTTGTTG CTGAATCCAT TTGAAAAGTT	200
	TCCGATGCAA AGTGTGTTA AACTGCATTT AGCTATGTTA GTTCTGCATC	250
	AGGTCGATCA GGGGAAACTG GATTTAAATC AGTCTGTTAC TGTTAATCGT	300
40	GCTGCAGTAT TACAAAATAC CTGGTCGCCA ATGATGAAAG ATCATCAGGG	350
	CGATGAATTT ACTGTTGCAG TACAGCAGTT ACTGCAGTAT TCGGTGTCAC	400
	ACAGCGACAA TGTGGCCTGC GATTTGTTAT TTGAACTGGT GGGCGGGCCG	450
	CAAGCTTTGC ATGCTTATAT CCAGTCTTTA GCGGTTAAAG AAGCTGCCGT	500
	GGTAGCAAAT GAAGCGCAAA TGCATGCGGA TGATCAGGTG CAATATCAAA	550
45	ACTGGACGTC GATGAAAGCC GCAGCACAAAG TTCTGCAAAA GTTTGAACAG	600
	AAAAAGCAGT TGTCTGAAAC CTCTCAGGCC TTGTTATGGA AATGGATGGT	650
	TGAAACCACC ACAGGACCAC AGCGGTAAA AGGCTTGTTA CCTGCTGGTA	700
	CTATAGTGGC GCATAAAACC GGTACTTCGG GCGTCAGAGC AGGAAAAACT	750
	GCGGCGACTA ATGATGCGGG CGTCATTATG TTGCCTGATG GACGGCCTTT	800
50	ATTGGTGGCG GTATTTGTCA AGGATTCGGC TGAATCAGAA CGAACCAATG	850
	AAGCTATTAT TGCGCAGGTT GCGCAAGCGG CTTATCAGTT TGAGCTGAAA	900
	AAACTCTCTG CAGTGAGTCC GGATTGA	927

2) INFORMATION FOR SEQ ID NO: 1446

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446

GGCCTGYGAT TTGTTATTTG AACTGGT

27

15

2) INFORMATION FOR SEQ ID NO: 1447

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447

CGCTSTGGTC CTGTGGTGGT TTC

23

30

2) INFORMATION FOR SEQ ID NO: 1448

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448

45 GATCAGGTGC ARTATCAAAA CTGGAC

26

50

2) INFORMATION FOR SEQ ID NO: 1449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449

AGCWGGTAAC AAYCCTTTTA ACCGCT

26

10

2) INFORMATION FOR SEQ ID NO: 1450

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450

ACCACTGGGA ATACACTTGT AATGGC

26

25

2) INFORMATION FOR SEQ ID NO: 1451

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451

40 ATCTACCTGG TCAATCATTG CTCGT

26

2) INFORMATION FOR SEQ ID NO: 1452

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: BM10393
(C) ACCESSION NUMBER: AF045472

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452

	ATGACATTAT	CAATAATTGT	CGCTCACGAT	AAACAAAGAG	TCATTGGGTA	50
	CCAAAATCAA	TTACCTTGGC	ACTTACCAAA	TGATTTAAAG	CATATTAAAC	100
10	AACTGACCAC	TGGGAATACA	CTTGTAATGG	CACGGAAAAC	TTTTAATTCT	150
	ATAGGGAAGC	CATTGCCAAA	TAGACGTAAC	GTCGTACTCA	CTAACCAAGC	200
	TTCATTTTAC	CATGAAGGGG	TAGATGTTAT	AAACTCTCTT	GATGAAATTA	250
	AAGAGTTATC	TGGTCATGTT	TTTATATTTG	GAGGACAAAC	GTTATACGAA	300
	GCAATGATTG	ACCAGGTAGA	TGATATGTAT	ATCACAGTAA	TAGATGGAAA	350
15	GTTTCAAGGA	GACACATTCT	TTCCACCATA	CACATTCGAA	AACTGGGAAG	400
	TCGAATCTTC	AGTAGAAGGT	CAACTAGATG	AAAAAAATAC	TATACCGCAT	450
	ACATTCTTAC	ATTTAGTGCG	TAGAAAAGGG	AAATAG		486

20

2) INFORMATION FOR SEQ ID NO: 1453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453

ATCGAAGAAT GGAGTTATCG GRAATG 26

35

2) INFORMATION FOR SEQ ID NO: 1454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454

CCTAAAYTR CTGGGGATTT CWGGA 25

50

2) INFORMATION FOR SEQ ID NO: 1455

764

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455
CAGGTGGTGG GGAGATATAC AAAA 24
- 15 2) INFORMATION FOR SEQ ID NO: 1456
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456
TATGTTAGAS RCGAAGTCTT GGKTAA 26
- 30 2) INFORMATION FOR SEQ ID NO: 1457
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457
CAAAGGTGAA CAGCTCCTGT TT 22
- 45 2) INFORMATION FOR SEQ ID NO: 1458
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458

TCCGTTATTT TCTTTAGGTT GGTAA

27

10

2) INFORMATION FOR SEQ ID NO: 1459

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1459

AAGGTGAACA GCTCCTGTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1460

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460

GATCACTACG TTCTCATTGT CA

22

40

2) INFORMATION FOR SEQ ID NO: 1461

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: AJ238350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461

5
GTGAAACTAT CACTAATGGT AGCTATATCG AAGAATGGAG TTATCGGGAA 50
TGGCCCTGAT ATTCCATGGA GTGCCAAAGG TGAACAGCTC CTGTTTAAAG 100
CTATTACCTA TAACCAATGG CTGTTGGTTG GACGCAAGAC TTTTGAATCA 150
ATGGGAGCAT TACCCAACCG AAAGTATGCG GTCGTAACAC GTCCAAGTTT 200
10 TACATCTGAC AATGAGAACG TAGTGATCTT TCCATCAATT AAAGATGCTT 250
TAACCAACCT AAAGAAAATA ACGGATCATG TCATTGTTTC AGGTGGTGGG 300
GAGATATACA AAAGCCTGAT CGATCAAGTA GATACACTAC ATATATCTAC 350
AATAGACATC GAGCCGGAAG GTGATGTTTA CTTTCCTGAA ATCCCCAGCA 400
ATTTTAGGCC AGTTTTTACC CAAGACTTCG CCTCTAACAT AAATTATAGT 450
15 TACCAAATCT GGCAAAAGGG TTAA 474

2) INFORMATION FOR SEQ ID NO: 1462

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462

30

GCACTCCCYA ATAGGAAATA CGC

23

35 2) INFORMATION FOR SEQ ID NO: 1463

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463

AGTGTTGCTC AAAAACAAC TCG

23

50

2) INFORMATION FOR SEQ ID NO: 1464

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464

10 ACGTTYGAAT CTATGGGMGC ACT

23

2) INFORMATION FOR SEQ ID NO: 1465

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465

25

GTCGATAAGT GGAGCGTAGA GGC

23

30 2) INFORMATION FOR SEQ ID NO: 1466

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466

AAGCATTGAC CTACAATCAG TGT

23

45

2) INFORMATION FOR SEQ ID NO: 1467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467

5 AATACAATA CATTGTCATC ATTTGAT

27

2) INFORMATION FOR SEQ ID NO: 1468

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468

20

CGTTACCCGC TCAGGTTGGA CATCAA

26

25 2) INFORMATION FOR SEQ ID NO: 1469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1469

CATCCCCCTC TGGCTCGATG TCG

23

40

2) INFORMATION FOR SEQ ID NO: 1470

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: Z50804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470

```

5   TTGAAAGTAT CATTGATAGC TGCGAAACGA AAAAACGGCG TGATTGGTTG      50
    CGGTCCAGAC ATACCGTGGT CCGCGAAAGG GGAGCAGCTA CTTTTTAAAG      100
    CATTGACCTA CAATCAGTGT CTTCTGGTGG GTCGCAAGAC GTTTGAATCT      150
    ATGGGCGCAC TCCCAATAG GAAATACGCG GTCGTTACCC GCTCAGGTTG      200
    GACATCAAAT GATGACAATG TAGTTGTATT TCAGTCAATC GAAGAGGCCA      250
    TGGACAGGCT AGCTGAATTC ACCGGTCACG TTATAGTGTC TGGTGGCGGA      300
10  GAAATTTACC GAGAAACATT ACCCATGGCC TCTACGCTCC ACTTATCGAC      350
    GATCGACATC GAGCCAGAGG GGGATGTTTT CTTCCCGAGT ATTCCAAATA      400
    CCTTCGAAGT TGTTTTTGAG CAACACTTTA CTTCAAACAT TAACTATTGC      450
    TATCAAATTT GGAAAAAGGG TTAA                                     474

```

15

2) INFORMATION FOR SEQ ID NO: 1471

```

20  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471

```

30  GATAATGACA ACGTAATAGT ATTCCC                                     26

```

2) INFORMATION FOR SEQ ID NO: 1472

```

35  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472

```

45  GCTCAATATC AATCGTCGAT ATA                                     23

```

2) INFORMATION FOR SEQ ID NO: 1473

50

```

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid

```

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473

TTAAAGCCTT GACGTACAAC CAGTGG

26

10

2) INFORMATION FOR SEQ ID NO: 1474

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474

TGGGCAATGT TTCTCTGTAA ATCTCC

26

25

2) INFORMATION FOR SEQ ID NO: 1475

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X12868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475

	GTGAAAGTAT	CATTAATGGC	TGCAAAAGCG	AAAAACGGAG	TGATTGGTTG	50
45	CGGTCCACAC	ATACCCTGGT	CCGCGAAAGG	AGAGCAGCTA	CTCTTTAAAG	100
	CCTTGACGTA	CAACCAGTGG	CTTTTGGTGG	GCCGCAAGAC	GTTCGAATCT	150
	ATGGGAGCAC	TCCCTAATAG	GAAATACGCG	GTCGTTACTC	GCTCAGCCTG	200
	GACGGCCGAT	AATGACAACG	TAATAGTATT	CCCGTCGATC	GAAGAGGCCA	250
	TGTACGGGCT	GGCTGAACTC	ACCGATCACG	TTATAGTGTC	TGGTGGCGGG	300
50	GAGATTTACA	GAGAAACATT	GCCCATGGCC	TCTACGCTCC	ATATATCGAC	350
	GATTGATATT	GAGCCGGAAG	GAGATGTTTT	CTTTCCGAAT	ATTCCCAATA	400
	CCTTCGAAGT	TGTTTTTGAG	CAACACTTTA	GCTCAAACAT	TAAC TATTGC	450
	TATCAAATTT	GGCAAAAGGG	TTAA			474

2) INFORMATION FOR SEQ ID NO: 1476

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476

GGCGAGCAGC TCCTATTCAA AG

22

15

2) INFORMATION FOR SEQ ID NO: 1477

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477

TAGGTAAGCT AATGCCGATT CAACA

25

30

2) INFORMATION FOR SEQ ID NO: 1478

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478

45 GAGAATGGAG TAATTGGCTC TGGATT

26

50

2) INFORMATION FOR SEQ ID NO: 1479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479

GCGAAATACA CAACATCAGG GTCAT

25

10

2) INFORMATION FOR SEQ ID NO: 1480

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 474 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
- (B) STRAIN: J120
- (C) ACCESSION NUMBER: Z86002

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480

ATGAAAATAT	CTCTTATGGC	AGCTGTTTCC	GAGAATGGAG	TAATTGGCTC	50
30	TGGATTGGAT	ATACCTTGGC	ATGTACAAGG	CGAGCAGCTC	100
	CCATGACTTA	CAATCAATGG	CTTCTAGTTG	GTCGTAAAAC	150
	ATGGGTAAAC	TTCCGAATAG	AAAATATGCA	GTGGTTACTC	200
	TATCTCGAAT	GACCCTGATG	TTGTGTATTT	CGCAAGTGTT	250
	TAGCTTACCT	AAACAATGCG	ACAGCACATA	TCTTTGTTTC	300
35	GAAATATATA	AAGCTTTAAT	CGATCAAGCA	GATGTTATCC	350
	GATTCACAAG	CATATCTCTG	GCGATGTGTT	TTTTCCCTCCA	400
	GCTTCAAGCA	AACATTTGAG	CAAAGTTTCA	GTTCAAATAT	450
	TACCAAATTT	GGGCAAAGGG	CTAA		474

40

2) INFORMATION FOR SEQ ID NO: 1481

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481

RTTACAGATC ATKTATATGT CTCT

24

5 2) INFORMATION FOR SEQ ID NO: 1482

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482

TAATTTATAT TAGACAWAAA AAACGTG

26

20

2) INFORMATION FOR SEQ ID NO: 1483

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483

CARYGTCAGA AAATGGCGTA ATC

23

35

2) INFORMATION FOR SEQ ID NO: 1484

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1484

TKCAAAGCRW TTTCTATTGA AGGAAA

26

50

2) INFORMATION FOR SEQ ID NO: 1485

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485
- AAAATGGCGT AATCGGTAAT GGC 23
- 15 2) INFORMATION FOR SEQ ID NO: 1486
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486
- CATTGAGCT TGAAATTCCT TTCCTC 26
- 30 2) INFORMATION FOR SEQ ID NO: 1487
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487
- AATCGAAAAT ATGCAGTAGT GTCGAG 26
- 45 2) INFORMATION FOR SEQ ID NO: 1488
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488

AGACTATTGT AGATTTGACC GCCA

24

10

2) INFORMATION FOR SEQ ID NO: 1489

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: VA292
(C) ACCESSION NUMBER: U31119

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489

30 TTGAAAATTT CATTGATTC TGCAACGTCA GAAAATGGCG TAATCGGTAA 50
TGGCCCTGAT ATCCCATGGT CAGCAAAGG TGAGCAGTTA CTCTTTAAAG 100
CGCTCACATA TAATCAGTGG CTCCTTGTTG GAAGGAAAAC ATTTGACTCT 150
ATGGGTGTTC TTCCAAATCG AAAATATGCA GTAGTGTCGA GGAAAGGAAT 200
TTCAAGCTCA AATGAAAATG TATTAGTCTT TCCTTCAATA GAAATCGCTT 250
TGCAAGAACT ATCGAAAATT ACAGATCATT TATATGTCTC TGGTGGCGGT 300
CAAATCTACA ATAGTCTTAT TGAAAAGCA GATATAATTC ATTTGTCTAC 350
35 TGTTCACGTT GAGGTTGAAG GTGATATCAA TTTTCCTAAA ATTCCAGAGA 400
ATTTCAATTT GGTTTTGTAG CAGTTTTTTT TGTCTAATAT AAATTACACA 450
TATCAGATTT GGAAAAAGG CTAA 474

40

2) INFORMATION FOR SEQ ID NO: 1490

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490

GACCTATGAG AGCTTGCCCG TCAAA

25

2) INFORMATION FOR SEQ ID NO: 1491

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491

TCGCCTTCGT ACAGTCGCTT AACAAA

26

15

2) INFORMATION FOR SEQ ID NO: 1492

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492

CATTTTAGCT GCCACCGCCA ATGGTT

26

30

2) INFORMATION FOR SEQ ID NO: 1493

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493

45 GCGTCGCTGA CGTTGTTTAC GAAGA

25

50

2) INFORMATION FOR SEQ ID NO: 1494

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: BL26A
(C) ACCESSION NUMBER: U10186

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494

ATGATCGAGC TTCATGCCAT TTTAGCTGCC ACCGCCAATG GTTGCATTGG 50
GAAGGACAAC GCACTTCCCT GGCCACCACT AAAAGGCGAT CTGGCCAGAT 100
15 TCAAAAAATT GACCATGGGG AAGGTGGTCA TTATGGGGCG CAAGACCTAT 150
GAGAGCTTGC CCGTCAAATT AGAAGGTCGC ACCTGCATCG TTATGACGCG 200
CCAAGCGCTG GAGCTTCCGG GTGTTCGTGA CGCTAACGGC GCTATCTTCG 250
TGAACAACGT CAGCGACGCC ATGCGGTTTC CTCAAGAAGA GAGCGTGGGC 300
GATGTGGCCT ACGTCATTGG TGGCGCTGAG ATATTCAAGC GACTTGCCTT 350
20 GATGATCACG CAGATTGAAT TGACCTTTGT TAAGCGACTG TACGAAGGCG 400
ACACCTACGT TGATCTGGCC GAAATGGTCA AAGACTACGA GCAGAATGGC 450
ATGGAAGAAC ATGACCTTCA CACTTACTTC ACTTACCGTA AAAAGGAGCT 500
TACAGAATGA 510

25

2) INFORMATION FOR SEQ ID NO: 1495

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495

TCTCTAAACA TGATTGTCGC TGTC

24

40

2) INFORMATION FOR SEQ ID NO: 1496

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496

CAGTGAGGCA AAAGTTTTTC TACC

24

5

2) INFORMATION FOR SEQ ID NO: 1497

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1497

CGGACGACTT CATGTGGTAG TCAGT

25

20

2) INFORMATION FOR SEQ ID NO: 1498

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498

TTTGTTTTCA GTAATGGTCG GGACCT

26

35

2) INFORMATION FOR SEQ ID NO: 1499

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X57730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499

	ATGGCTTCTC	TAAACATGAT	TGTCGCTGTC	AATAAGACAG	GAGGTATCGG	50
	ATTTGAAAAT	CAGATTCCGT	GGCATGAACC	AGAAGATTTA	AAACACTTCA	100
	AAGCTGTTAC	AATGAACTCA	GTTTTGATTA	TGGGTAGAAA	AACTTTTGCC	150
	TCACTGCCTA	AAGTGCTGCC	CGGACGACTT	CATGTGGTAG	TCAGTAAAC	200
5	AGTACCACCC	ACCCAGAACA	CTGATCAAGT	TGTGTATGTA	AGTACATACC	250
	AGATCGCAGT	AAGAACTGCA	AGCTTGTTGG	TTGACAAACC	AGAGTATTCT	300
	CAAATTTTGT	TAATTGGTGG	GAAGAGTGCG	TACGAGAACT	TAGCTGCCTA	350
	CGTGGACAAA	CTCTACTTAA	CTAGAGTACA	GCTCAACACA	CAACAAGACA	400
	CTGAACTGGA	TTTATCCCTA	TTCAAGTCAT	GGAAACTCGT	ATCTGAGGTC	450
10	CCGACCATTA	CTGAAAACAA	AACAAAACCT	ATTTTCCAAA	TTTGGATTAA	500
	CCCTAACCCCT	ATTAGTGAGG	AACCCACATG	TTAG		534

15 2) INFORMATION FOR SEQ ID NO: 1500

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500

ATCGGGTTAT TGGCAATGGT CCTA

24

30

2) INFORMATION FOR SEQ ID NO: 1501

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501

GCGGTAGTTA GCTTGCGGTG AGATT

25

45

2) INFORMATION FOR SEQ ID NO: 1502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502

5

GCGGGCGGAG CTGAGATATA CA

22

10 2) INFORMATION FOR SEQ ID NO: 1503

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503

AACGGAGTGG GTGTACGGAA TTACAG

26

25

2) INFORMATION FOR SEQ ID NO: 1504

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: TKS84

(C) ACCESSION NUMBER: Z21672

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504

	ATGAACTCGG AATCAGTACG CATTTATCTC GTTGCTGCGA TGGGAGCCAA	50
	TCGGGTTATT GGCAATGGTC CTAATATCCC CTGGAAAATT CCGGGTGAGC	100
45	AGAAGATTTT TCGCAGACTC ACTGAGGGAA AAGTCGTTGT CATGGGGCGA	150
	AAGACCTTTG AGTCTATCGG CAAGCCTCTA CCGAACCGTC ACACATTGGT	200
	AATCTCACGC CAAGCTAACT ACCGCGCCAC TGGCTGCGTA GTTGTTTCAA	250
	CGCTGTCGCA CGCTATCGCT TTGGCATCCG AACTCGGCAA TGAACCTAC	300
	GTCGCGGGCG GAGCTGAGAT ATACACTCTG GCACTACCTC ACGCCCACGG	350
50	CGTGTTTCTA TCTGAGGTAC ATCAAACCTT CGAGGGTGAC GCCTTCTTCC	400
	CAATGCTCAA CGAAACAGAA TTCGAGCTTG TCTCAACCGA AACCATTCAA	450
	GCTGTAATTC CGTACACCCA CTCCGTTTAT GCGCGTCGAA ACGGCTAA	498

2) INFORMATION FOR SEQ ID NO: 1505

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505

ATTTTTCGCA GGCTCACCGA GAGC

24

2) INFORMATION FOR SEQ ID NO: 1506

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506

CGGATGAGAC AACCTCGAAT TCTGCTG

27

2) INFORMATION FOR SEQ ID NO: 1507

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: RA33.2
(C) ACCESSION NUMBER: Z50802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507

ATGAACCCGG	AATCGGTCCG	CATTTATCTG	GTCGCTGCCA	TGGGTGCCAA	50
TCGGGTATT	GGCAATGGTC	CCGATATCCC	CTGGAAAATC	CCAGGTGAGC	100
AGAAGATTTT	TCGCAGGCTC	ACCGAGAGCA	AAGTGGTCGT	TATGGGCCGC	150
AAGACATTTG	AGTCCATAGG	CAAGCCCTTA	CCAAACCGCC	ACACAGTGGT	200

	GCTCTCGCGC	CAAGCTGGTT	ATAGCGCTCC	TGGTTGTGCA	GTTGTTTCAA	250
	CGCTGTCACA	CGTATCGCCA	TCGACAGCCG	AACACGGCAA	AGAACTCTAC	300
	ETAGCGCGCG	GAGCCGAGGT	ATATGCGCTG	GCGCTACCGC	ATGCCAACGG	350
	CGTCTTTCTA	TCTGAGGTAC	ATCAAACCTT	TGAGGGTGAC	GCCTTCTTCC	400
5	CAGTGCTTAA	CGCAGCAGAA	TTGAGGTTG	TCTCATCCGA	AACCATTCAA	450
	GGCACAATCA	CGTACACGCA	CTCCGTCTAT	GCGCGTCGTA	ACGGCTAA	498

10 2) INFORMATION FOR SEQ ID NO: 1508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- 15 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508

AGAATGTATT GGTATTTCCA TCTATCG

27

25

2) INFORMATION FOR SEQ ID NO: 1509

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- 30 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509

CAATGTCGAT TGTTGAAATA TGTAAA

26

40

2) INFORMATION FOR SEQ ID NO: 1510

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 45 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510

TGGAGTGCCA AAGGGGAACA AT

5 2) INFORMATION FOR SEQ ID NO: 1511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511

CAGACACAAT CACATGATCC GTTATCG

27

20

2) INFORMATION FOR SEQ ID NO: 1512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: UI14
 (C) ACCESSION NUMBER: Z83331

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512

GTGAAACTAT CACTAATGGC AGCAATTTTCG AAGAATGGAG TTATCGGAAA 50
 TGGCCCAGAT ATTCCATGGA GTGCCAAAGG GGAACAATTA CTCTTCAAAG 100
 40 CGATTACCTA TAATCAGTGG CTTTGGTAG GCCGAAAGAC TTTCGAGTCA 150
 ATGGGGGCTT TACCCAACCG AAAATATGCC GTTGTAAGCTC GTTCAAGCTT 200
 CACTTCCAGT GATGAGAATG TATTGGTATT TCCATCTATC GATGAAGCGC 250
 TAAATCATCT GAAGACGATA ACGGATCATG TGATTGTGTC TGGTGGTGGT 300
 GAAATATACA AAAGCCTGAT CGATAAAGTT GATACTTTAC ATATTTCAAC 350
 45 AATCGACATT GAGCCAGAAG GTGATGTCTA TTTTCCAGAA ATCCCCAGTA 400
 GTTTTAGGCC AGTTTTTAGC CAAGACTTCG TGTCTAACAT AAATTATAGT 450
 TACCAAATCT GGCAAAAGGG TTAA 474

50

2) INFORMATION FOR SEQ ID NO: 1513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513

10 TTCAAGCTCA AATGAAAACG TCC

23

2) INFORMATION FOR SEQ ID NO: 1514

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514

25

GAAATTCTCA GGCATTATAG GGAAT

25

30 2) INFORMATION FOR SEQ ID NO: 1515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515

GTGGTCAGTA AAAGGTGAGC AAC

23

45

2) INFORMATION FOR SEQ ID NO: 1516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

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MISSING AT THE TIME OF PUBLICATION

CTATGTCTCA AGGCCGTGCA ACATACTCTA TGGAAATTTGC TAAATATGCT 50
 GAAACTCCAC GTAACGTGGC TGAAGGCATC ATTTCTAAAT TTCAGTCTGG 100
 CGGTAAAAAA GGTGACGACG AGTAA 125

5

2) INFORMATION FOR SEQ ID NO: 1519

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
 20 (B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519

TCTTTTCGATT ACTATAAGCC CAAACTAATT CATAGTTAAA AACCAAGTGC 50
 25 TCATGCAGTG ATCCTGCATG AGTAGTTTAA AAAGGAAGAT CTC 93

2) INFORMATION FOR SEQ ID NO: 1520

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
 40 (B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520

45 ATGGCTAAGG CTAAGTTTGA ACGTAATAAG CCACACGTTA ACGTGGGCAC 50
 AATCGGTCAC GTTGACCATG GTAAAACAAC TTTAACAGCT GCAATTGCAA 100
 CTGTATGTGC GAAGAAATTC GGTGGCGAAG CGAAAGACTA CGCTGCAATT 150
 GACTCTGCAC CAGAAGAAAA AGCACGTGGT ATTACAATTA ATACTTCACA 200
 CGTAGAATAC GATTCTCCAA CTCGTCAC TA CGCACACGTA GACTGCCCGG 250
 50 GCCACGCCGA TTATGTTAAA AACATGATTA CTGGTGCTGC TCAGATGGAC 300
 GGCGCGATCC TTGTATGTGC TGCGACTGAT GGTCCAATGC CACAGACTCG 350
 TGAACACATC CTTCTTTCTC GTCAGGTTGG TGTACCTTAC ATTCTTGTAT 400
 TCCTTAACAA GTGTGACCTT GTTGATGATG AAGAACTTCT TGAGCTAGTG 450

5 GAAATGGAAG TTCGTGAACT TCTTTCTACT TATGACTTCC CAGGTGATGA 500
 CACTCCAGTT ATCCGTGGTT CAGCTCTTCT TGCACCTAAC GGTGACGCTG 550
 GTCAGTATGG CGAAGAAGCA GTTGTGCGC TTGTTGACGC ACTTGACACT 600
 TACATTCCAG AGCCAGTACG TGCAATCGAC CAAGCATTCT TAATGCCAAT 650
 10 CGAAGACGTA TTCTCTATTT CTGGTCGTGG TACAGTAGTA ACTGGCCGTG 700
 TAGAACTGG TATTGTGAAA GTAGGCGAAT CAGTTGAAAT CGTTGGTATC 750
 CGTGATACTC AAGTAACTAC AGTTACTGGC GTAGAAATGT TCCGTAAATT 800
 GCTTGACGAA GGTCTGTCGG GCGAGAACTG TGGTGTCTT CTACGTGGTA 850
 CTAAGCGTGA AGACGTACAA CGTGGTCAAG TACTTGCTAA ACCAGGTGCA 900
 15 ATCAAGCCAC AACTAAATT CGATGCAGAA GTATACGTAC TTTCTAAAGA 950
 AGAAGGTGGT CGTCACACTC CATTCTTAA CGGTTACCGT CCACAGTTCT 1000
 ACTTCCGTAC AACTGACGTA ACTGGCGCGA TCAAATTACA AGATGGCGTT 1050
 GAAATGGTTA TGCCTGGTGA CAACGTAGAA ATGTCAGTAG AATTAATCCA 1100
 CCCAAT 1106
 15

2) INFORMATION FOR SEQ ID NO: 1521

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Haemophilus influenzae*
 30 (B) STRAIN: ATCC 9006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521

35 ACAAAC TCAA GGTCGTGCAT CTTACTCAAT GGAACCGTTA AAATATGCTG 50
 AAGCTCCAAC AAGTGTTGCG GCTGCAGTAA TTGAAGCGCG TAAAAAATAA 100

2) INFORMATION FOR SEQ ID NO: 1522

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: ATCC 9006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522

TTTTTGTAAG CCAGCGGTGT AAAATATGAT TGTTTTATAC CGCACTTCTT 50
 AGGAAACATT AGAA 64

5

2) INFORMATION FOR SEQ ID NO: 1523

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: ATCC 9006

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523

ATGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTAA ACGTGGGTAC 50
 AATCGGCCAC GTTGACCACG GTAAAACAAC TTTAACAGCA GCAATTACAA 100
 25 CCGTATTAGC AAAACACTAC GGTGGTGCAG CGCGTGCATT TGACCAAATC 150
 GATAACGCGC CAGAAGAAAA AGCGCGTGGT ATTACCATCA ACACTTCACA 200
 TGTTGAATAC GATACACCAA CTCGCCACTA TGCACACGTA GACTGTCCAG 250
 GACACGCCGA CTATGTTAAA AACATGATTA CCGGTGCGGC GCAAATGGAT 300
 GGTGCTATTT TAGTAGTAGC AGCAACAGAT GGTCCATATGC CACAAACTCG 350
 30 TGAACATATC TTATTAGGTC GCCAAGTAGG TGTTCCATAC ATCATCGTAT 400
 TCTTAAACAA ATGCGACATG GTAGATGATG AAGAGTTATT AGAATTAGTA 450
 GAAATGGAAG TCGGTGAACT TCTATCTCAA TATGACTTCC CAGGTGACGA 500
 TACACCAATC GTACGTGGTT CAGCATTACA AGCATTGAAC GGCGTAGCAG 550
 AATGGGAAGA AAAAATCCTT GAATTAGCTG GTCACCTAGA TACTTACATC 600
 35 CCAGAACCAG AACGTGCGAT TGACCAACCG TTCCTTCTTC CAATTGAAGA 650
 CGTATTCTCA ATTTAGGTC GTGGTACAGT AGTAACTGGT CGTGTAGAAC 700
 GTGGTATCAT CCGTACTGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT 750
 ACAGCGAAAA CTACTGTAAC AGGTGTTGAA ATGTTCCGTA AATTACTTGA 800
 CGAAGGTCGT GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC 850
 40 GTGAAGAAAT CGAACGTGGT CAAGTATTAG CGAAACCAGG TTCAATCACA 900
 CCACACACTG ATTTTGAATC AGAAGTATAC GTATTATCAA AAGATGAAGG 950
 TGGTCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAA TTCTATTTCC 1000
 GTACAACAGA CGTAACTGGT ACAATTGAAT TACCAGAAGG CGTGGAAATG 1050
 GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCCA 1098

45

2) INFORMATION FOR SEQ ID NO: 1524

- 50 (i) SEQUENCE CHARACTERISTICS:,
 (A) LENGTH: 77 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524

10

CAATGGAGTT CTTGAAGTAC AACGAAGCGC CTAGCAACGT CGCTCAGGCT 50
ATTATCGAAG CTCGTAAAGC GAAATAA 77

15

2) INFORMATION FOR SEQ ID NO: 1525

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 67 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525

GATCCTTTTCG AGTTCAATTT AGTTTACGCT CCCTCTGTGA GAGGGAGCGA 50
TATTAAGGAA TATAGTC 67

35

2) INFORMATION FOR SEQ ID NO: 1526

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1112 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526

GTGTCTAAAG AAAAATTTGA ACGTTCAAAA CCGCACGTTA ACGTTGGTAC 50

	TATCGGCCAC	GTTGACCACG	GTAAAACAAC	TCTGACTGCT	GCAATCACTA	100
	CAGTTTTAGC	TAAAACTTAC	GGTGGTGCTG	CTCGTGCATT	CGACCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCGCGTGGT	ATCACCATCT	CTACTTCACA	200
	CGTAGAATAC	GATACTCCAA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
5	GTCACGCCGA	CTATGTTAAA	AACATGATCA	CTGGTGCTGC	GCAAATGGAC	300
	GGCGCTATTC	TGGTAGTAGC	AGCAACTGAT	GGTCCAATGC	CACAACTCG	350
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTCC	CAGGTGATGA	500
10	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCTTATATC	600
	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCTTGTTAC	CAATCGAAGA	650
	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	TATCAAAGAA	750
15	ACCACCAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	800
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACAAAAC	850
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CAAAACCAGG	CTCAATCAAC	900
	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAC	ACACCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
20	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	1050
	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGAACTGA	TCCACCCAAT	1100
	CGCAATGGAC	GA				1112

25

2) INFORMATION FOR SEQ ID NO: 1527

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527

	ATCAACGAAG	CTATCGAGGT	TTATTTTGAG	GTTGAGGGCA	AGAAAAATAG	50
	ATTGATCCTG	GAGGTCGCGG	CTCACTTGGG	TGATAACCGC	GTCAGAACGA	100
	TCGCTATGGA	TATGAGTGAG	GGGCTTACTC	GCGGGCTTGA	AGCTACCGCT	150
45	CTTGGTGCGC	CTATTAGTGT	GCCGGTTGGC	GAGAAGGTTT	TGGGAAGAAT	200
	TTTTAACGTC	GTCGGCGATC	TCATCGACGA	GGGCGAGGGC	GTAAATTTTG	250
	ATAAACATTG	GTCTATCCAC	CGCGATCCGC	CACCATTTGA	AGAACAAAGC	300
	ACGAAAAGTG	AAATTTTGA	AACCGGTATA	AAGGTTGTGG	ATCTTCTTGC	350
	GCCTTACGCA	AAGGGCGGTA	AGGTCGGACT	ATTTGGCGGT	GCAGGTGTCTG	400
50	GTA AACGGT	CATCATCATG	GAGCTCATCC	ACAATGTCGC	CTTCAAACAC	450
	AGCGGATACT	CTGTATTTGC	AGGTGTTGGC	GAGAGGACGC	GCGAAGGAAA	500
	CGACCTTTAT	CACGAGATGA	AAGAAAGTAA	CGTTTTGGAT	AAAGTCGCCT	550
	TGTGCTACGG	ACAGATGAAC	GAGCCGCCAG	GGGCGAGAAA	TCGTATCGCA	600

CTGACTGGTC	TAACGATGGC	TGAGTATTTT	CGCGATGAGA	TGGGACTTGA	650
TGTGCTTATG	TTTATCGACA	ACATCTTCCG	CTTCTCTCAA	TCTGGTGCAG	700
AGATGTCGGC	ACTCCTCGGA	CGTATCCCAT	CAGCCGTTGG	TTACCAGCCG	750
ACGCTGGCAA	GCGAGATGGG	TAAATTTCAA	GAAAGGATCA	CATCGACTAA	800

5

2) INFORMATION FOR SEQ ID NO: 1528

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528

20 AACTTGAGCG ATTTTCGGAT ACCCTG

26

2) INFORMATION FOR SEQ ID NO: 1529

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529

35

TTGCCGATGA AATAACCGCC GACT

24

40 2) INFORMATION FOR SEQ ID NO: 1530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: M11277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530

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5  ATGCGATTGG TTTGGAAATG TGGGGCGATT CAGGCATCCC GGTTATCTGA      50
   ATGGCTCAAC TCAACAGCCG GTGCTCATGA ACTTGAGCGA TTTTCGGATA      100
   CCCTGACCTT TTCTGTGTAT GGCTCAGTGC TGATCTGGCT GAAATCATAT      150
   CTCCGCGAAT CAGGAAGAAA ACTGCAGTTA GTCGGAATCG CCTTACCCAA      200
   CACCCTGAAC CCAAGGGACG ACCTAGCGCA ATTGGCCGAA ATTATCCAGC      250
   TCATCGATCA CCTCATGAAA CCGCACGTTG ATATGTTGAC TCACTTGTTG      300
   GCGTCCATTG ATGGCCAGTC GCGGTTATT TCATCGGCAA AATGGGGGGA      350
10 GCTAGAAACG GCTCGGCAGG AGAAAGCTAT CTCAGGGGTA ACCAGATTGA      400
   AGCTCCGCTT GCGGTCGCTT GCGGCGTCC TGAAAAACA CGTCAACAGC      450
   GATTTGTTCC GAAAAGCCTC TGATCGAATA GAGTCGATAG AGTATACGTT      500
   GGAAACCTTG CGTATAATGA AAACCTTCTT CGATGGTACC TCTCTTGAGG      550
   GAGATACTTC CGTACGTGAC TCGTATATGG CGGGCGTAGT AGATGGAATG      600
15 GTTCGAGCGA ATCCGGATGT GAAGATAATT CTGCTGGCGC ACAACAATCA      650
   TCTACAAAAA ACTCCAGTCT CCTTTTCAGG CGAGCTTACG GCTGTTCCCA      700
   TGGGGCAGCA CCTCGCAGAG AGGGTGAATT ACCGTGCGAT TGCATTACCC      750
   CATCTTGAC CCACCGTGCC GGAAATGCAT TTCCCATCGC CAAAAAGTCC      800
   TCTTGATTG TCTGTTGTGA CCACGCCTGC CGATGCAATC CGTGAGGATA      850
20 GTATGGAACA GTATGTCATC GACGCTGTG GTACGGAGAA TTCATGTCTG      900
   ACATTGACAG ATGCCCCCAT GGAAGCAAAG CGAATGCGGT CTCAAAGCGC      950
   CTCTGTAGAA ACGAAATTGA GCGAGGCATT TGATGCCATC GTCTGTGTTA     1000
   CAAGCGCCGG CAAGGACAGC CTGGTTGCC TATAG                      1035

```

25

2) INFORMATION FOR SEQ ID NO: 1531

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30 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

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35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531

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40 TCTTTTTGTT ACGACATACG CTTTT

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25

2) INFORMATION FOR SEQ ID NO: 1532

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45 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 24 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532

AGTGCTTCTT TATCCGCTGT TCTA

24

5

2) INFORMATION FOR SEQ ID NO: 1533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533

CAGCGGATAA AGAAGCACTA CACATT

26

20

2) INFORMATION FOR SEQ ID NO: 1534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534

CCTCCTGAAA TAAAGCCCGA CAT

23

35

2) INFORMATION FOR SEQ ID NO: 1535

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: A15097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535

50

	ATGAGGTTTCG	AAGAATGGGT	CAAAGATAAG	CATATTCCTT	NCAAACNGAA	50
	TCACCCTGAT	GATAATTACG	ATGATTTTAA	GCCATTAAGA	AANATAATTG	100
	GAGATACCCG	AGTTGTAGCA	TTAGGTGAAA	ATTCTCATTT	CATAAAAGAA	150
	TTCTTTTTGT	TACGACATAC	GCTTTTGCGT	TTTTTTATCG	AAGATCTAGG	200
5	TTTTACTACG	TTTGCTTTTG	AATTTGGTTT	TGCTGAGGGT	CAAATCATCA	250
	ATAACTGGAT	ACATGGACAA	GGAAGTGACG	ATGAAATAGG	CAGATTCTTA	300
	AAACACTTCT	ATTATCCAGA	AGAGCTCAAA	ACCACATTTT	TATGGCTAAG	350
	GGAGTACAAT	AAAGCAGCAA	AAGAAAAAAT	CACATTTCTT	GGCATTGATA	400
	TACCCAGAAA	TGGAGGTTCA	TACTTACCAA	ATATGGAGAT	AGTGCATGAC	450
10	TTTTTTTAGAA	CAGCGGATAA	AGAAGCACTA	CACATTATCG	ATGATGCATT	500
	TAATATTGCA	AAAAAGATTG	ATTACTTCTC	CACATCACAG	GCAGCCTTAA	550
	ATTTACATGA	GCTAACAGAT	TCTGAGAAAT	GCCGTTTAAC	TAGCCAATTA	600
	GCTCGAGTAA	AAGTTCGCCT	TGAAGCTATG	GCTCCAATTC	ACATTGAAAA	650
	ATATGGGATT	GATAAATATG	AGACAATTCT	GCATTATGCC	AACGGTATGA	700
15	TATACTTGGA	CTATAACATT	CAAGCTATGT	CGGGCTTTAT	TTCAGGAGGC	750
	GGAATGCAGG	GCGATATGGG	TGCAAAAGAC	AAATACATGG	CAGATTCTGT	800
	GCTGTGGCAT	TTAAAAAACC	CACAAAGTGA	GCAGAAAGTG	ATAGTAGTAG	850
	CACATAATGC	ACATATTCAA	AAAACACCCA	TTCTGTATGA	TGGATTTCTA	900
	AGTTGCCTAC	CAATGGGCCA	AAGACTTAAA	AATGCCATTG	GTGATGATTA	950
20	TATGTCTTTA	GGTATTACTT	CTTATAGTGG	GCATACTGCA	GCCCTCTATC	1000
	CGGAAGTTGA	TACAAAATAT	GGTTTTTCGAG	TTGATAACTT	CCAAGTGCAG	1050
	GAACCAAATG	AAGGTTCTGT	CGAGAAAGCT	ATTTCTGGTT	GTGGAGTTAC	1100
	TAATTCTTTT	GTCTTTTTTT	GAAATATTCC	TGAAGATTTA	CAATCCATCC	1150
	CGAACATGAT	TCGATTTGAN	TCTATTTACA	TGAAAGCAGA	ACTCGAGAAA	1200
25	GCTTTCGATG	GAATATTTCA	AATTGAAAAG	TCATCTGTAT	CTGAGGTCGT	1250
	TTATGAATAA					1260

30 2) INFORMATION FOR SEQ ID NO: 1536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536

AGATGTATTA ACTGGAAAAC AACAA

25

45

2) INFORMATION FOR SEQ ID NO: 1537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537

5 CTTTGTAATT AGTTTCTGAA AACCA

25

2) INFORMATION FOR SEQ ID NO: 1538

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538

20

TTAGAAGATA TAGGATACAA AATAGAAG

28

25 2) INFORMATION FOR SEQ ID NO: 1539

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539

GAATGAAAAA GAAGTTGAGC TT

22

40

2) INFORMATION FOR SEQ ID NO: 1540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

(C) ACCESSION NUMBER: M14039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540

```

5  ATGAAAAATA ATAATGTAAC AGAAAAAGAA TTATTTTATA TTTTAGATTT      50
   ATTTGAACAC ATGAAAGTAA CTTATTGGTT AGATGGTGGC TGGGGGGTAG      100
   ATGTATTAAC TGGAAAACAA CAAAGAGAAC ACAGAGATAT AGATATAGAT      150
   TTTGACGCTC AACACACTCA AAAAGTTATA CAAAAATTAG AAGATATAGG      200
   ATACAAAATA GAAGTTCATT GGATGCCTTC ACGTATGGAA CTTAAGCATG      250
   AAGAATATGG GTATTTAGAT ATTCATCCTA TAAATCTAAA TGATGATGGA      300
10 TCAATTACCC AAGCAAACCC AGAAGGTGGT AATTATGTTT TCCAAAATGA      350
   CTGGTTTTCA GAACTAATT ACAAAGATCG AAAAATACCA TGTATTTCAA      400
   AAGAAGCTCA ACTTCTTTT CATTCTGGTT ATGATTTAAC AGAAACAGAC      450
   CATTTTGATA TAAAAAATTT AAAATCAATA ACATAA                      486

```

15

2) INFORMATION FOR SEQ ID NO: 1541

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541

```

30 TGATAATCTT ATACGTGGGG AATTT                      25

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2) INFORMATION FOR SEQ ID NO: 1542

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35 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542

```

45 ATAATTTTCT AATTGCCCTG TTTCAT                      26

```

2) INFORMATION FOR SEQ ID NO: 1543

50

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid

```

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543

GGGCAATTAG AAAATTATTT ATCAGA

26

10

2) INFORMATION FOR SEQ ID NO: 1544

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544

TTTTACTCAT GTTTAGCCAA TTATCA

26

25

2) INFORMATION FOR SEQ ID NO: 1545

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Enterococcus faecium*
(C) ACCESSION NUMBER: AF110130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545

	ATGTTAAAAC	AAAAAGAATT	AATTGCAAAC	GTTAAGAATC	TTACTGAGTC	50
45	AGATGAACGA	ATTACAGCTT	GTATGATGTA	TGGATCGTTT	ACCAAAGGAG	100
	AAGGTGACCA	ATACTCTGAT	ATAGAGTTCT	ATATATTTTT	GAAACATAGT	150
	ATAACCTCGA	ACTTTGATTC	ATCCAACCTGG	TTGTTTGACG	TAGCTCCGTA	200
	CTTGATGCTT	TATAAAAATG	AGTACGGAAC	AGAGGTAGTT	ATTTTTGATA	250
	ATCTTATACG	TGGGGAATTT	CATTTCCCTT	CTGAAAAAGA	TATGAACATA	300
50	ATCCCCTCGT	TTAAAGATTC	AGGTTATATT	CCTGATACGA	AGGCTATGCT	350
	TATTTACGAT	GAAACAGGGC	AATTAGAAAA	TTATTTATCA	GAGATAAGTG	400
	GTGCAAGACC	AAATAGACTT	ACTGAAGAAA	ATGCTAATTT	TTTGTTGTGT	450
	AATTTCTCTA	ATCTATGGTT	GATGGGAATC	AACGTTCTAA	AAAGAGGAGA	500

ATATGCTCGT TCATTAGAAC TCTTATCACA ACTTCAAAAA AATACACTAC 550
 AACTTATACG TATGGCAGAA AAAAATGCTG ATAATTGGCT AAACATGAGT 600
 AAAAACCTTG AAAAAGAAAT TAGCCTTGAA AATTATAAAA AATTTGCAAA 650
 GACCACTGCT CGATTAGATA AGGTAGAATT ATTTGAAGCC TATAAAAATT 700
 5 CTTTGCTATT AGTTATGGAT TTGCAAAGTC ACCTTATTGA ACAATACAAC 750
 TTAAAAGTTA CACATGACAT TTTAGAAAGA TTGTTGAATT ACATTAGTGA 800
 ATAG 804

10

2) INFORMATION FOR SEQ ID NO: 1546

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - 15 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546

CAAGAAGGAA TGGCTGTACT AC

22

25

2) INFORMATION FOR SEQ ID NO: 1547

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 27 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- 35 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1547

TAATTCCCAA ATAACCCTAA TAATAGA

27

40

2) INFORMATION FOR SEQ ID NO: 1548

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1218 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

50

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*
(C) ACCESSION NUMBER: U70055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548

5
ATGGAAAAAT ACAACAATTG GAAACTTAAG TTTTATACAA TATGGGCAGG 50
GCAAGCAGTA TCATTAATCA CTAGTGCCAT CTTGCAAATG GCGATTATTT 100
TTTACCTTAC AGAAAAAACT GGATCCGCGA TGGTCTTGTC TATGGCTTCA 150
CTATTAGGTT TTTTACCCTA TGCGGTCTTT GGACCTGCAA TTGGTGTGCT 200
10 AGTGGATCGT CATGATAGGA AGAAGATAAT GATTGGTGCT GATTTAATTA 250
TCGCAGCAGC TGGTTCGGTG CTTACTATTG TTGCATTCTA TATGGAGCTA 300
CCTGTCTGGA TGGTTATGAT AGTATTGTTT ATCCGTAGCA TTGGAACAGC 350
TTTTCACACC CCGGCTCTCA ATGCGGTTAC GCCACTTTTA GTACCAGAAG 400
AACAGCTTAC GAAATGTGCA GGCTATAGTC AGTCTTTGCA GTCTATAAGC 450
15 TATATTGTTA GTCCGGCGGT TGCAGCACTC TTATACTCCG TTTGGGAACT 500
AAATGCTATT ATTGCCATCG ATGTATTGGG TGCTGTGATT GCATCTATTA 550
CGGTAGCAAT TGTACGTATT CCTAAGCTGG GTGATCGCGT GCAAAGTTTG 600
GACCCAAATT TCATAAGAGA AATGCAAGAA GGAATGGCTG TACTACGGCA 650
AAATAAAGGA TTATTTGCTT TATTACTCGT TGGAACATTA TATATGTTTG 700
20 TTTATATGCC AATTAATGCA CTATTCCTT TAATTAGCAT GGATTACTTT 750
AATGGAACAC CTGTGCATAT TTCTATTACG GAAATTTCTT TTGCATCTGG 800
AATGTTGATA GGGGGTCTAT TATTAGGGTT ATTTGGGAAT TACCAAAGC 850
GAATCTTATT AATAACGGCA TCCATTTTTA TGATGGGGAT AAGCTTAACC 900
ATTTCAAGAT TACTTCCCCA AAGTGGATTT TTCATTTTTG TAGTCTGCTG 950
25 TGCAATAATG GGGCTTTCTG TTCCGTTTTA CAGCGGTGTG CAAACAGCTC 1000
TTTTTCAGGA GAAAATTAAG CCTGAATATT TAGGACGTGT ATTTTCTTTA 1050
ACTGGAAGTA TCATGTCTCT TGCTATGCCA ATTGGATTAA TTCTTTCTGC 1100
ACTCTTTGCT GATAGAATCG GTGTAAATCA TTGGTTTTTA CTATCAGGTA 1150
CTTTAATTAT TTGCATTGCA ATAGTTTGCC CAATGATAAA TGAGATTAGA 1200
30 AAATTAGATT TAAAATAA 1218

2) INFORMATION FOR SEQ ID NO: 1549

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549

45 GCTTATTATT AGGAAGATTA GGGGGC 26

50 2) INFORMATION FOR SEQ ID NO: 1550

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases

800

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550

10 TAGCAAGTGA CATGATACTT CCGA

24

2) INFORMATION FOR SEQ ID NO: 1551

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1218 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Streptococcus pneumoniae*
(C) ACCESSION NUMBER: U83667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551

	ATGGAAAAAT	ACAACAATTG	GAAACGAAAA	TTTTATGCAA	TATGGGCAGG	50
30	GCAAGCAGTA	TCATTAATCA	CTAGTGCCAT	CCTGCAAATG	GCGATTATTT	100
	TTTACCTTAC	AGAAAAACA	GGATCTGCGA	TGGTCTTGTC	TATGGCTTCA	150
	TTAGTAGGTT	TTTTACCCTA	TGCGATTTTG	GGACCTGCCA	TTGGTGTGCT	200
	AGTGGATCGT	CATGATAGGA	AGAAGATAAT	GATTGGTGCC	GATTTAATTA	250
	TCGCAGCAGC	TGGTGCAGTG	CTTGCTATTG	TTGCATTCTG	TATGGAGCTA	300
35	CCTGTCTGGA	TGATTATGAT	AGTATTGTTT	ATCCGTAGCA	TTGGAACAGC	350
	TTTTTCATACC	CCAGCACTCA	ATGCGGTTAC	ACCACTTTTA	GTACCAGAAG	400
	AACAGCTAAC	GAAATGCGCA	GGCTATAGTC	AGTCTTTGCA	GTCTATAAGC	450
	TATATTGTTA	GTCCGGCAGT	TGCAGCACTC	TTATACTCCG	TTTGGGATTT	500
	AAATGCTATT	ATTGCCATCG	ACGTATTGGG	TGCTGTGATT	GCATCTATTA	550
40	CGGTAGCAAT	TGTACGTATA	CCTAAGCTGG	GTAATCAAGT	GCAAAGTTTA	600
	GAACCAAATT	TCATAAGGGA	GATGAAAGAA	GGAGTTGTGG	TTCTGAGACA	650
	AAACAAAGGA	TTGTTTGCCT	TATTACTCTT	AGGAACACTA	TATACTTTTG	700
	TTTATATGCC	AATCAATGCA	CTATTTCTTT	TAATAAGCAT	GGAACACTTT	750
	AATGGAACGC	CTGTGCATAT	TTCTATTACG	GAAATTTTCT	TTGCATTTTG	800
45	GATGCTAGCA	GGAGGCTTAT	TATTAGGAAG	ATTAGGGGGC	TTCGAAAAGC	850
	ATGTATTACT	AATAACAAGT	TCATTTTTTA	TAATGGGGAC	CAGTTTAGCC	900
	GTTTCGGGAA	TACTTCCTCC	AAATGGATTT	GTAATATTCG	TAGTTTGCTG	950
	TGCAATAATG	GGGCTTTCGG	TGCCATTTTA	TAGCGGTGTG	CAAACAGCTC	1000
	TTTTTCAGGA	GAAAATTAAG	CCTGAATATT	TAGGACGTGT	ATTTTCTTTG	1050
50	ATCGGAAGTA	TCATGTCACT	TGCTATGCCA	ATTGGGTAA	TTCTTTCTGG	1100
	ATTCTTTGCT	GATAAAATCG	GTGTAAATCA	TTGGTTTTTA	CTATCAGGTA	1150
	TTTTAATTAT	TGGCATTGCT	ATAGTTTGCC	AAATGATAAC	TGAGGTTAGA	1200
	AAATTAGATT	TAAAATAA				1218

2) INFORMATION FOR SEQ ID NO: 1552

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552

GGCAAGCAGT ATCATTAATC ACTA

24

15

2) INFORMATION FOR SEQ ID NO: 1553

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553

CAATGCTACG GATAACAAT ACTATC

26

30

2) INFORMATION FOR SEQ ID NO: 1554

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554

45 AGAAAATTAA GCCTGAATAT TTAGGAC

27

2) INFORMATION FOR SEQ ID NO: 1555

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555

TAGTAAAAAC CAATGATTTA CACCG

25

10

2) INFORMATION FOR SEQ ID NO: 1556

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556

ACTGTACGCA CTTGCAGCCC GACAT

25

25

2) INFORMATION FOR SEQ ID NO: 1557

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557

40

GAACGGCAGG CGATTCTTGA GCAT

24

2) INFORMATION FOR SEQ ID NO: 1558

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558

GTGGTGGTGC ATGGCGATCT CT

22

5

2) INFORMATION FOR SEQ ID NO: 1559

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559

GCCGCAGCGA GGTACTCTTC GTTA

24

20

2) INFORMATION FOR SEQ ID NO: 1560

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 35 (C) ACCESSION NUMBER: D16251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560

	ATGACCGTAG TCACGACCGC CGATACCTCC CAACTGTACG CACTTGCAGC	50
40	CCGACATGGG CTCAAGCTCC ATGGCCCGCT GACTGTCAAT GAGCTTGGGC	100
	TCGACTATAG GATCGTGATC GCCACCGTCG ACGATGGACG TCGGTGGGTG	150
	CTGCGCATCC CGCGCCGAGC CGAGGTAAGC GCGAAGGTCG AACCAGAGGC	200
	GCGGGTGCTG GCAATGCTCA AGAATCGCCT GCCGTTCGCG GTGCCGGA	250
	GGCGCGTGGC CAACGCCGAG CTCGTTGCCT ATCCCATGCT CGAAGACTCG	300
45	ACTGCGATGG TCATCCAGCC TGGTTCGTCC ACGCCCGACT GGGTCGTGCC	350
	GCAGGACTCG GAGGTCTTCG CGGAGAGCTT CGCGACCGCG CTCGCCGCC	400
	TGCATGCCGT CCCCATTTCC GCCGCCGTGG ATGCGGGGAT GCTCATCCGT	450
	ACACCGACGC AGGCCCGTCA GAAGGTGGCC GACGACGTTG ACCGCGTCCG	500
	ACGCGAGTTC GTGGTGAACG ACAAGCGCCT CCACCGGTGG CAGCGCTGGC	550
50	TCGACGACGA TTCGTCGTGG CCAGATTTCT CCGTGGTGGT GCATGGCGAT	600
	CTCTACGTGG GCCATGTGCT CATCGACAAC ACGGAGCGCG TCAGCGGGAT	650
	GATCGACTGG AGCGAGGCCG GCGTTGATGA CCCTGCCATC GACATGGCCG	700
	CGCACCTTAT GGTCTTTGGT GAAGAGGGGC TCGCGAAGCT CCTCCTCACG	750

TATGAAGCGG CCGGTGGCCG GGTGTGGCCG CGGCTCGCCC ACCACATCGC 800
 GGAGCGCCTT GCGTTCGGGG CGGTCACCTA CGCACTCTTC GCCCTCGACT 850
 CGGGTAACGA AGAGTACCTC GCTGCGGCGA AGGCGCAGCT CGCCGCAGCG 900
 GAATGA 906

5

2) INFORMATION FOR SEQ ID NO: 1561

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 20 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1561

GATCATGGTA AAACCTACATT GACTGCTGCT ATCACCAAAG TTTTAGCCGA 50
 25 ACAAGGTGGT GCCAACTTCT TGGATTAYGG TTCTATTGAT AGAGCTCCAG 100
 AAGAAAGAGC TAGAGGTATC ACTATTTCCA CTGCCCACGT TGAATACGAA 150
 ACCAAGAACA GACACTATGC CCACGTTGAT TGTCCAGGAC ACGCTGATTA 200
 TATCAAAAAT ATGATTACTG GTGCCGCTCA AATGGATGGT GCTATCATTG 250
 TTGTTGCTGC CACTGATGGT CAAATGCCTC AAACCAGAGA ACATTTGTTA 300
 30 TTGGCCAGAC AAGTTGGTGT TCAAGACTTG GTTGTGTTTG TCAACAAAGT 350
 CGATACTATT GATGACCCTG AAATGTTGGA ATTAGTCGAA ATGGAAATGA 400
 GAGAATTGTT ATCCACCTAC GGTTTTGATG GTGACAACAC TCCAGTTATT 450
 ATGGGATCTG CTTTAATGGC TTTGGAAGAC AAGAAACCAG AAATTGGTAA 500
 GGAAGCTATC TTGAAATTGT TAGATGCTGT CGATGAACAC ATTCCAACCTC 550
 35 CATCAAGAGA CTTGGAACAA CCATTTTGTG TACCAGTTGA AGACGTGTTC 600
 TCCATCTCCG GTAGAGGAAC TGTTGTCCTG GGTAGAGTTG AAAGAGGTGT 650
 TTTGAAGAAG GGTGAAGAAA TCGAAATTGT TGGTGGTTTT GACAAACCTT 700
 ACAAGACTAC TGTTACCGGT ATTGAAATGT TCAAAAAAGA ATTAGACTCT 750
 GCTATGGCTG GTGACAACTG TGGTGTTTTG TTAAGAGGTG TTAAAAGAGA 800
 40 TGAAATCAAG AGAGGTATGG TTTTGCCCAA ACCAGGTACT GCCACTTCTC 850
 ACAAGAAGTT CTTGGCTTCC TTGTATATTT TGAAGGAGGT AGAAGGTGGY 900
 CGTTCCACTC CATTTGGTGA AGGTTACAAG CCTCAATGCT TCTTCAGAAC 950
 TAACGATGTC ACTACCACAT TTTCATTCCT AGAAGGAGAA GGTGTTGACC 1000
 ATTCTCAAAT GATCATGCCA GGTGACAACA TTGAAATGGT TGGTGAAT 1048

45

2) INFORMATION FOR SEQ ID NO: 1562

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562

```

10 TGATCACGGT AAAACCACAT TAACTGCTGC CATTACCAAA GTATTAGCTG      50
   AACAAGGTGG TGCCAACTTT TTGGATTACG GTTCCATTGA TAGAGCTCCA      100
   GAAGAAAGAG CCAGAGGTAT CACTATTTCC ACTGCCCACG TTGAATACGA      150
   AACCAAGAAC AGACACTATG CCCACGTTGA TTGTCCAGGA CACGCTGATT      200
15 ATATCAAAAA CATGATTACT GGTGCTGCTC AAATGGATGG TGCTATCATT      250
   GTTGTGCTG CTACTGACGG TCAAATGCCA CAAACCAGAG AACATTTATT      300
   GTTGGCAAGA CAAGTTGGTG TTCAAGACTT GGTGTCTTT GTCAACAAAG      350
   TTGATACTAT TGATGACCCT GAGATGTTGG AATTAGTCGA AATGGAAATG      400
   AGAGAATTGT TGTCCACCTA CGGTTTGTGAT GGTGACAACA CTCCTGTTAT      450
20 TATGGGATCT GCTTTAATGG CCTTGGAAGG CAAAAAACCA GAAATTGGTA      500
   AGGAAGCTAT TTTGAGATTG TTAGATGCTG TCGATGAACA CATTCCAAC      550
   CCATCAAGAG ACTTGGAACA ACCATTTTGT TTGCCAGTTG AAGACGTGTT      600
   CTCCATCTCT GGTAGAGGAA CTGTTGTCAC CGGTAGAGTT GAAAGAGGTG      650
   TCTTGAAGAA GGGTGAAGAA ATCGAAATTG TTGGTGGTTT TGACAAACCA      700
25 TACAAGACCA CTGTTACTGG TATTGAAATG TTCAAAAAGG AATTAGATTC      750
   TGCTATAGCT GGTGACAAC      GTGGTGT      GTTGAGAGGT GTTAAAAGAG      800
   ATGAAATCAA GAGAGGTATG GTTTTGGCCA AGCCAGGTAC TGCTACTTCT      850
   CACAAGAAAT TTTTAGCATC TTTGTATATT TTGACTTCAG AAGAAGGTGG      900
   TCGTTCCACT CCATTTGGAG AAGGTTACAA GCCTCAATGT TTCTTCAGAA      950
30 CTAATGACGT CACTACCACA TTTTCATTCC CAGAAGGAGA AGGTGTTGAC      1000
   CACTCCCAAA TGGTCATGCC AGGTGATAAC ATTGAAATGG TTGGTGAATT      1050
   GATCAAATCA TGTCCATTGG AAGT      1074

```

35 2) INFORMATION FOR SEQ ID NO: 1563

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1033 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida famata*

(B) STRAIN: ATCC 62894

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563

```

GATCACGGGA AGACTACTTT GACCGCTGCC ATCACCAAAG TTTTAGCCGA      50
AAAAGGTGGT GCTAACTTCT TGGACTACGG TTCTATCGAT AAAGCTCCAG      100

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	AAGAAAGAGC	CAGAGGTATT	ACTATTTCTG	CTGCCCATGT	TGAATACGAA	150
	ACTGACAAGA	GACACTATGC	CCATGTTGAT	TGTCCAGGTC	ACGCAGATTA	200
	TATCAAGAAT	ATGATTACTG	GTGCTGCTCA	AATGGATGGT	GCCATTATTG	250
	TTGTTGCTGC	TTCCGATGGT	CAAATGCCTC	AAACCAGAGA	ACATTTGTTA	300
5	TTGGCCAGAC	AAGTTGGTGT	TCAACACTTG	GTTGTTTTTCG	TCAACAAGGT	350
	CGACACCATT	GACGATCCAG	AAATGTTGGA	ATTGGTTGAA	ATGGAAATGA	400
	GAGATTTGTT	AAC TACTTAC	GGTTTTGATG	GTGATAACAC	CCCAGTTATC	450
	ATGGGATCTG	CTTTGTGTGC	TTTGGAATCC	AGAGAACCAG	AAATTGGTCA	500
	AAAAGCCATT	GAAAAATTGT	TAGATGCCGT	CGATGAATAC	ATTCCAACCC	550
10	CAGTCAGAGA	CTTGAACAA	CCATTCTTGA	TGCCAGTTGA	AGAAGTTTTTC	600
	TCCATTTCCG	G TAGAGGTAC	CGTTGTTGCT	GGTAGAGTCG	AAAGAGGTAC	650
	CTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTC	GACAAGCCAT	700
	TCAAGGCCAC	TGTTACTGGT	ATTGAAATGT	TCAAGAAGGA	ATTGGACTCC	750
	GCTCTTGCTG	GTGACAAC TG	TGGTATCTTG	TTGAGAGGTG	TCAAGAGAGA	800
15	CGAAGTTAAG	AGAGGTATGG	TCTTGACCAA	GCCAAACACC	GTCACTTCCC	850
	ACAAGAAGAT	CTTGGCCTCG	TTGTATATCT	TGACCAAGGA	AGAAGGTGGT	900
	AGACACTCTC	CATTTGGAGC	CAACTACAAG	CCCCAATTGT	TCATGAGAAC	950
	CACCGATGTT	ACCGGTACCA	TGACCTTCCC	AGAAGGTGCC	GACCAATCTG	1000
	CCATGGTCAT	GCCAGGTGAC	AACGTTGAAA	TGC		1033
20						

2) INFORMATION FOR SEQ ID NO: 1564

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
- (B) STRAIN: ATCC 66032

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564

	GATCACGGTA	AGACTACATT	GACAGCTGCT	ATCACCAAGA	CATTGGCCAA	50
40	GAACGGTGGT	GCTGATTTCT	TGGACTACTC	TTCCATTGAC	AAAGCTCCAG	100
	AGGAGAGAGC	CCGTGGTATC	ACTATCTCTA	CTGCCCATGT	CGAGTACGAG	150
	ACCGCCAAGA	GACATTACTC	CCACGTCGAC	TGTCCAGGTC	ACGCCGACTA	200
	CATCAAGAAC	ATGATTACTG	GTGCTGCCCA	AATGGACGGT	GCTATCATCG	250
	TTGTCGCCGC	CACCGATGGT	CAAATGCCAC	AAACTAGAGA	GCATTTGCTG	300
45	TTGGCCAGAC	AAGTCGGTGT	TCAACGTATC	GTTGTCTTTG	TCAACAAGGT	350
	GGACACCATC	GATGACCCTG	AAATGTTGGA	ATTAGTGGA	ATGGAAATGA	400
	GAGAATTGTT	GAACGAATAC	GGTTTTGACG	GTGACAATGC	CCCTATCATT	450
	ATGGGTTCCG	CTTTGTGTGC	CCTAGAAGGT	CGTCAACCTG	AAATTGGTGA	500
	GCAAGCTATC	ATGAAACTAT	TGGACGCTGT	TGATGAATAC	ATTCCAACCC	550
50	CAGAAAGAGA	CTTGAACAAG	CCATTCTTGA	TGCCTGTTGA	AGACATCTTC	600
	TCCATCTCTG	G TAGAGGTAC	CGTCGTCACT	GGACGTGTCG	AAAGAGGTAA	650
	CTTGAAGAAG	GGTGAAGAAG	TTGAAATTGT	TGGTCACAAC	ACTACCCCAT	700
	TGAAGACCAC	CGTTACTGGT	ATCGAAATGT	TCAGAAAGGA	ATTGGACCAA	750

	GCTATGGCTG	GTGACAACGC	CGGTATCCTA	TTGAGAGGTA	TCAGAAGAGA	800
	CCAATTGAAG	AGAGGTATGG	TCATGGCCAA	GCCAGGTACC	GTCAAGGCTC	850
	ACACCAAGAT	TTTGGCTTCT	TTGTACATCT	TGTCTAAGGA	AGAAGGTGGT	900
	AGACATTCTG	GTTTCGGTGA	AAACTACAGA	CCTCAGATGT	TTATCAGAAC	950
5	CGCAGATGTC	ACTGTTGTGA	TGAAGTTCCC	AGAATCTGTG	GAAGACCACT	1000
	CTATGCAAGT	TATGCCAGGT	GACAACGTCG	AAATGGTCTG	TGAACTAGTC	1050
	CACCCA					1056

10

2) INFORMATION FOR SEQ ID NO: 1565

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565

	GATCATGGTA	AGACCACTTT	GACCGCTGCT	ATCACCAAGG	TTTTGTGCGGA	50
	AAAAGGAGGT	GCTAATTTCT	TGGATTACGG	CTCCATCGAC	AGAGCTCCAG	100
	AAGAGAGAGC	CAGAGGTATC	ACCATTTCCA	CTGCCCATGT	TGAGTACCAA	150
30	ACTGATAAGA	GACATTATGC	CCACGTTGAC	TGTCCAGGTC	ACGCCGATTA	200
	CATTAGAAT	ATGATTACTG	GTGCCGCCCA	GATGGACGGT	GCCATTATTG	250
	TTGTTGCTGC	CACTGACGGT	CAAATGCCTC	AGACCAGAGA	GCACTTGTTG	300
	TTGGCCAGAC	AAGTTGGTGT	GCAACACTTG	GTAGTTTTTG	TGAACAAGGT	350
	GGACACCAT	GACGATCCCG	AGATGTTGGA	ATTGGTCGAG	ATGGAAATGA	400
35	GAGAATTGTT	GAGTCAGTAC	GGTTTCGATG	GTGACAACAC	CCCAGTTATC	450
	ATGGGATCTG	CTTTGTGTGC	TTTGGAAGT	AAGCAGCCAG	AAATTGGTGT	500
	GCAAGCCATT	GAAAAATTGT	TGGACGCTGT	CGATGAGCAC	ATTCCTACTC	550
	CTACCCGTGA	CTTGGAACAG	CCATTCTTGT	TGCCTGTTGA	AGATGTGTTC	600
	TCCATTTCTG	GTAGAGGAAC	TGTGGTTACT	GGTAGAGTCG	AAAGAGGTTC	650
40	GTTGAAGAAG	GGTGAGGAAA	TCGAGATTGT	TGGTGACTTT	GACAAGCCAT	700
	TCAAGACCAC	TGTGACTGGA	ATTGAAATGT	TCAAGAAGGA	ATTGGATGCT	750
	GCTATGGCTG	GTGACAATGC	TGGTATCTTG	TTGAGAGGTG	TCAAGAGAGA	800
	CGATGTCAAG	AGAGGTATGG	TTTTGGCCAA	GCCTTCCACC	GTCACTTCTC	850
	ACAAGAAGGT	GTTGGCTTCC	TTGTACATCT	TGAGTAAGGA	AGAAGGTGGC	900
45	CGTCACTCTC	CTTTTGGTGA	GAACAACAAG	CCTCAATTGT	TCATCAGAAC	950
	TACTGACGTT	ACCGGTACTT	TAAGATTCCC	AGCCGGCGAG	GGTGTGCGAC	1000
	ACTCGCAAAT	GGTTATGCCA	GGTGACAATG	TTGAGATGGA	AATTGAGCTT	1050
	GTGAGAAAGA	C				1061

50

2) INFORMATION FOR SEQ ID NO: 1566

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566

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15  GATCACGGTA AGACTACCTT GACTGCTGCT ATCACCAAGG TTTTGGCTTC      50
    TAAGGGTGGT GCTAGCTTCT TGGACTATGG TTCCATTGAC AGAGCCCCAG      100
    AGGAGAGAGC TAGAGGTATT ACTATTTCTA CTGCCCACGT TGAGTACCAA      150
    ACCGAAAAGA GACACTACGC CCACGTCGAC TGTCCAGGTC ACGCTGATTA      200
    CATTAGAAT  ATGATTACTG GTGCCGCCCA GATGGACGGT GCTATCATTC      250
20  TTGTTGCTGC TTCTGATGGT CAGATGCCTC AGACCAGAGA GCACCTTTTG      300
    TTGGCCAGAC AGGTTGGTGT TCAGAACTTG GTTGTTTTCG TTAACAAGGT      350
    TGACACCATT GACGACCCTG AAATGTTGGA ATTGTTTGAG ATGGAAATGA      400
    GAGAATTGTT GACTACTTAC GGTTTTGACG GTGATGAGAC TCCTGTTATC      450
    ATGGGTCTCG CTTTGTGCGC TTTGGAAGAG AAGCAACCAG AGATTGGTGA      500
25  GCAGGCTATC ATGAAGTTGT TGGACGCTGT CGATGAGTAC ATTCCAACCC      550
    CACAGCGTGA CTTGGAGCAG CCATTCTTGA TGCCTGTTGA GGATGTTTTTC      600
    TCCATTTCTG GTAGAGGTAC TGTCGTTACT GGTAGAGTTG AGAGAGGTTTC      650
    TTTGAAGAAG GGTGAGGAAA TCGAGATTGT CGGTGA CTTC GCCAAGACTT      700
    TCAAGGCTAC CGTTACTGGT ATTGAGATGT TCAAGAAGGA ATTGATGCT      750
30  GCTATGGCTG GTGACAACGC CGGTATCTTG TTGAGAGGTG TCAAGAGAGA      800
    TGAGATCTCC CGTGGTGATG TCTTGCCAA GCCAGGTACT GTTACTCCAC      850
    ACAAGAAGAT CTTGGCTTCT TTGTACGTTT TGACCAAGGA AGAAGGTGGT      900
    CGTCACAACC CATTCGCTGA GAACTACAAG CCACAGTTGT TCCTCAGAAC      950
    CACCAACGTC ACTGGTACCA TGAGATTCCC AGAAGGTGAA GATGTTGACC     1000
35  ACTCTGCCAT GGTTAACCCA GGTGACAACG TTGAGATGGA AATCGAGTTG     1050
    GGTAGAAAGG CCCCACTTGA GTT                                     1073
  
```

40 2) INFORMATION FOR SEQ ID NO: 1567

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567

	CATGGTAAGA	CCACTTTGAC	TGCTGCCATC	ACCAAGACTC	TAGCTGAACG	50
	TGGTGGTGCT	GACTTTTGG	ACTACTCTTC	TATTGACAAG	GCTCCAGAAG	100
5	AAAGAGCYAG	AGGTATCACT	ATTTCTACTG	CTCATGTTGA	ATACGAGACT	150
	GAAAAGAGAC	ATTACTCCCA	CGTTGACTGT	CCAGGTCACG	CTGATTACAT	200
	CAAGAACATG	ATTACTGGTG	CTGCTCAAAT	GGACGGTGCT	ATTATTGTTG	250
	TTGCTGCTAC	TGATGGTCAA	ATGCCTCAAA	CCAGAGAGCA	TTTGTGTTG	300
	GCCAGACAAG	TTGGTGTTCA	ACACATTGTT	GTTTTCGTTA	ACAAGGTTGA	350
10	CACCATCGAT	GATCCAGAAA	TGTTGGAATT	GGTTGAAATG	GAAATGAGAG	400
	AATTRTTGAC	TCAATATGGC	TTTGACGGTG	ACAACACTCC	AGTGATCATG	450
	GGTTCTGCTT	TGTGTGCCTT	GGAAGGTAAG	CAACCAGAAA	TTGGTGAGCA	500
	AGCCATCATG	AAGTTGTTGG	ACGCTGTTGA	CGAATACATC	CCAACCCAG	550
	CCCGTGACTT	GGAAAAVCCA	TTCTTGATGC	CTGTTGAAGA	TATCTTCTCC	600
15	ATTTCCGGTA	GAGGTACTGT	CGTCACTGGT	AGAGTTGAAC	GTGGTAACTT	650
	GAAGAAGGGT	GAAGAAATCG	AAATTGTTGG	TCACAACACC	ACTCCTTTCA	700
	AGACTACTGT	TACTGGTATT	GAAATGTTCA	GAAAGGAATT	GGACCAAGCC	750
	ATGGCTGGTG	ACAACGCTGG	TGTCCTTTTG	AGAGGTGTCA	GAAGAGACCA	800
	ATTGAAGAGA	GGTATGGTTT	TGGCTAAGCC	AGGTACTGTT	AAGGCCCA	850
20	CCAAGTTCTT	GGCTTCCTTG	TACATTTTGA	CCAAGGAAGA	AGGTGGTAGA	900
	CACTCCGGTT	TCGGTGAAAA	CTACAGACCA	CAAATCTACG	TCAGAACTGC	950
	TGACGTTACC	GTDGTCTTGA	AGTTCCCAGA	ATCTGTTGAA	GACCATTCCA	1000
	TGCAAGTCAT	GCCAGGTGAC	AATGTCCGAA	TGGAGTGTGA	ATTGGTTCAC	1050
	CCAACTCCAT	TG				1062

25

2) INFORMATION FOR SEQ ID NO: 1568

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
- (B) STRAIN: ATCC 66035

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568

	CGGAAAGACC	ACCTTGACCG	CCGCCATTAC	CAAGGTTTTG	GCTGACAAGG	50
45	GTGGCGCCAA	CTTCTTGAC	TACGGTGCCA	TTGACAAGGC	TCCTGAAGAA	100
	AGAGCACGTG	GTATCACCAT	TTCCACTGCC	CACGTTGAAT	ACGAGACCGA	150
	CAACAGACAC	TACGCCCACG	TTGACTGTCC	AGGTCACGCC	GATTACATCA	200
	AGAACATGAT	CACGGGTGCC	GCTCAAATGG	ACGGTGCCAT	TATTGTTGTT	250
	GCAGCCACCG	ACGGCCAAAT	GCCTCAAACC	AGAGAGCACT	TGTTGTTGGC	300
50	CAGACAAGTT	GGTGTGCAAC	ACTTGGTTGT	TTTCGTGAAC	AAGGTTGATA	350
	CCATCGACGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGAGAA	400
	TTGTTGACTC	AATACGGATT	TGACGGCGAT	GAAACCCCTG	TTGTTATGGG	450
	CTCTGCTCTT	TGCGCTTTGG	AAGGTAGAGA	ACCAGAGATT	GGTGAGCAAG	500

	CCATCACCAA	GTTGTTGGAG	GCTGTTGACG	AGTACATCCC	AACCCACAA	550
	CGTGACTTGG	AACAACCATT	CTTGATGCCT	GTTGAAGATG	TTTTCTCCAT	600
	TTCTGGTAGA	GGTACTGTTG	TCACTGGTAG	AGTGGAGAGA	GGTTCCTTGA	650
	AGAAGGGTGA	GGAGATCGAG	ATTGTTGGTG	ACTTTGACAA	GCCTTTCAAG	700
5	ACTACTGTTA	CTGGTATTGA	GATGTTCAAG	AAGGAATTGG	ACGCTGCTAT	750
	GGCTGGTGAC	AATGCTGGTA	TCTTGTTGAG	AGGTGTCAAG	AGAGAACAAG	800
	TTTCCCGTGG	TATGGTTTTG	GCCAAGCCAG	GCACTGTGAC	CTCGCACAAAG	850
	AAGGTTTTGG	CTTCTTTGTA	CATTTTGTCT	AAGGAAGAAG	GTGGTCGTCA	900
	CTCTCCATTT	GGCGAGAACT	ACAAGCCTCA	ATTGTTTCCTT	AGAACTACCG	950
10	ATGTCACTGG	TACTTTGAGA	TTCCCAGCAG	GTGAGGACGT	TGACCACTCC	1000
	GCTATGGTTT	CTCCAGGTGA	CAATGTCGAG	ATGGAAATCG	AGTTGGTCAG	1050
	AAAGACTCCT	CT				1062

15

2) INFORMATION FOR SEQ ID NO: 1569

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 990 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida sphaerica</i>
	(B)	STRAIN: ATCC 2504

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569

	TCACCAAGAC	TTTGGCTGAA	CGTGGTGGTG	CTGATTTCTT	GGACTIONCT	50
35	TCCATTGACA	AGGCTCCAGA	AGAAAGAGCR	AGAGGTATCA	CTATTTCTAC	100
	TGCACATGTT	GAATATGAAA	CTGACAAGAG	ACATTACTCT	CACGTCGACT	150
	GTCCAGGTCA	TGCTGATTAC	ATCAAGAATA	TGATTACTGG	TGCTGCCCAA	200
	ATGGATGGTG	CTATCATTTG	TGTTGCTGCT	ACAGATGGTC	AAATGCCTCA	250
	AACCAGAGAA	CATTTGTTGT	TGGCTAGACA	AGTTGGTGTT	CAACAYATCG	300
40	TTGTTTTTCG	TAACAAGGTT	GACACTATCG	ATGACCCTGA	AATGTTAGAA	350
	TTGGTTGAAA	TGAAATGAG	AGAATTATTG	ACCCAATACG	GTTTCGATGG	400
	TGACAACACT	CCAGTCATCA	TGGGTTCTGC	TTTGTGTGCT	TTAGAAGGTA	450
	AGCAACCAGA	AATTGGTGAA	CAAGCAATCA	TGAAGTTATT	GGACGCTGTT	500
	GACGAATACA	TCCCAACTCC	AGCTCGTGAT	TTGGAAAAGC	CTTTCTTGAT	550
45	GCCTGTTGAA	GATATCTTCT	CCATCTCCGG	TAGAGGTACC	GTCGTAAGTG	600
	GTAGAGTTGA	ACGTGGTAAC	TTGAACAAGG	GTRAAGAAAT	CGAAATCGTT	650
	GGTCACAACA	CCACTCCATT	CAAGACCACT	GTTACTGGTA	TTGAAATGTT	700
	CAGAAAGGAA	TTGGACCAAG	CTATGGCTGG	TGATAACGCT	GGTGTCWTGT	750
	TGAGAGGTGT	CAGAAGAGAC	CAATTAAAGA	GAGGTATGGT	CTTGGCCAAG	800
50	CCAGGTACTG	TCAAGGCTCA	CACCRAATTC	TTGGCCTCTT	TGTATATCTT	850
	GACCAAGGAA	GAAGGTGGTA	GACATTCCGG	TTTCGGTGAA	AATTACAGAC	900
	CTCAAATCTA	CGTTAGAAGT	GCTGATGTCA	CCGTTGTTTT	GAAGTTCCCA	950
	GAAGCTGTTG	AAGATCACTC	TATGCAAGTC	ATGCCAGGTG		990

2) INFORMATION FOR SEQ ID NO: 1570

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1184 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 750

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570

	GATCATGGTA	AAACCACTTT	GACTGCTGCC	ATTACTAAAG	TCTTGGCTGA	50
	TAAAGGTCAA	GCTAACTTCT	TAGATTACGG	TTCTATTGAT	AGAGCTCCAG	100
	AAGAAAGAGC	CAGAGGTATC	ACCATCTCTA	CTGCCCACGT	TGAATATGAA	150
20	ACCGAAAAAA	GACATTACGC	CCATGTTGAG	TATGTATACT	TTTTTTTGTT	200
	GTGTAATTGT	TTTAAAGATT	TTCTTTAAAG	CTGAAGAAGT	CAAATCAGTT	250
	CTTTGATAAC	TTCTATTAAA	AAAAGGGAAA	AATTAACAAG	ATATACTAAC	300
	ACTATAACAG	TTGTCCTGGA	CATCAAGATT	ATATCAAGAA	TATGATTACC	350
	GGTGCCGCTC	AAATGGATGG	TGCTATTATT	GTTGTTGCTG	CCACTGATGG	400
25	TCAAATGCCA	CAAACCAGAG	AACATTTGTT	GTTGGCTAGA	CAAGTCGGTG	450
	TTCAAGATTT	GGTTGTCTTT	GTTAACAAAG	TCGACACTAT	TGATGACCCA	500
	GAAATGTTGG	AATTGGTTGA	AATGGAAATG	AGAGAATTAT	TGACTACTTA	550
	CGGTTTTGAT	GGTGATAACA	CTCCTGTTAT	CATGGGTTCT	GCTTTGATGG	600
	CCTTGCAAGG	TAAACAACCA	GAAATTGGTG	AACAAGCTAT	CATGAAATTG	650
30	ATGGACGCTA	TTGATGAACA	CATTCCAACC	CCAACCAGAG	ACTTGGAACA	700
	ATCTTTCTTG	ATGCCAGTTG	AAGATGTTTT	CTCCATTTCT	GGTAGAGGTA	750
	CTGTTGTAC	TGGTAGAGTC	GAAAGAGGTG	TCTTAAAGAA	GGGTGAAGAA	800
	ATTGAAATTG	TTGGTGGTTT	CGAAAAACCA	TTCAAGACCA	CTGTTACTGG	850
	TATTGAAATG	TTCAAGAAAG	AATTAGATGC	TGCTATGGCT	GGTGACAACT	900
35	GTGGTGTCTT	GTTGAGAGGT	GTCAAGAGAG	ACGAAATCAA	GAGAGGTATG	950
	GTTTTGGCTA	AACCAGGTAC	TGCTACTTCC	CACAAGAAAT	TCTTGGCTTC	1000
	CATGTATATC	TTAACTGCTG	AAGAAGGTGG	TCGTTCCACT	CCATTCGGTG	1050
	AAGGTTACAA	GCCACAATGT	TTCTTCAGAA	CTAACGATGT	TACCACTTCC	1100
	TTCTCTTTCC	CAGAAGGTGA	AGGTGTTGAC	CACTCCCAA	TGGTTATGCC	1150
40	AGGTGACAAC	ATTGAAATGG	TCGGTGAATT	GATT		1184

2) INFORMATION FOR SEQ ID NO: 1571

45

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571

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CGATCACGGT AAGACCACCT TGACCGCCGC CATCACCAAG GTCTTGGCCG      50
ACAAGGGTCA GGCTAACTTC TTGGACTACG GATCCATTGA CAGAGCCCCT      100
GAAGAAAGAG CAAGAGGTAT CACTATCTCC ACTGCCACG TTGAATACGA      150
10 GACTGATAAG AGACACTATG CCCACGTTGA TTGCCCCGGC CATCAAGATT      200
ATATCAAGAA TATGATCACT GGTGCTGCCC AAATGGACGG TGCTATCATT      250
GTTGTTGCTG CTACTGACGG TCAGATGCCA CAAACCAGAG AACACTTGTT      300
GTTGGCTAGA CAAGTTGGTG TCCAAGACTT GGTGTTTTTC GTTAACAAGG      350
TTGACACTAT CGATGACCCA GAAATGTTGG AATTGGTTGA AATGGAAATG      400
15 AGAGAATTAT TATCTTCTTA YGGCTTTGAC GGTGACAACA CCCAGTTGT      450
CATGGGTTCG GCTTTGATGG CTTTGCAAGG TAAGCAACCA GAAATTGGTG      500
AACAAGCTAT TATTAAGTTG ATGGACGCTA TTGATGAACA CATYCCAACC      550
CCAACCAGAG ACTTGAACA ACCATTCTTG TTGCCAGTTG AAGATGTCTT      600
TTCTATTTCC GGTAGAGGTA CCGTCGTCAC TGGTAGAGTC GAAAGAGGTG      650
20 TCTTGAAGAA GGGTGAAGAA ATTGAAATTG TCGGTAACCT TGAAAAGCCA      700
TTCAAGACCA CCGTTACTGG TATTGAAATG TTCAAGAAGG AATTGGATGC      750
TGCTATGGCT GGTGACAACT GTGGTGTCTT GTTGAAGAGG GTCAAGAGAG      800
ACGAAATCAG CAGAGGTATG GTTTTGGCCA AGCCAGGTAC CGTCACTTCC      850
CACAAGAAGT TCTTGGCCTC CATGTACATC TTGACTGGTG AAGAAGGTGG      900
25 TCGTCGTACC CCATTCGGTG AAGGTTACAA GCCACAATGT TTCTTCAGAA      950
CCAATGACAT CACCACCACT TTCACTTTCC CAGAAGGTGA AGGTGTCGAC      1000
CACTCCCAA TGGTTATGCC AGGTGACAAC ATCGAAATGG TTGGTGAATT      1050
GTACAAGGCT TGTCTTGA A A                                     1071

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30

2) INFORMATION FOR SEQ ID NO: 1572

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
 (B) STRAIN: ATCC 8750

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572

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TATCTTGGTT WGCTCGGCCG CTGACGGCCC AATGCCTCAG ACTCGCGAGC      50
ACATCCTGCT GAGCCGTCAG GTTGGCGTTC CTTACATCAT CGTGTTCCCTG      100
50 AACAAGGCCG ACATGGTTGA TGACGAAGAG CTGATCGAAC TGGTTGAAAT      150
GGAAGTTCGC GAGCTGTTGT CCAAGTACGA CTTCCTGGC GACGACACCC      200
CGATCATCAA GGGTTCGGCC AAAGTGGCTC TGGAAGGCGA CGAAGGCCCA      250
CTGGGCAGCC AAGCCGTTCT GGCTCTGGCC GAAGCGCTGG ACAACTACAT      300

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	TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	GTTCTTGATG	CCTGTTGAAG	350
	ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
	CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
	CACGGTCAAG	ACCATTTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
	CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
	GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
10	GGTTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
	TCGCCATGGA	AGAAGGT				817

15 2) INFORMATION FOR SEQ ID NO: 1573

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 796 bases
- (B) TYPE: Nucleic acid
- 20 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella buccalis*
- (B) STRAIN: ATCC 35310

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573

30	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTC	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAACCTCTTG	AGCAATACGA	ATTCGAAGAG	GATACTCCAA	200
35	TCGTTTCGTGG	TTCTGCACTG	GGTGCAATTGA	ATGGTGTTGA	CAAGTGGGTT	250
	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAACAG	GACGTATTGA	GACTGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450
40	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCACTTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
45	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GGCGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	GTAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

50 2) INFORMATION FOR SEQ ID NO: 1574

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 820 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574

	GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
	GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
15	TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
	ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
	TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
	GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTC	ATACATTCCA	300
	GAGCCAAAGC	GTGATATCGA	TGATCCATTC	CTATTACCAA	TCGAAGATAT	350
20	CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
	GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
	ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
	AGGTCGTGCA	GGTGATAACG	TTGGTGTCT	ACTACGTGGT	ACCAAGCGTG	550
	ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
25	CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
	TCGTCACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
	CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
	ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
	TATGGCTGAA	GCGGAGAGAT				820

30

2) INFORMATION FOR SEQ ID NO: 1575

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
- (B) STRAIN: ATCC 33315

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575

	GGTAGTGTCT	GCAGCTGACG	GCCCAATGCC	ACAACTCGT	GAACATATCC	50
50	TATTGTCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGACGATGA	AGAATTACTT	GAATTAGTTG	AAATGGAAGT	150
	ACGTGATCTA	TTAACTGAAT	ACGACTTCCC	AGGTGATGAT	ACTCCTGTTA	200
	TTTCTGTTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	ATATGAACAA	250

AAAGTCTTAG ACTTAATGGC AGCTGTAGAT GATTTCATCC CAACTCCTGA 300
 ACGTGACCAT GACAAACCGT TCATGATGCC GATTGAAGAT GTTTTCTCAA 350
 TCACTGGTCG TGGAAGTGT GCTACAGGTC GTGTTGAACG TGGAAGTATT 400
 AAAGTCGGTG ATGAAGTTGA TATCATCGGT ATTCATGAAA ATGTTAAAAA 450
 5 GACAACTGTT ACGGGTGTAG AAATGTTCCG TAAATTGTTG GATTACGCTG 500
 AAGCTGGCGA TAACATCGGT ACATTATTGC GTGGTGTTTC TCGTGATGAT 550
 ATCGAACGTG GTCAAGTGT GGCTAAACCA GGCACAATCA CACCACATAC 600
 AAAATTCTCA GCTGAAGTTT ATGTATTAAC AAAAGAAGAA GGCGGACGTC 650
 ATACTCCATT CTTCTCAAAC TATCGCCAC AATTTTACTT CCGTACAACT 700
 10 GACATCACTG GTGTCATTGA ATTGCCAGAA GGTACTGAAA TGGTTATGCC 750
 AGGTGATAAC GTAGCAATGG AAGTTGAATT AATTCACCCT GTTGCTATTG 800
 AAA 803

15

2) INFORMATION FOR SEQ ID NO: 1576

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33292

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576

TTAATGAAGC AATTGTTGTA AATTTTGAAA GCGAAGGAAA AAAACATAAA 50
 CTGTGTTTAG AAGTAGCAGC TCATTTAGGA GATAATAGAG TTAGAAGTAT 100
 TGCTATGGAT ATGACAGATG GTTTGGTAAG GGGCTTAAAA GCTGAGGCTT 150
 35 TAGGTGCTCC TATTAGTGTT CCTGTTGGTG AGAAAGTTTT AGGAAGAATT 200
 TTCAATGTTA CTGGAGATTT GATCGATGAA GGTGAAGAAA TTTCTTTTGA 250
 TAAAAAATGG GCAATTCATA GAGATCCGCC AGCTTTTGAA GATCAAAGCA 300
 CAAAAGTGA GATTTTGTAA ACAGGGATTA AAGTTGTAGA TTTGCTTGCT 350
 CCTTATGCAA AAGGTGGTAA AGTAGGCTTT TTTGGTGGTG CAGGTGTTGG 400
 40 TAAACTGTT ATTATTATGG AGCTTATTCA CAATGTTGCA TTTAAGCATA 450
 GCGGCTATTC TGTATTTGCA GGTGTGGGTG AGAGAACTCG TGAAGGAAAT 500
 GACCTTTATA ATGAAATGAA AGAAAGTAAT GTTTTAGACA AAGTTGCTCT 550
 ATGTTATGGA CAAATGAATG AACCACCAGG AGCAAGAAAT CGTATTGCTT 600
 TAACAGGTTT AACAATGGCT GAGTATTTTA GAGATGAAAT GGGTCTTGAT 650
 45 GTGCTTATGT TTATTGATAA TATCTTTAGA TTTTCACAAT CAGGTTCTGA 700
 AATGTCAGCA CTTTATAGGAA GAATTCCATC AGCTGTGGGT TATCAACCAA 750
 CCCTAGCAAG TGAAATGGGT AAATTCCAAG AAAGAATTAC TTCAACTAAA 800
 AAAGG 805

50

2) INFORMATION FOR SEQ ID NO: 1577

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*
 (B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577

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15  ATTTACCCAA GATCAACGAA GCCGTCGAAG TAAATTTCTGA GGTGAGGGC      50
    AAGCAAAACA GACTTGTGTT AGAGGTTGCC GCACACCTTG GCGATAACCG      100
    CGTAAGAACG ATCGCTATGG ATATGAGCGA AGGCTTAACC AGAGGCCTTG      150
    AGGCTACGGC TCTTGGCGCG CCTATTAGCG TTCCGGTCGG CGAAAAGTT      200
    TTGGGAAGGA TTTTAAACGT CGTCGGCGAT CTGATCGACG AGGGTGAAGG      250
20  CATAGAATTT GATAAAAAAT GGTCTATCCA CCGCGATCCT CCGCCGTTTG      300
    AAGAGCAAAG CACGAAGAGT GAAATTTTTG AAACGGGTAT AAAAGTGGTC      350
    GATCTTCTAG CCCCTTATGC AAAAGGCGGT AAGGTCGGAT TATTCGGCGG      400
    TGCCGGCGTC GGTAAGACGG TTATTATCAT GGAGCTTATC CACAACGTTG      450
    CATTTAAGCA TAGCGGTTAT TCCGTGTTTG CCGGCGTGGG CGAGCGAACC      500
25  CGCGAAGGAA ACGACCTTTA TCACGAGATG AAAGAGAGTA ACGTTTTGGA      550
    CAAAGTCGCC TTGTGCTACG GCCAGATGAA CGAGCCGCCG GGAGCAAGAA      600
    ACCGCATCGC TCTAACAGGC CTAACGATGG CTGAATACTT CCGCGACGAG      650
    ATGGGACTTG ACGTTTTGAT GTTTATAGAC AACATCTTCC GTTTCTCTCA      700
    GTCTGGCGCT GAGATGTCGG CGCTTCTTGG ACGTATCCCG TCAGCCGTTG      750
30  GTTATCAGCC GACTTTGGCG AGCGAAATGG GCAAATTCCA AGAGAGAATT      800
    ACATCAACC                                     809
  
```

35 2) INFORMATION FOR SEQ ID NO: 1578

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578

```

50  AATCGAAGTG CAACGTTTCAT TGCGTGACT TGATGGTGCT GTAAGTGTGT      50
    TGGACTCACA ATCAGGTGTA GAACCTCAA CAGAAACAGT TTGGCGTCAA      100
    GCGACAGATT ACCGCGTACC GCGTGTTGTA TTCTGTAACA AAATGGACAA      150
  
```

	AATTGGTGCA	GACTTCTTAT	ACTCTGTATC	AACTTTACAT	GATCGTTTAC	200
	AAGCAAATGC	TCACCCAATC	CAATTACCAA	TTGGTGCGGA	AGATGACTTT	250
	ACTGGTATTA	TCGACTTAGT	AAAAATGAAA	GCTGAAATCT	ACACAAATGA	300
	CTTAGGAACT	GAAATCCAAG	AGACTGAAAT	TCCTGAAGAA	TACGTAGAAT	350
5	TAGCTGAAGA	ATGGCGCGAA	AAATTAATTG	AAGCTGTTGC	TGATACTGAT	400
	GAAGAACTAA	TGATGAAATT	CTTGGAAGGT	GAAGAAATCA	CTGAAGAAGA	450
	ATTGAAAGCT	GGTATTCGTC	AAGCAACATT	GACTGTTGAC	TTTTTCCCTG	500
	TTCTTTGCGG	ATCTGCCTTT	AAAAACAAAG	GGGTTCAATT	GATGTTGGAT	550
	GCAGTCATCG	ACTACTTGCC	TTCACCACTT	GATGTTCCCTG	CGATTAAAGG	600
10	GATCAATCCT	AAAACAGACG	AAGAACTGA	TCGTCCGGCT	GACGATGAAG	650
	CACCATTTGC	TTCATTAGCA	TTTAAAGTAA	TGACTGACCC	ATTCTGTARGT	700
	CGTTTGACAT	TCTTYCGTGT	GTATTCARGT	ATCTTGAAC	CTGGATCATA	750
	CGTATTGAAT	GCTTCAAAAG	GCAAACGCGA	ACGTATCGGT	CGGATCCTAC	800
	AAATGCACGC	CAACACTCGT	GCTGAAATCC	AAACAGTATA	CTCAGGCGAT	850
15	ATCGCCGCTG	CTGTTGGTTT	GAAAGACACA	ACAACCTGGGG	ATCCACTATG	900
	TGATGAAAAA	TCCCCAGTAA	TCCTTGAATC	AATCGAATTC	CCAGAACCAG	950
	TTATCGAAGT	CGCTGTTGAG	CTTAAATCAA	AAGCTGACCA	AGATAAAATG	1000
	GGGGTTGCTT	TACAAAAACT	TGCTGAAGAA	GATCCATCAT	TCCGTGTGGA	1050
	AMCAAACGCT	GAAACAGGCG	AAACTGTTAT	CGCTGGTATG	GGAGAACTTC	1100
20	ACTTGGACGT	CTTAGTTGAC	CGTATGCGTC	GCGAATTTAA	AGTTGAAGCA	1150
	AACGTAGGTG	CGCCTCAAGT	TTCTTATCGT	GAAACATTCC	GTGCAGCAAC	1200
	ACAAGCGGAA	GGTAAATTTG	TACGTCAGTC	TGGTGGTAAA	GGTCAATACG	1250
	GTCACGTATG	GGTCGAATTT	ACACCAAACG	AAGAAGGTAA	AGGCTTCGAA	1300
	TTCGAAAACG	CGATTGTCGG	TGGTGTGGTT	CCTCGTGAAT	ACATCCCAGC	1350
25	AGTTGAAAAA	GGACTTGAAG	AATCAATGGC	GAACGGTGTC	TTAGCCGGTT	1400
	ACCCATTAGT	AGACATCAAA	GCAAAACTTT	ATGATGGTTC	ATACCATGAT	1450
	GTCGATTCAA	GTGAAACTGC	CTTCCGTGTT	GCAGCTTCTA	TGGCTTTACG	1500
	TGCTGCAGCG	AAGAAAGCAA	ACCCAGTAAT	TCTTGAACCA	ATGATGAAAG	1550
	TAGTTATCAC	TGTACCAGAA	GATTACTTAG	GTGATGTTAT	GGGTCACGTA	1600
30	ACTGCTCGTC	GTGGACGCGT	AGAAGGAATG	GAAGCACWCG	GTAACTCACA	1650
	AATCGTGAAC	GCAATCGTGC	C			1671

35 2) INFORMATION FOR SEQ ID NO: 1579

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1662 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579

50	GAAGTACAAC	GTTCACTACG	GGTTCTTGAC	GGWGCTGTAA	CAGTATTGGA	50
	CTCACAATCT	GGTGTAAGAC	CACAACTGA	AACAGTTTGG	CGTCAAGCGA	100
	CAGATTACCG	CGTACCACGT	ATCGTATTCT	GTAACAAAAT	GGATAAAATC	150

	GGTGCAGACT	TCTTATACTC	TGTATCTACT	TTACATGATC	GCTTGCAAGC	200
	AAATGCTCAT	CCAATCCAAT	TACCAATTGG	TGCGGAAGAT	GACTTTACTG	250
	GTATCATCGA	TCTAGTAAAA	ATGAAAGCTG	AGATCTATAC	AAACGATTTA	300
	GGAACAGAGA	TTCAAGAAAC	TGAAATTCTT	GAAGAGTACA	AAGAATTAGC	350
5	TGAAGAATGG	CGCGAAAAAT	TAGTTGAAGC	TGTTGCAGAT	ACTGACGAAG	400
	AGCTAATGAT	GAAATTCTTG	GAAGGTGAAG	AAATCACTGA	AGAAGAATTG	450
	AAAGCTGGTA	TCCGTCAAGC	GACATTGACT	GTTGAATTTT	TCCCAGTTCT	500
	TTGTGGTTCA	GCCTTCAAAA	ACAAAGGGGT	TCAATTGATG	TTGGATGCAG	550
	TCATCGACTA	CCTTCCTTCA	CCACTTGATG	TTCCTGCAAT	CAAAGGGATC	600
10	AATCCTAAAA	CTGACGAAGA	AACTGATCGT	CCTGCTGACG	ATGAAGCGCC	650
	TTTTGCTTCA	CTAGCATTTA	AAGTAATGAC	TGACCCATTC	GTAGGTCGTT	700
	TGACATTCTT	CCGTGTGTAT	TCAGGTGTCT	TGAACTCTGG	ATCATATGTC	750
	TTGAATGCTT	CAAAAGACAA	ACGCGAACGT	ATCGGTCGTA	TTCTGCAAAT	800
	GCACGCGAAC	ACTTGTGCAG	AAATCCAAAC	AGTTTATTCA	GGCGATATCG	850
15	CTGCAGCTGT	TGGTTTGAAA	GATTCCACAA	CAGGGGATAC	ATTGTGTGCG	900
	AAAAATCACC	CAGTAATCCT	TGAATCAATC	GAATTCCCAG	AMCCAGTTAT	950
	CGAAGTAGCT	GTTGAACYTA	AATCAAAAGC	TGACCAAGAT	AAAATGGGTG	1000
	TGGCTTTACA	AAAACCTGCT	GAAGAAGATC	CTTCATTCCG	TGTAGAAMCA	1050
	AACGCTGAAA	CTGGCGAAAC	TGTTATCGCA	GGGATGGGTG	AACTTCACTT	1100
20	GGACGTCCTT	GTTGACCGTA	TGCGTCGCGA	ATTTAAAGTT	GAAGCAAACG	1150
	TTGGTGCGCC	TCAAGTTTCT	TACCGCGAAA	CATTCCGTGC	TTCTACGCAA	1200
	GCCGAAGGTA	AATTTGTACG	TCAGTCTGGT	GGTAAAGGTC	AATACGGTCA	1250
	CGTATGGATC	GAATTTACAC	CAAACGAAGA	AGGTAAAGGC	TTCGAATTCG	1300
	AAAACGCAAT	TGTCGGTGGT	GTGGTTCCAC	GTGAATACAT	CCCAGCAGTT	1350
25	GAAAAAGGAC	TTGAAGACTC	AATGGCTAAC	GGTGTCTAG	CTGGTTATCC	1400
	ATTGGTTGAC	ATCAAAGCCA	AGCTTTACGA	TGGTTCATAC	CATGATGTGC	1450
	ATTCAAGTGA	AACAGCCTTC	CGTGTGGCAG	CTTCAATGGC	TTTACGTGCT	1500
	GCAGCGAAGA	AAGCTAATCC	AGTGATTCTT	GAACCAATGA	TGAAAGTTGT	1550
	TATCACTGTT	CCTGAAGATT	ACTTAGGTGA	TATTATGGGA	CACGTAAGTG	1600
30	CTCGTCGTGG	ACGTGTTGAA	GGTATGGAAG	CGCATGGTAA	CTCACAAATC	1650
	GTTAACGCGA	TT				1662

35 2) INFORMATION FOR SEQ ID NO: 1580

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1669 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580

50	CAATCGAAGT	ACAACGTTCT	CTTCGTGTAT	TGGATGGTGC	TGTTACCGTT	50
	CTTGACTCAC	AATCAGGTGT	TGAGCCTCAA	ACTGAAACAG	TTTGGCGTCA	100
	AGCAACTGAG	TATGGAGTTC	CACCTATCGT	ATTTGCCAAC	AAAATGGACA	150

	AAATCGGTGC	TGACTTCCTT	TACTCTGTAA	GCACACTTCA	CGATCGTCTT	200
	CAAGCAAATG	CACACCCAAT	CCAATTGCCA	ATCGGTTCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGACA	TCCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGATC	GAAGCAGTTG	CTGAAACTGA	400
	CGAAGAATTG	ATGATGAAAT	ACCTCGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGGTATCCGT	AAAGCGACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GCTCTGCCTT	CAAGAACAAA	GGTGTTCAAT	TGATGCTTGA	550
	TGCGGTTATT	GACTACCTTC	CAAGCCCACT	TGACATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGATGAA	650
	GAGCCATTTG	CAGCTCTTGC	CTTCAAGATC	ATGACAGACC	CATTCGTAAG	700
	TCGTTTGACA	TTCTTCCGTG	TTTACTCARG	TGKTCTTCAA	TCAGGTTTCA	750
	ACGTATTGAA	CACCTCTAAA	GGKAAACGTG	AGCGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CCAACAGCCG	TCAAGAAATT	GACACTGGTT	ACTCAAGAGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TCCAACGGT	GACTCATTGC	900
	CAGATGAAAA	AGCTAAAATC	ATTCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGCCAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCTGGTAT	GGGTGAGCTT	1100
20	CACCTTGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTTGAAGC	1150
	AAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTCGA	1300
	ATTGCAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	ACTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	TGCGGCTTCA	CTTGCTCTTA	1500
	AAGAAGCTGC	TAAATCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACAATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTC	TGCTTACGT				1669

35 2) INFORMATION FOR SEQ ID NO: 1581

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581

AATTGGGGAC TACACCTATT ATGATG

26

50

2) INFORMATION FOR SEQ ID NO: 1582

(i) SEQUENCE CHARACTERISTICS:

820

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582

10 GGCAAATCAG TCAGTTCAGG AGT

23

2) INFORMATION FOR SEQ ID NO: 1583

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583

25

CGATTGGCAA CAATACACTC CTG

23

30 2) INFORMATION FOR SEQ ID NO: 1584

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584

TCACCTATTT TTACGCCTGG TAGGAC

26

45

2) INFORMATION FOR SEQ ID NO: 1585

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Enterococcus faecium*
(C) ACCESSION NUMBER: AF139725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585

```
10 ATGACTATAC CTGACGCAAA TGCAATCTAT CCTAACTCAG CCATCAAAGA      50
   GGTGTGCTTT ATCAAGAACG TGATCAAAAG TCCCAATATT GAAATTGGGG      100
   ACTACACCTA TTATGATGAC CCAGTAAATC CCACCGATTT TGAGAAACAC      150
   GTTACCCATC ACTATGAATT TCTAGGCGAC AAATTAATCA TCGGTAAATT      200
   TTGTTCTATC GCCAGTGGCA TTGAATTTAT CATGAACGGT GCCAACCACG      250
   TAATGAAAGG TATTTCGACT TATCCATTTA ATATTTTAGG TGGCGATTGG      300
15 CAACAATACA CTCCTGAAC TACTGATTG CCGTTGAAAG GTGATACTGT      350
   AGTCGGAAAT GACGTGTGGT TTGGGCAAAA TGTGACCGTC CTACCAGGCG      400
   TAAAAATAGG TGACGGTGCC ATTATCGGAG CAAATAGTGT TGTAACAAAA      450
   GACGTCGCTC CATATACAAT TGTCGGTGGC AATCCAATTC AACTCATCGG      500
   ACCAAGATTT GAACCGGAAG TTATTCAAGC ATTAGAAAAT CTGGCATGGT      550
20 GGAATAAAGA TATTGAATGG ATAACGCTA ATGTTTCCTAA ACTAATGCAA      600
   ACAACACCCA CACTTGAATT GATAAACAGT TTAATGGAAA AATAA          645
```

25 2) INFORMATION FOR SEQ ID NO: 1586

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586

ATTCCCACAA TCTTTTTTAT CAATAA 26

40

2) INFORMATION FOR SEQ ID NO: 1587

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587

CATTGTTTCTG ATTCGGTAAA GTTC 24

2) INFORMATION FOR SEQ ID NO: 1588

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588

GTTTTTGAAG TTAAATAGTG TTCTT

2) INFORMATION FOR SEQ ID NO: 1589

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589

CTTCCATTTG TACTTCCCT A

2) INFORMATION FOR SEQ ID NO: 1590

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1920 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Cloning vector pFW16
(C) ACCESSION NUMBER: U50983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1590

ATGAAAATTA	TTAATATTGG	AGTTTTAGCT	CATGTTGATG	CAGGAAAAAC	50
TACCTTAACA	GAAAGCTTAT	TATATAACAG	TGGAGCGATT	ACAGAATTAG	100
GAAGCGTGGA	CAAAGGTACA	ACGAGGACGG	ATAATACGCT	TTAGAACGT	150
CAGAGAGGAA	TTACAATTCA	GACAGGAATA	ACCTCTTTTC	AGTGGGAAAA	200
TACGAAGGTG	AACATCATAG	ACACGCCAGG	ACATATGGAT	TTCTTAGCAG	250

	AAGTATATCG	TTCATTATCA	GTTTTAGATG	GGGCAATTCT	ACTGATTTCT	300
	GCAAAAGATG	GCGTACAAGC	ACAAACTCGT	ATATTATTTT	ATGCACTTAG	350
	GAAAATGGGG	ATTCCCACAA	TCTTTTTTAT	CAATAAGATT	GACCAAAATG	400
	GAATTGATTT	ATCAACGGTT	TATCAGGATA	TTAAAGAGAA	ACTTTCTGCC	450
5	GAAATTGTAA	TCAAACAGAA	GGTAGAACTG	TATCCTAATG	TGTGTGTGAC	500
	GAACTTTACC	GAATCTGAAC	AATGGGATAC	GGTAATAGAG	GGAAACGATG	550
	ACCTTTTAGA	GAAATATATG	TCCGGTAAAT	CATTAGAAGC	ATTGGAACCTC	600
	GAACAAGAGG	AAAGCATAAG	ATTTTCAGAAT	TGTTCTCTGT	TCCCTCTTTA	650
	TCATGGAAGT	GCAAAAAGTA	ATATAGGGAT	TGATAACCTT	ATAGAAGTTA	700
10	TTACTAATAA	ATTTTATTCA	TCAACACATC	GAGGTCCGTC	TGAACTTTGC	750
	GGAAATGTTT	TCAAAATTGA	ATATACAAAA	AAAAGACAAC	GTCTTGCATA	800
	TATACGCCCT	TATAGTGGAG	TACTACATTT	ACGAGATTCG	GTTAGAGTAT	850
	CAGAAAAGGA	AAAAATAAAA	GTTACAGAAA	TGTATACTTC	AATAAATGGT	900
	GAATTATGTA	AGATTGATAG	AGCTTATTCT	GGAGAAATTG	TTATTTTGCA	950
15	AAATGAGTTT	TTGAAGTTAA	ATAGTGTTCT	TGGAGATACA	AACTATTGC	1000
	CACAGAGAAA	AAAGATTGAA	AATCCGCACC	CTCTACTACA	AACAACGTGT	1050
	GAACCGAGTA	AACCTGAACA	GAGAGAAATG	TTGCTTGATG	CCCTTTTGGA	1100
	AATCTCAGAT	AGTGATCCGC	TTCTACGATA	TTACGTGGAT	TCTACGACAC	1150
	ATGAAATTAT	ACTTCTTTT	TTAGGGAAAG	TACAAATGGA	AGTGATTAGT	1200
20	GCACTGTTGC	AAGAAAAGTA	TCATGTGGAG	ATAGAAATAA	CAGAGCCTAC	1250
	AGTCATTTAT	ATGGAGAGAC	CGTTAAAAAA	TGCAGAATAT	ACCATTACAC	1300
	TCGAAGTGCC	GCCAAATCCT	TTCTGGGCTT	CCATTGGTCT	ATCTGTATCA	1350
	CCGCTTCCGT	TGGGAAGTGG	AATGCAGTAT	GAGAGCTCGG	TTTCTCTTGG	1400
	ATACTTAAAT	CAATCATTTT	AAAATGCAGT	TATGGAAGGG	ATACGCTATG	1450
25	GTTGTGAACA	AGGATTGTAT	GGTTGGAATG	TGACGGACTG	TAAAATCTGT	1500
	TTTAAGTATG	GCTTATACTA	TAGCCCTGTT	AGTACCCAG	CAGATTTTCG	1550
	GATGCTTGCT	CCTATTGTAT	TGGAACAAGT	CTTAAAAAAA	GCTGGAACAG	1600
	AATTGTTAGA	GCCATATCTT	AGTTTTAAAA	TTTATGCGCC	ACAGGAATAT	1650
	CTTTCACGAG	CATACAACGA	TGCTCCTAAA	TATTGTGCGA	ACATCGTAGA	1700
30	CACTCAATTG	AAAAATAATG	AGGTCATTCT	TAGTGGAGAA	ATCCCTGCTC	1750
	GGTGTATTCA	AGAATATCGT	AGTGATTTAA	CTTCTTTTAC	AAATGGACGT	1800
	AGTGTTTGTT	TAACAGAGTT	AAAAGGGTAC	CATGTTACTA	CCGGTGAACC	1850
	TGTTTGCCAG	CCCCGTCGTC	CAAATAGTCG	GATAGATAAA	GTACGATATA	1900
	TGTTCAATAA	AATAACTTAG				1920
35						

2) INFORMATION FOR SEQ ID NO: 1591

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- 45 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591

50 ATGAGGTAAT AGAACGGATT

20

2) INFORMATION FOR SEQ ID NO: 1592

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592

CAGTATTTCA GTAAGCGTAA A

21

15

2) INFORMATION FOR SEQ ID NO: 1593

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593

CCGAGCGATT TACCGGATAC TTGGCTGCIC GCTCGG

36

30

2) INFORMATION FOR SEQ ID NO: 1594

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 1032 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: N97-330
45 (C) ACCESSION NUMBER: AF175293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594

ATGTTTAGAA TTAAAGTTGC AGTTCTGTTT GGGGGCTGTT CAGAGGAACA 50
50 TAATGTTTCG ATAAAATCTG CGATGGAGAT TGCCGCAAAC ATAGATACAA 100
AAAAGTATCA GCCTTATTAT ATTGGAATCA CAAAATCCGG CGTTTGGAAG 150
ATGTGTGAAA AACCTTGTTT GGAGTGGGAA CAATATGCGG GGGATCCGGT 200
TGTTTTTTCA CCGGACAGAA GTACGCATGG TCTGCTGATA CAAAAGACA 250

CTGGGTATGA AATCCAGCCT GTGGATGTGG GATTACCGAT GATTCATGGC 300
 AAGTTTGGCG AGGATGGCTC CATACAAGGC TTGCTTGAAT TGTCAGGCAT 350
 TCCGTATGTG GGATGCGATA TTCAAAGCTC CGTGACCTGC ATGGATAAGG 400
 CGCTTGCATA TACCGTTGTG AAAAATGCGG GTATCGCTGT GCCTGGGTTC 450
 5 CGGATCCTTC AGGAGGGGGA TCGCCTGGAA ACAGAGGATT TCGTATATCC 500
 CGTTTTTGTA AAGCCTGCCC GTTCCGGCTC ATCCTTTGGC GTAAACAAGG 550
 TATGCAAGGC AGAAGAAGT CAGGCAGCAA TCGAAGATGC AAGAAAATAT 600
 GACAGCAAGA TTTTGATTGA AGAGGCCGTT ACCGGGAGTG AGGTAGGCTG 650
 CGCCATACTG GGAAACGGAA ATGATCTCAT GGCTGGCGAG GTGGATCAGA 700
 10 TTGAGCTGAG ACACGGCTTT TTTAAGATTC ATCAGGAAGC ACAGCCGGAG 750
 AAAGGATCTG AAAATGCAGT CATCCGAGTT CCAGCCGCCT TACCGGATGA 800
 GGTAATAGAA CGGATTCAGA AAACAGCAAT GAAGATTTAC CGGATACTTG 850
 GCTGCAGAGG ATTGGCCCGC ATTGACCTGT TTTTGCGGGA GGACGGCTGC 900
 ATTGTGTTGA ATGAAGTGAA TACCATGCCG GGTTTACTT CCTACAGCCG 950
 15 TTATCCCCGC ATGATGACAG CAGCCGTTT TACGCTTACT GAAATACTGG 1000
 ATCGCTTGAT TGAACCTTCA CTTAGGAGGT AA 1032

20 2) INFORMATION FOR SEQ ID NO: 1595

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595

AAATAATGCT CCATCAATTT GCTGA

25

35

2) INFORMATION FOR SEQ ID NO: 1596

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596

ATAGTCGAAA AAGCCATCCA CAAG

24

50

2) INFORMATION FOR SEQ ID NO: 1597

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597
10 GATGAATTTC CGAAAATACA TGGA 24

15 2) INFORMATION FOR SEQ ID NO: 1598

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598
CAGCCAATTT CTACCCCTTT CAC 23

30 2) INFORMATION FOR SEQ ID NO: 1599

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 604 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 40 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: BM4405
(C) ACCESSION NUMBER: AF136925

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599

CAGGGAGTAT TTGAGTTATT AGATATTCCA TATGTAGGTT GTGGTATCGG 50
AGCTGCAGCA ATTTCCATGA ATAAAATAAT GCTCCATCAA TTTGCTGAAA 100
50 TAGTTGGTGT AAAAAGCACT CCTAGTATGA TTATAGAAAA GGGACAAGAC 150
CTACAAAAAG TCGATGAATT TGCGAAAATA CATGGATTTC CTTTATATAT 200
CAAACCGAAT GAGGCAGGCT CATCAAAAGG AATTAGCAAG GTAGAACAAA 250
AAAGTGATTT ATATAAAGCA ATAGACGAAG CTTCAAAATA TGATAGCCGT 300

ATTTTAATTC AAAAGGAAGT GAAAGGGGTA GAAATTGGCT GTGGGATTTT 350
 AGGGAATGAA CAATTGGTCG TTGGAGAATG TGATCAAATT AGTCTTGTGG 400
 ATGGCTTTT CGACTATGAA GAGAAATACA ATTTAGTAAC AGCAGAAATT 450
 TTGTTACCAG CTAAACTATC AATAGACAAA AAAGAAGACA TCCAGATAAA 500
 5 AGCAAAAAA CTATACAGAC TATTAGGGTG CAAAGGATTA GCGAGAATCG 550
 ACTTTTTCTT AACGGATGAC GGAGAAATTT TATTAAATGA GATCAACACC 600
 CTCC 604

10

2) INFORMATION FOR SEQ ID NO: 1600

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
 (B) STRAIN: ATCC 49349

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600

ACCTCAAATT AATGAAGCAA TTGTTGTAAA TTTTGAAAGC GAAGGAAAAA 50
 AACATAAACT TGTTTTAGAA GTAGCAGCTC ATTTAGGAGA TAATAGAGTT 100
 AGAACTATTG CTATGGATAT GACAGATGGT TTGGTAAGGG GCTTAAAAGC 150
 30 TGAGGCTTTA GGTGCTCCTA TTAGTGTTCC TGTGTTGAG AAAGTTTTAG 200
 GAAGAATTTT CAATGTTACT GGAGATTGTA TCGATGAAGG TGAAGAAATT 250
 CCTTTTGATA AAAAATGGGC AATTCATAGA GATCCGCCAG CTTTGAAGA 300
 TCAAAGCACA AAAAGTGAGA TTTTGAAC AGGGATTAAA GTTGTAGATT 350
 TACTTGCTCC TTATGCAAAA GGTGGTAAAG TAGGTCTTTT TGGTGGTGCA 400
 35 GGTGTTGGTA AAAGTGTAT TATTATGGAG CTTATTCACA ATGTTGCATT 450
 TAAGCATAGC GGCTATTCTG TATTTGCAGG TGTGGGTGAG AGAACTCGTG 500
 AAGGAAATGA CCTTTATAAT GAAATGAAAG AAAGTAATGT TTTAGACAAA 550
 GTTGCTCTAT GTTATGGACA AATGAATGAA CCACCAGGAG CAAGAAATCG 600
 TATTGCTTTA ACAGGTTTAA CAATGGCTGA GTATTTTAGA GATGAAATGG 650
 40 GTCTTGATGT GCTTATGTTT ATTGATAATA TCTTTAGATT TTCACAATCA 700
 GGTTCTGAAA TGTCAGCACT TTTAGGAAGA ATTCCATCAG CTGTGGGTTA 750
 TCAACCAACC CTAGCAAGTG AAATGGGTAA ATTCCAAGAA AGAATTACTT 800
 CAACT 805

45

2) INFORMATION FOR SEQ ID NO: 1601

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus sulfureus*
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601

```

10 CTCCTTACCA GATATCAACA ATGCGCTGGT TGTATATAAA AATGATGCCA      50
   ATAAACAAA AGTTGTTTTA GAAGCAGCGT TAGAATTAGG TGACGGAATC      100
   ATTCGTGCGA TTGCAATGGA ATCGACTGAT GGATTGCAAC GTGGGATGGA      150
   AGTTGTGCGAT ATGGGAGAAT CTATTTCTGT ACCAGTTGGA ACAGAACTT      200
   TAGGACGTGT GTTTAATGTA TTAGGAGATA CGATTGACTT AGAAGCTCCT      250
15 TTTCTTAAAG ATGCACCGCG TAGTGGAATC CATAAAAAG CCCCTAATTT      300
   TGATGAATTA AGTACAAGCA CAGAAATTCT AGAAACAGGG ATCAAAGTCA      350
   TCGATCTATT AGCCCCTTAT TTAAGAGGTG GTAAAGTTGG ATTGTTTGGG      400
   GGAGCCGGTG TAGGAAAAC GGTATTGATT CAAGAGTTGA TTCACAATAT      450
   CGCACAAGAA CACGGTGGGA TTTCGGTCTT TACTGGTGTT GGTGAGCGTA      500
20 CACGTGAAGG AAACGATTTG TATTATGAAA TGAAAGATTC AGGAGTCATT      550
   GAAAAACAG CGATGGTGTT TGGACAAATG AATGAGCCAC CTGGTGCACG      600
   GATGCGTGTA GCCTTGACTG GATTAACGAT TGCTGAATAT TTCCGTGATG      650
   TTGAAGGACA GGATGTACTG TTGTTTATCG ACAATATCTT CCGTTTTACA      700
   CAAGCTGGTT CTGAAGTGTC TGCCTTGTTA GGTCGTATGC CATCAGCTGT      750
25 GGGATATCAA CCAACATTAG CTACCGAAAT GGGGCAATTG CAAGAGCGGA      800
   TCACGTCAAC GAAAAAGGA TCGATC      826

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30 2) INFORMATION FOR SEQ ID NO: 1602

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus solitarius*
(B) STRAIN: ATCC 49428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602

```

45 TGATACTTTA CCAGATATTA ATAATGCATT AGTAGTATAT AAAAAGGACG      50
   AGGACAAGAC ACGCGTTGTC TTAGAAGCCA CCTTGGAAC TGGAGATGGC      100
   ATGATTCGTG CAATCTCTAT GGGATCGACT GATGGCTTGC AACGGGGAAT      150
   GGAAGTTGTG GACACACAAG CACCTATTTT TGTTCCAGTA GGAAATGAAA      200
50 CCTTAGGACG TGTTTTTAAT GTCTTAGGAG AAACGATTGA TAAACAGGCA      250
   CCGTTTCCTG AAGATGCCAA AAAAAGTGGT ATTCAATAAA AAGCACCCGC      300
   TTTTGATGAA TTAAGTACCA GTTCTGAAAT ATTGGAAACC GGGATTAAAG      350
   TAATCGATTT GCTAGCTCCT TATTTACGAG GTGGTAAAGT TGGATTATTT      400

```

GCGGGTGCTG GCGTGGGTAA AACGGTATTA ATTCAAGAAT TAATTCATAA 450
 CGTTGCCCAA GAACATGGGG GAATTTCTGT TTTTACGGGT GTCGGAGAGC 500
 GTACTCGTGA AGGAAATGAC CTATATTATG AAATGCAGGA TTCAGGCGTT 550
 ATTGAAAAAA CGGCTATGGT ATTTGGACAA ATGAACGAAC CCCCTGGTGC 600
 5 ACGTATGCGT GTAGCGTTAA CTGGTTTGAC ACTTGCTGAG TACTTCCGTG 650
 ATGTACAAGG TCAAGACGTA TTATTATTTA TAGATAATAT TTTCCGCTTT 700
 ACTCAAGCAG GAACAGAAGT ATCTGCTTTA TTAGGACGGA TGCCGTCTGC 750
 CGTTGGTTAC CAACCAACTC TAGCAACGGA AATGGGACAG TTGCAAGAAC 800
 GAATCACATC GACAGATAAA GGATCAATTA CCT 833
 10

2) INFORMATION FOR SEQ ID NO: 1603

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*
 25 (B) STRAIN: ATCC 35980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603

ATCAGCCTAA AATTAACGAA GCAATAGAAG TTAATTATGA ATTAGATGGT 50
 30 AAAAAAATAA GACTTATTCT TGAAGTAGCT GGACATCTTG GCGATAATAG 100
 AGCAAGAACC ATTGCTATGG ATATGAGTGA TGGTTTACAA AGAGGATTAG 150
 AAGTTACGGC TCTTGGTGCT CCTATAACAG TTCCTGTTGG AGATAAAGTT 200
 TTAGGTAGAA TGTTTAATGT TGTAGGTGAC TTAATAGATG AAGGTGAAGT 250
 AACAGATTTT GATAAAAGAT GGGCTATCCA TAGAGATCCT CCTTCGTTTG 300
 35 AAGATCAAAG TACAAAAAGT GAAATTTTTG AAACAGGTAT AAAAGTAGTT 350
 GATCTTCTTG CACCTTATGC AAAAGGTGGT AAAGTTGGCT TATTTGGTGG 400
 TGCTGGCGTT GGAAAAACAG TTATCATAAT GGAGCTTATA CATAATGTTG 450
 CATTTAAACA CAGCGGTTAT TCAATTTTTG CCGGTGTTGG AGAGAGAACA 500
 AGAGAGGGAA ATGATCTTTA TAATGAGATG AAAGAGTCTG GTGTTTGGGA 550
 40 TAAAGTTGCC TTATGTTATG GACAAATGAA TGAACCACCA GGAGCAAGAA 600
 ACCGTATAGC ATTAACAGGT CTTACAATGG CTGAATATTT CCGTGATGAA 650
 ATGGGGCTTG ATGTGTTGAT GTTTATAGAT AATATTTTGA GATTTTCTCA 700
 ATCAGGTTCT GAAATGTCAG CGCTGCTTGG TAGAATTCCA TCTGCTGTTG 750
 GTTATCAACC AACATTAGCA AGTGAGATGG GAAAACTTCA AGAAAGAATT 800
 45 ACTTCC 833

2) INFORMATION FOR SEQ ID NO: 1604

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 738 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus pseudoavium*

(B) STRAIN: ATCC 49372

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604

```

GGTGTATCC GCACAATCGC TATGGAATCT ACAGATGGAT TGCAACGGGG      50
GATGGAAGTT GTCGATACCG GCAAACCAAT CTCTGTTCTT GTAGGTAAAG      100
AAACATTAGG TCGTGTGTTT AACGTATTAG GTGAAACGAT CGACAAAGAA      150
GCACCTTTTC CAGAAGATGT AGAAAAGAGC GGTATTCACA AAAAGGCCCC      200
CGCTTTTGAA GACCTTAGCA CCAGTAATGA GATTTTAGAA ACTGGGATCA      250
AGGTTATCGA CTTATTAGCC CCTTACTTAA AAGGTGGTAA AGTTGGACTA      300
TTCGGTGGTG CCGGTGTTGG TAAAACCGTC TTAATTCAAG AACTGATTCA      350
TAATATCGCC CAAGAACACG GTGGGATTTC TGTCTTTACC GGGGTTGGGG      400
20 AACGGACTCG TGAAGGGAAC GACCTTTATT ATGAAATGAA AGAATCCGGC      450
GTTATTGAAA AAACAGCGAT GGTCTTCGGA CAAATGAATG AGCCACCAGG      500
TGCGCGGATG CGCGTTGCCT TGAAGTGGTT GACATTAGCT GAATATTTCC      550
GTGATGAAGA AGGTCAAGAT GTGTTGCTAT TTATCGATAA CATTTTCCGC      600
TTCACACAAG CCGGATCAGA AGTTTCGGCG CTATTAGGTC GGATGCCATC      650
25 TGCCGTTGGT TATCAACCAA CCTTGGCAAC AGAAATGGGT CAATTACAAG      700
AACGAATCAC TTCAACGAAA AAAGGCTCAA TTACATCG      738

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30 2) INFORMATION FOR SEQ ID NO: 1605

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605

ATYATYGAAR TITAYGCICC

20

45

2) INFORMATION FOR SEQ ID NO: 1606

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606

5 CCRAACATIA YICCIAC TTT TTC

23

2) INFORMATION FOR SEQ ID NO: 1607

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Klebsiella ornithinolytica*
- (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607

25	CTGGATTATG CGATGTCGGT CATTGTTGGC CGTGCGCTGC CGGATGTCCG	50
	AGATGGCCTG AAACCGGTAC ACCGTCGCGT ACTTTACGCC ATGAACGTAT	100
	TGGGCAATGA CTGGAACAAA GCCTATAAAA AATCCGCCCG TGTCGTTGGT	150
	GACGTAATCG GTAAATACCA CCCTCATGGT GATACCGCCG TTTATGACAC	200
	CATTGTACGT ATGGCACAGC CATTCTCCTT GCGTTATATG CTGGTCGATG	250
30	GCCAGGGTAA CTTCCGTTCT GTCGATGGCG ACTCCGCCGC AGCGATGCGT	300
	TATACGGAAA TCCGTATGTC GAAAATCGCC CACGAG	336

35 2) INFORMATION FOR SEQ ID NO: 1608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608

50

CTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG CTGCCGGATG	50
TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTATA CGCCATGAAC	100
GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCTG CCCGTGTCGT	150

GGGTGACGTC	ATCGGTAAAT	ACCACCCTCA	TGGTGATACT	GCCGTATACG	200
ACACCATGT	ACGTATGGCG	CAGCCATTCT	CCCTGCGTTA	CATGCTGGTA	250
GATGGCCAGG	GTAACCTTGG	TTCGGTCGAC	GGCGACTCCG	CCGCAGCGAT	300
GCGTTATACG	GAAATCCGTA	TGTCGAAGAT	CGCCCATGAA	C	341

5

2) INFORMATION FOR SEQ ID NO: 1609

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single,
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609

20 GCCCTGATCC AAATAGCATA TA

22

2) INFORMATION FOR SEQ ID NO: 1610

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610

35

CCTGGCATAA CAGTAACATT CTG

23

40 2) INFORMATION FOR SEQ ID NO: 1611

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611

TGGGAAAAAG CAACTCCATC TC

22

2) INFORMATION FOR SEQ ID NO: 1612

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612

ACAACTGAAT TCGCAGCAAC AAT

23

15

2) INFORMATION FOR SEQ ID NO: 1613

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 639 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: U19459

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613

ATGAAATATG GCCCTGATCC AAATAGCATA TATCCACATG AAGAAATAAA 50
AAGTGT TTTTATTA AAA ATACAATTAC CAATCCAAAT ATTATAGTTG 100
35 GAGATTATAC TTACTATTCC GATGTTAACG GAGCTGAAAA ATTTGAAGAA 150
CATGTGACAC ATCATTATGA ATTTAGGGGT GATAAACTTG TAATTGGCAA 200
GTTTTGTGCA ATAGCTGAAG GTATAGAATT TATTATGAAT GGAGCAAACC 250
ATAGAATGAA TTCAATAACA ACTTATCCTT TTAATATAAT GGGAAATGGT 300
TGGGAAAAAG CAACTCCATC TCTTGAAGAT TTACCATTTA AGGGAGATAC 350
40 TGTTGTTGGA AATGATGTGT GGATTGGTCA GAATGTTACT GTTATGCCAG 400
GAATTCAAAT AGGAGATGGA GCAATTGTTG CTGCGAATTC AGTTGTTACA 450
AAAGATGTAC CACCATATCG TATTATTGGT GGAAATCCGA GTAGAATTAT 500
AAAGAAAAGG TTTGAAGATG AATTGATAGA TTATTTATTG CAAATAAAAT 550
GGTGGGATTG GTCAGCACAA AAAATATTTT CTAATCTTGA AACACTTTGT 600
45 AGCTCTGATT TAGAGAAAAT AAAATCTATT CGAGATTAG 639

2) INFORMATION FOR SEQ ID NO: 1614

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614

CCAATCCAGA AGAAATATAC CC

22

10

2) INFORMATION FOR SEQ ID NO: 1615

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615

ATTAGTTTAT CCCCAATCAA TTCA

24

25

2) INFORMATION FOR SEQ ID NO: 1616

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616

40 ATAATGAATG GGGCTAATCA TCGTAT

26

2) INFORMATION FOR SEQ ID NO: 1617

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617

GCCAACAACT GAATAAGGAT CAAC

24

5

2) INFORMATION FOR SEQ ID NO: 1618

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (C) ACCESSION NUMBER: AF015628

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618

	ATGAAATGGC AAAATCAGCA AGGCCCCAAT CCAGAAGAAA TATACCCTAT	50
	AGAAGGTAAT AAACATGTTC AATTTATTAA ACCATCTATA ACAAAGCCCA	100
25	ATATTTTAGT TGGGGAATAT TCATATTACG ATAGTAAAGA TGGTGAATCT	150
	TTTGAAAGCC AAGTTCTTTA TCACTATGAA TTGATTGGGG ATAAACTAAT	200
	ATTAGGGAAG TTTTGTCTTA TTGGACCCGG AACGACATTT ATAATGAATG	250
	GGGCTAATCA TCGTATGGAT GGTTCACAT TTCCATTCAA TCTTTTCGGA	300
	AATGGTTGGG AGAAGCATAC CCCTACATTG GAAGACCTTC CTTATAAGGG	350
30	TAACACGGAA ATTGGGAACG ATGTTTGGAT TGGACGAGAT GTGACAATTA	400
	TGCCCCGGTG AAAAATAGGA AACGGGGCTA TTATTGCAGC AAAATCGGTT	450
	GTGACAAAGA ACGTTGATCC TTATTGAGTT GTTGCGGTA ATCCTTCACG	500
	ATTAATTAAG ATAAGGTTT CCAAGGAAAA AATCGCAGCA TTAATAAAG	550
	TAAGGTGGTG GGACCTAGAG ATAGAGACGA TAAATGAAAA TATTGATTGC	600
35	ATCCTGAATG GTGATATAAA AAAGGTTAAA AGAAGTTAG	639

2) INFORMATION FOR SEQ ID NO: 1619

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619

50

AAGGCAAAAT AAAAGGAGCA AAGC

24

2) INFORMATION FOR SEQ ID NO: 1620

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620

15 TGTACCCGAG ACATCTTCAC CAC 23

2) INFORMATION FOR SEQ ID NO: 1621

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621

30 AATTGAAGGA CGGGTATTGT GGAAAG 26

2) INFORMATION FOR SEQ ID NO: 1622

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622

45 CGATTTTGAC AGATGGCGAT AATGAA 26

2) INFORMATION FOR SEQ ID NO: 1623

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1569 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M90056

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623

	ATGAAAATAA	TGTTAGAGGG	ACTTAATATA	AAACATTATG	TTCAAGATCG	50
	TTTATTGTTG	AACATAAATC	GCCTAAAGAT	TTATCAGAAT	GATCGTATTG	100
	GTTTAATTGG	TAAAAATGGA	AGTGGAAAAA	CAACGTTACT	TCACATATTA	150
15	TATAAAAAAA	TTGTGCCTGA	AGAAGGTATT	GTAAAACAAT	TTTCACATTG	200
	TGAACTTATT	CCTCAATTGA	AGCTCATAGA	ATCAACTAAA	AGTGGTGGTG	250
	AAGTAACACG	AAACTATATT	CGGCAAGCGC	TTGATAAAAA	TCCAGAACTG	300
	CTATTAGCAG	ATGAACCAAC	AACTAACTTA	GATAATAACT	ATATAGAAAA	350
	ATTAGAACAG	GATTTAAAAA	ATTGGCATGG	AGCATTTTATT	ATAGTTTCAC	400
20	ATGATCGCGC	TTTTTTTAGAT	AACTTGTGTA	CTACTATATG	GGAAATTGAC	450
	GAGGGAAGAA	TAAGTGAATA	TAAGGGGAAT	TATAGTAACT	ATGTTGAACA	500
	AAAAGAATTA	GAAAGACATC	GAGAAGAATT	AGAATATGAA	AAATATGAAA	550
	AAGAAAAGAA	ACGATTGGAA	AAAGCTATAA	ATATAAAAGA	ACAGAAAGCT	600
	CAACGAGCAA	CTAAAAAACC	GAAAAACTTA	AGTTTATCTG	AAGGCAAAT	650
25	AAAAGGAGCA	AAGCCATACT	TTGCAGGTAA	GCAAAAGAAG	TTACGAAAAA	700
	CTGTAAAATC	TCTAGAAACC	AGACTAGAAA	AACTTGAAAG	CGTCGAAAAG	750
	AGAAACGAAC	TTCCTCCACT	TAAAATGGAT	TTAGTGAAGT	TAGAAAGTGT	800
	AAAAAATAGA	ACTATAATAC	GTGGTGAAGA	TGTCTCGGGT	ACAATTGAAG	850
	GACGGGTATT	GTGGAAAGCA	AAAAGTTTTA	GTATTTCGCG	AGGAGACAAG	900
30	ATGGCAATTA	TCGGATCTAA	TGGTACAGGA	AAGACAACGT	TTATTAAAAA	950
	AATTGTGCAT	GGGAATCCTG	GTATTTTCATT	ATCGCCATCT	GTCAAATCG	1000
	GTTATTTTAG	CCAAAAAATA	GATACATTAG	AATTAGATAA	GAGCATTTTA	1050
	GAAAATGTTC	AATCTTCTTC	ACAACAAAAT	GAAACTCTTA	TTCGAACTAT	1100
	TCTAGCTAGA	ATGCATTTT	TTAGAGATGA	TGTTTATAAA	CCAATAAGTG	1150
35	TCTTAAGTGG	TGGAGAGCGA	GTTAAAGTAG	CACTAACTAA	AGTATTCTTA	1200
	AGTGAAGTTA	ATACGTTGGT	ACTAGATGAA	CCAACAACT	TTCTTGATAT	1250
	GGAAGCTATA	GAGGCGTTTG	AATCTTTGTT	AAAGGAATAT	AATGGCAGTA	1300
	TAATCTTTGT	ATCTCACGAT	CGTAAATTTA	TCGAAAAAGT	AGCCACTCGA	1350
	ATAATGACAA	TTGATAATAA	AGAAATAAAA	ATATTTGATG	GCACATATGA	1400
40	ACAATTTAAA	CAAGCTGAAA	AGCCAACAAG	GAATATTAAA	GAAGATAAAA	1450
	AACTTTTACT	TGAGACAAAA	ATTACAGAAG	TACTCAGTCG	ATTGAGTATT	1500
	GAACCTTCGG	AAGAATTAGA	ACAAGAGTTT	CAAACTTAA	TAAATGAAAA	1550
	AAGAAATTTG	GATAAATAA				1569

45

2) INFORMATION FOR SEQ ID NO: 1624

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624

5

TTCTTTAATG CTCGTAGATG AACCTA

26

10 2) INFORMATION FOR SEQ ID NO: 1625

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1625

TTTTCGTATT CTTCTTGTTG CTTTC

25

25

2) INFORMATION FOR SEQ ID NO: 1626

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626

AGGAATGATT AAGCCCCCTT CAAAAA

26

40

2) INFORMATION FOR SEQ ID NO: 1627

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627

TTACATTGCG ACCATGAAAT TGCTCT

26

2) INFORMATION FOR SEQ ID NO: 1628

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (C) ACCESSION NUMBER: U82085

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628

20	ATGCTTAAAA	TCGACATGAA	GAATGTAAAA	AAATATTATG	CAGATAAATT	50
	AATTTTAAAT	ATAAAAGAAC	TAAAGATTTA	TAGTGGGGAT	AAAAATAGGTA	100
	TTGTAGGTAA	GAATGGAGTT	GGCAAAACAA	CACCTTTTAA	AATAATAAAA	150
	GGACTAATAG	AGATTGACGA	AGGAAATATA	ATTATAAGTG	AAAAACAAC	200
	TATTAAATAT	ATCTCTCAAT	TAGAAGAACC	ACATAGTAAG	ATAATTGATG	250
25	GAAAATATGC	TTCAATATTT	CAAGTTGAAA	ATAAGTGGAA	TGACAATATG	300
	AGTGGTGGTG	AAAAAACTAG	ATTTAAACTA	GCAGAGGGAT	TTCAAGATCA	350
	ATGTTCTTTA	ATGCTCGTAG	ATGAACCTAC	AAGTAATTTA	GATATCGAAG	400
	GAATAGAGTT	GATAACAAAT	ACTTTTAAAG	AGTACCGTGA	TACTTTTTTG	450
	GTAGTATCTC	ATGATAGAAT	TTTTTTAGAT	CAAGTTTGTA	CAAAAATTTT	500
30	TGAAATTGAA	AATGGATATA	TTAGAGAATT	CATCGGTAAT	TATACAAACT	550
	ATATAGAGCA	AAAAGAAATG	CTTCTACGAA	AGCAACAAGA	AGAATACGAA	600
	AAGTATAATT	CTAAAAGAAA	GCAATTGGAG	CAAGCTATAA	AGCTAAAAGA	650
	GAATAAGGCG	CAAGGAATGA	TTAAGCCCCC	TTCAAAAACA	ATGGGAACAT	700
	CTGAATCTAG	AATATGGAAA	ATGCAACATG	CTACTAAACA	AAAAAAGATG	750
35	CATAGAAATA	CGAAATCGTT	GGAAACACGA	ATAGATAAAT	TAAATCATGT	800
	AGAAAAAATA	AAAGAGCTTC	CTTCTATTAA	AATGGATTTA	CCTAATAGAG	850
	AGCAATTTCA	TGGTCGCAAT	GTAATTAGTT	TAAAAAACTT	ATCTATAAAA	900
	TTTAATAATC	AATTTCTTTG	GAGAGATGCT	TCATTTGTCA	TTAAAGGTGG	950
	AGAAAAGGTT	GCTATAATTG	GTAACAATGG	TGTAGGAAAA	ACAACATTGT	1000
40	TGAAGCTGAT	TCTAGAAAAA	GTAGAATCAG	TAATAATATC	ACCATCAGTT	1050
	AAAATTGGAT	ACGTCAGTCA	AAACTTAGAT	GTTCTACAAT	CTCATAAATC	1100
	TATCTTAGAA	AATGTTATGT	CTACCTCCAT	TCAAGATGAA	ACAATAGCAA	1150
	GAATTGTTCT	AGCAAGATTA	CATTTTTATC	GCAATGATGT	TCATAAAGAA	1200
	ATAAATGTTT	TGAGTGGTGG	AGAACAAATA	AAGGTTGCTT	TTGCCAAGCT	1250
45	ATTTGTTAGC	GATTGTAATA	CATTAATTCT	TGATGAACCA	ACAAACTATT	1300
	TGGATATCGA	TGCTGTTGAG	GCATTAGAAG	AATTGTTAAT	TACCTATGAA	1350
	GGTGTTGTGT	TATTTGCTTC	CCATGATAAA	AAATTTTATC	AAAACCTAGC	1400
	TGAACAATTG	TTAATAATAG	AAAATAATAA	AGTGAAAAAA	TTCGAAGGAA	1450
	CATATATAGA	ATATTTAAAA	ATTAAAGATA	AACCAAAATT	AAATACAAAT	1500
50	GAAAAGAAC	TCAAAGAAAA	AAAGATGATA	CTAGAAATGC	AAATTTTCATC	1550
	ATTATTAAGT	AAAATCTCAA	TGGAAGAAAA	TGAAGAAAAA	AACAAAGAAT	1600
	TAGATGAAAA	GTACAAATTG	AAATTAAAAG	AATTGAAAAG	CCTAAATAAA	1650
	AATATTTA					1658

2) INFORMATION FOR SEQ ID NO: 1629

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629

AAGGGGAAAG TTTGGATTAC ACAACA 26

15

2) INFORMATION FOR SEQ ID NO: 1630

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630

GAACCACAGG GCATTATCAG AACC 24

30

2) INFORMATION FOR SEQ ID NO: 1631

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631

45 CGACGATGCT TTATGGTTTG T 21

2) INFORMATION FOR SEQ ID NO: 1632

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632

GTTAATTTGC CTATCTTGTC ACACTC

26

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2) INFORMATION FOR SEQ ID NO: 1633

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M36022

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633

ATGGAATTTA AATTACAAGA ATTAAATCTT ACTAACCAAG ATACAGGACC 50
ATATGGTATA ACCGTTTCAG ATAAGGGGAA AGTTTGGATT ACACAACATA 100
AAGCAAATAT GATAAGTTGC ATCAATTTAG ATGGAAAAAT TACAGAGTAC 150
30 CCACTACCGA CACCAGATGC AAAAGTCATG TGTTTAACTA TATCCTCAGA 200
TGGGGAAGTT TGGTTTACTG AGAATGCAGC AAACAAAATA GGGAGGATTA 250
CAAAAAAAGG GATTATTAAG GAATATACAT TGCCTAACCC AGATTCAGCA 300
CCCTACGGTA TTACAGAAGG ACCAAATGGA GATATATGGT TTACAGAAAT 350
GAATGGCAAC CGTATTGGAC GTATTACGGA CGACGGTAAA ATTCGTGAAT 400
35 ACGAGCTGCC TAATAAAGGA TCTTACCCTT CTTTATCAC TTTGGGTTCT 450
GATAATGCCC TGTGGTTCAC AGAAAATCAA AATAATGCTA TTGGTAGAAT 500
TACAGAAAGT GGGGATATTA CAGAGTTTAA AATTCCTACA CCTGCATCAG 550
GACCAGTTGG TATTACAAAG GGAACGACG ATGCTTTATG GTTTGTGGAA 600
ATTATCGGTA ATAAGATAGG GCGAATAACT CCTCTGGGGG AAATTACCGA 650
40 ATTCAAAATT CCAACGCCAA ACGCTCGACC TCATGCAATT ACTGCTGGAG 700
CAGGAATTGA TTTATGGTTT ACTGAATGGG GGGCTAATAA AATAGGAAGG 750
CTGACAAGCA ATAATATAAT TGAGGAATAC CCAATTCAA TCAAAAGTGG 800
TGAACCACAT GGCATTTGTT TCGATGGTGA AACAATTTGG TTTGCAATGG 850
AGTGTGACAA GATAGGCAA TTAACCTCTCA TTAAGGATAA TATGGAGTGA 900
45

2) INFORMATION FOR SEQ ID NO: 1634

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634

TTAACTTGTC TATTCCCGAT TCAGG

25

10

2) INFORMATION FOR SEQ ID NO: 1635

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635

GCTGTGGCAA TGGATATTCT GTA

23.

25

2) INFORMATION FOR SEQ ID NO: 1636

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636

TTCCTACCCC TGATGCTAAA GTGA

24

40

2) INFORMATION FOR SEQ ID NO: 1637

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637

CAAAGTGCCT TATCCGAACC TAA

23

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2) INFORMATION FOR SEQ ID NO: 1638

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638

	GGTGGGGAAG	ACTGTCTTCA	TCCAGGAATT	GATTGTGAGT	CGTTCCACAT	50
	GCTCACCTAG	TTTTCGCTCG	ATCTTTTCAC	TAACGCAAAC	CATGTAGAAC	100
	AACATTGCCA	AGGCCACGG	TGGTTACTCC	GTCTTCACTG	GTGTTGGTGA	150
25	GCGTACTCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	GAGACTGGTG	200
	TCATTAGCT	CGAGGGTGAA	TCCAAGGTCG	CACTGGTGTT	CGGACAGATG	250
	AACGAGCCCC	CCGGTGCCCC	TGCCCCGTGC	GCCCTTACCG	GTCTGACCAT	300
	TGCCGAGTAC	TTCCGTGACG	AGGAGGGTCA	GGACGTGCTG	CTCTTCATTG	350
	ACAACATTTT	CCGTTTCACC	CAGGCCGGTT	CTGAGGTGTC	TGCCCTTCTC	400
30	GGTCGTATCC	CCTCTGCCGT	CGGTTACCAG	CCCACCCTGG	CCGTCGACAT	450
	GGGTGGTATG	CAGGAGCGTA	TCACCACCAC	CAAGAAGGGT	TCTATTACCT	500
	CCGTCCARGC	CGTCTACGTC	CCCGCGA			527

35

2) INFORMATION FOR SEQ ID NO: 1639

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639

	ACTGTCTTGA	TTCAAGAACT	TATTAACAAC	ATTGCTAAAG	CCCATGGTGG	50
	TTACTCTATT	TTCTGTGGTG	TTGGTGAACG	TACTCGTGAA	GGTAACGATT	100

TATACCACGA AATGATGGAA ACTGGTGTCA TTAAACTTGA AGGTGACTCC 150
 AAGTGTGCTC TTGTATTCGG TCAAATGAAC GAACCTCCTG GTGCTCGTGC 200
 CCGTGTGCT TTAAGTGGTT TAACCATGTC TGAATACTTC CGTGATGAAG 250
 AAGGTCAAGA TGTGTTACTT TTCATTGATA ACATTTTCCG TTCACTCAA 300
 5 GCTGGTTCTG AAGTATCTGC CCTTTTAGGT CGTATTCCAT CTGCTGTAGG 350
 TTACCAACCC ACTTTATCTA CTGATATGGG TGGTATGCAA GAACGTATTA 400
 CTACTACCAA GAATGGTTCC ATTACCTCTG TACARGCCGT CTACGTCCCC 450
 GC 452

10

2) INFORMATION FOR SEQ ID NO: 1640

- (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 783 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462
 25 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640

ACGCCCTTAC GGTAACAA AGCAACGAA ACGGAAGCAT GAACTTAACA 50
 30 TTTGAAGTTG CACTTCATTT AGGTGATGAT ACAGTTCGTA CAGTTGCGAT 100
 GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA GATACTGGTA 150
 AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG TGTATTCAAC 200
 GTATTAGGTG ATGCAATTGA CTTAGATGGT GAACTTCCTG CGGATGTACA 250
 CCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCAAGAA TTATCTACTA 300
 35 AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT ACTTGCTCCT 350
 TACATTAAGG GTGGTAAGAT CGGCCTATTC GGTGGTGCCG GCGTAGGTAA 400
 AACAGTATTA ATTCAAGAAT TAATTAACAA CATCGCACAA GAGCACGGTG 450
 GTATCTCTGT ATTGCTGGT GTAGGTGAGC GTACTCGTGA GGGTAATGAC 500
 TTATACCATG AAATGAGCGA TTCTGGCGTA ATCAAGAAAA CTGCGATGGT 550
 40 ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT GTTGCAATTA 600
 CAGGTTTAAAC AATGGCTGAG CATTTCCGTG ATGAGCAAGG ACAAGACGTA 650
 CTTCTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCGG GTTCTGAAGT 700
 ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC CAACCAACAC 750
 TTGCAACAGA AATGGGTCAA TTACAAGAGC GTA 783

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2) INFORMATION FOR SEQ ID NO: 1641

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL NRS-319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641

10 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAGCAAGCAT 50
 TAACTTAACA TTTGAAGTTG CACTTCATTT AGGTGATGAC ACAGTTCGTA 100
 CAGTTGCAAT GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA 150
 GATACTGGTA AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG 200
 15 TGTATTCAAC GTATTAGGTG ATGCAATTGA CTTAGATGGT GATGTTCTTG 250
 CGGATGTACG TCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA 300
 CTATCTACTA AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT 350
 ACTTGCTCCT TACATTAAGG GTGGTAAGAT CGGTCTATTC GGTGGTGCCG 400
 GTGTAGGTAA AACAGTATTA ATTCAGGAAT TAATTAACAA CATCGCACAA 450
 20 GAACACGGTG GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA 500
 GGGTAACGAC TTATACCATG AAATGAGCGA TTCTGGCGTA ATTAAGAAAA 550
 CTGCGATGGT ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT 600
 GTTGCAATTAA CAGGTTTAA AATGGCTGAA CATTTCCGTG ATGAGCAAGG 650
 ACAAGACGTA CTATTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCAG 700
 25 GTTCTGAAGT ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC 750
 CAACCAACAC TTGCAACAGA AATGGGTCAA TTACAAGAGC GTATTACATC 800
 TACAAATAAA GGATCTATCA CGT 823

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2) INFORMATION FOR SEQ ID NO: 1642

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases

35 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL BD-15

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642

GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAAAG 50
 CAACGAAAAC GGAGCAAACA TTAACCTAAC ATTTGAAGTT GCACTTCATT 100
 TAGGTGATGA TACAGTTCGT ACAGTTGCCA TGTCTTCCAC AGATGGACTT 150
 50 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
 TGGTGATGTA ACACTTGGTC GTGTATTCAA CGTATTAGGT GATGCAATTG 250
 ACTTAGATGG TGAAGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
 CAAGCACCTG CATTCGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350

	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAAG	GGTGGTAAGA	400
	TTGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACAGTATT	AATTCAGGAA	450
	TTAATTAACA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCCGG	500
	TGTAGGTGAG	CGTACTCGTG	AAGGTAACGA	CTTATACCAC	GAAATGAGCG	550
5	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCATTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGACGT	ACTACTGTTC	ATCGATAACA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	750
	ATGCCATCTG	CGGTAGGTTA	CCAGCCAACA	CTTGCAACAG	AAATGGGTCA	800
10	ATTACAAGAG	CGTATTACAT	CTACAAATA			829

2) INFORMATION FOR SEQ ID NO: 1643

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Bacillus pseudomycoides*
 (B) STRAIN: NRRL BD-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643

30	AATCTACAAT	GCCCTTACGG	TAAAACAAAG	CAACGAAAAC	GGAGCAAGCA	50
	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	TAGGTGATGA	CACAGTTCGT	100
	ACAGTTGCGA	TGTCTTCCAC	AGATGGACTT	GTTCGTGGCA	CAGAAGTAGA	150
	AGATACTGGT	AAACCAATCT	CTGTACCGGT	TGGTGATGCA	ACACTTGGTC	200
	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	ACTTAGATGG	TGAAGTTCCT	250
35	GCGGATGTAC	GCCGTGATCC	AATTCACCGT	CAAGCACCTG	CGTTCGAAGA	300
	GTTATCTACG	AAAGTAGAAA	TTCTTGAAAC	TGGTATTAAA	GTAGTAGACT	350
	TACTTGCTCC	TTACATTAAA	GGTGGTAAAA	TCCGGTCTATT	CGGTGGTGCC	400
	GGTGTAGGTA	AAACAGTATT	AATCCAGGAA	TTAATTAACA	ACATCGCACA	450
	AGAGCACGGT	GGTATTTCTG	TATTCGCTGG	TGTAGGTGAG	CGTACTCGTG	500
40	AAGGTAATGA	CTTATACCAC	GAAATGAGCG	ATTCTGGCGT	AATCAAGAAA	550
	ACAGCGATGG	TATTCGGACA	AATGAACGAG	CCACCTGGTG	CACGTCAACG	600
	TGTTGCATTA	ACAGGATTAA	CAATGGCTGA	ACATTTCCGT	GATGAGCAAG	650
	GACAAGACGT	ACTATTGTTC	ATCGATAACA	TCTTCCGTTT	CACGCAAGCG	700
	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	ATGCCATCTG	CGGTAGGTTA	750
45	CCAACCAACT	CTTGCAACAG	AAATGGGTCA	ATTACAAGAG	CGTATTACAT	800
	CTACAAATAA	AGGATCTATC	ACG			823

50 2) INFORMATION FOR SEQ ID NO: 1644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL B-617

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644

	GGAAAGCTAC	CTGAAATCTA	CAATGCCCTT	AGAATTAAAC	AAGACGCAGT	50
	TAAGTTAACT	TTAGAAGTTG	CACTTCACTT	AGGTGATGAT	ACAGTTCGTA	100
15	CAGTTGCGAT	GTCTTCCACA	GACGGACTTG	TTCGTGGTAC	TGCAGTAGAA	150
	GATACTGGCA	AAGCGATTTC	TGTTCCAGTT	GGTGATGCAA	CACTTGGTTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGT	GAGGTTCCAG	250
	CAGATGTACG	CCGTGATCCA	ATTCACCGTC	AAGCACCTGC	ATTCCAAGAG	300
	TTATCTACAA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
20	ACTTGCTCCT	TACATTAAAG	GTGGTAAAT	CGGTCTATTC	GGTGGTGCCG	400
	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTACTCGTGA	500
	AGGTAACGAC	TTATAACCATG	AAATGAGCGA	TTCTGGCGTA	ATCAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGTGC	ACGTCAACGT	600
25	GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
	ACAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
	GTTCTGAA					708

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2) INFORMATION FOR SEQ ID NO: 1645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- 35 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
- (B) STRAIN: ATCC 35567

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645

	GTACGATGCG	CTTGAAGTTC	AAAACGATGT	CAAAC TAGTG	CTGGAAGTTC	50
	AACAGCAGCT	CGGTGGTGGT	GTCGTTTCGT	GTATCGCTAT	GGGTACCTCA	100
	GATGGCCTAA	GCCGCGGTCT	GAAAGTACTT	GATTTAGAAC	ACCCTATCGA	150
50	AGTTCCTGTC	GGTGTGGCAA	CTCTGGGCCG	TATTATGAAC	GTGCTTGGTG	200
	AGCCTATCGA	TATGAAGGGT	GACATTGGTG	AAGAAGAGCG	TTGGGCTATC	250
	CATCGCGCTG	CACCAAGCTA	CGAAGATTTA	TCCAGTGCTA	ACGAACTGCT	300
	GGAAACGGGC	ATCAAGGTTA	TCGACCTGAT	TTGTCCGTTT	GCCAAAGGCG	350

GTAAAGTTGG TCTGTTTGGT GGTGCCGGCG TAGGTAAAAC GGTAACATG 400
 ATGGAGCTGA TTCGTAATAT TGCGACTGAG CACTCAGGTT ACTCTGTATT 450
 TGCCGGCGTT GGTGAGCGTA CTCGTGAGGG TAATGACTTC TACCACGAAA 500
 TGACAGAATC TAACGTATTA GACAAAGTAT CTCTGGTTTA TGGCCAAATG 550
 5 AATGAGCCAC CGGGAAACCG TCTGCGCGTT GCGTTAACCG GCCTGACCAT 600
 GGC GGAAAAA TTCCGTGATG AAGGCCGTGA CGTTCTGCTG TTTATCGATA 650
 ACATTTATCG TTATACCTTA GCCGGTACAG AAGTATCAGC ACTGTTAGGT 700
 CGTATGCCAT CAGCGGTAGG TTACCAACCA ACGCTGGCGG AAGAGATGGG 750
 TACACTGCAA GAACGTATCA CYTCAACC 778
 10

2) INFORMATION FOR SEQ ID NO: 1646

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Buttiauxella agrestis*
 25 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646

GATGCCGTAC CAAAAGTGTA CGACGCTCTT GAGGTTACAA ATGGTAAAGA 50
 30 CCGTCTGGTG CTGGAAGTTC AGCAACAGTT AGGTGGTGGC GTAGTGC GTA
 CTATCGCCAT GGGTACTTCT GATGGTTTGC GTCGTGGTCT GGAAGTTTCT 150
 AACCTCGATC ACCCAATTGA AGTGCCAGTA GGTAAAGCAA CTCTGGGCCG 200
 TATCATGAAC GTCCTGGGCG AGCCTATCGA CATGAAAGGC GATATCGGCG 250
 AAGAAGAGCG TTGGGCGATT CACCGTGCTG CTCCTAGCTA CGAAGAACTG 300
 35 TCTAGCTCCC AGGATCTGCT GGAAACCGGC ATCAAAGTAA TGGACCTGAT 350
 TTGCCCGTTC GCTAAGGGTG GTAAAGTCGG TCTGTTCCGT GGTGCGGGTG 400
 TGGGTAAAAC TGTAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCAGTGT TGCAGGCGTG GGGGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCATGAAA TGACCGATTC CAACGTTCTG GACAAAGTAT 550
 40 CACTGGTTTA TGGCCAGATG AACGAGCCAC CAGGTAACCG TCTGCGCGTT 600
 GCGTTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
 CGTTCTGCTG TTCGTTGATA ACATTTACCG TTATACCCTG GCCGGTACAG 700
 AAGTATCTGC GCTGCTGGGT CGTATGCCAT CTGCGGTAGG TTACCAGCCA 750
 ACTCTGGCAG AAGAGATGGG TGTTTTGCAG GAGCGTATTA CCTCCACCAA 800
 45 AACTGG 806

2) INFORMATION FOR SEQ ID NO: 1647

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1122 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida norvegica*
(B) STRAIN: ATCC 36586

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647

	GAAACCGTTG	TTGACACTGG	TTCCCCAATC	ACCGTCCCAG	TTGGTCGTGA	50
	AACCTTGGGT	CGTATCATT	ACGTTATCGG	TGAACCAATC	GATGAACGTG	100
	GTCCAATCAA	CACCAAGCAA	AGAAACCCAA	TCCATGCTGA	TCCTCCTTCA	150
15	TTTGCTGAAC	AATCCACTTC	TGCTGAAGTT	TTAGAAACCG	GTATTAAAGT	200
	TGTCGATTTA	TTGGCTCCTT	ATGCCAGAGG	TGGTAAAATT	GGTTTATTCG	250
	GTGGTGCCGG	TGTCGGTAAA	ACCGTCTTTA	TCCAAGAATT	GATTAACAAC	300
	ATTGCTAAAG	CTCATGGTGG	TTTCTCAGTC	TTCACCGGTG	TCGGTGAAAG	350
	AACCAGAGAA	GGTAACGATT	TATACCGTGA	AATGAAAGAA	ACCGGTGTCA	400
20	TTAACTTGGA	AGGTGACTCT	AAAGTCGCTT	TAGTCTTCGG	TCAAATGAAC	450
	GAACCTCCAG	GTGCTAGAGC	CCGTGTTGCC	TTAACCGGTC	TAACCATTCG	500
	TGAATACTTC	AGAGATGAAG	AAGGTCAAGA	TGTCTTGTTA	TTCGTTGATA	550
	ACATTTTCAG	ATTCAACCAA	GCTGGTTCAG	AAGTCTCTGC	CTTATTAGGT	600
	CGTATTCCAT	CTGCTGTCGG	TTATCAACCA	ACCTTGGCCA	CTGATATGGG	650
25	TTTGTTGCAA	GAACGTATCA	CCACCACCAG	AAAAGGTTCC	GTCACTTCTG	700
	TCCAAGCTGT	TTATGTCCCA	GCTGATGATT	TGACTGATCC	TGCCCCAGCC	750
	ACCACTTTTCG	CGCATTTGGA	TGCTACTACT	GTCTTGCTCT	GTGGTATCTC	800
	AGAATTGGGT	ATCTACCCAG	CTGTCGATCC	ATTGGATTCC	AAATCAAGAT	850
	TATTAGATGC	CGCTGTTGTT	GGTCAAGAAC	ATTACGATGT	TGCTACTCAA	900
30	GTTCAACAAA	CTTTACAAGC	CTACAAATCT	TTACAAGATA	TTATCGCTAT	950
	TTTAGGTATG	GATGAATTAT	CAGAACAAGA	TAAATTGACC	GTTGAAAGAG	1000
	CTAGAAAGAT	CCAACGTTTC	TTATCTCAAC	CATTTGCTGT	CGCTGAAGTT	1050
	TTCACTGGTA	TTCCAGGTAG	ATTAGTTAGA	TTGAAAGAAA	CCGTTGCTTC	1100
	ATTCAGAGAC	GTTTTAGCTG	GT			1122

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2) INFORMATION FOR SEQ ID NO: 1648

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
50 (B) STRAIN: ATCC 700677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648

TACGTCTCTT ACCCTGACGA TGATTTGCAA GTCGCATCTA CGGTCGTAGA 50
 TGTTCCTAAAT GGTAAAGTCA TCGCCCAACT TGGAGCTCGT CACCAAGCAA 100
 GTAACGTTTC ATTTGGTACC AACCAAGCTG TGGAAACCAA TCGTGAAGTGG 150
 GGATCAACTA TGAAACCAAT CACAGACTAT GCTCCTGCCT TGGAGTACGG 200
 5 TGTCTACGAT TCAACTGCTA CTATCGTTCA CGATGAGCCC TATAACTACC 250
 CTGGGACAGA TATCCCTCTC TATAACTGGG ATCGAGCATA TTTCGGTAAT 300
 ATTACTCTGC AATATGCCCT TCAACAATCT CGTAACGTAC CTGCCGTTGA 350
 AACACTAAAC AAGGTCGGTC TAGATAAGGC TAAAACCTTC CTTAATGGTC 400
 TTGGTATCGA CTATCCAAGC ATGCATTATG CAAACGCCAT TTCAAGTAAT 450
 10 ACAACTGAAT CCAACAAAAA ATATGGTGCA AGTAGTGAAA AAATAGCTAC 500
 CGCCTATGCC GCATTTCGCA ATGGTGGTAT TTACCACAAA CCAATGTACA 550
 TCAATAAAGT TGTCTTTAGC GATGGTAGCG AAAAAGAATT TTCTGACCCT 600
 GGCACAAGAG CCATGAAAGA AACGACTGCT TACATGATGA CAGAAATGAT 650
 GAAAACAGTC TGGACGTACG GAACTGGTGC TGGTGCCTAC CTGCCTTGGC 700
 15 TTCCTCAAGC TGGTAAAACA GGTACCTCTA ACTATACTGA CGAAGAAATT 750
 GAAAAGTATA TCAAGAACAC TGGTTACGTA GCTCCAGATG AAATGTTTGT 800
 GGGTTATACC CGT 813

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2) INFORMATION FOR SEQ ID NO: 1649

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*
 (B) STRAIN: ATCC 43675

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649

ATTAATGAAG CTATTGTTGT TAATTATGAA TTAGAAGGAA AAGAATGCAA 50
 GCTAGTTCTT GAAGTAGCTG CACATTAGG CGATAATAAA GTAAGAACCA 100
 TCGCTATGGA TATGACAGAT GGTCTTGTTA GAGGTTTAAC AGCCGTCGCA 150
 40 ACTGGAAATC CAATTAGTGT TCCAGTAGGC GAAAAAGTTC TTGGAAGAAT 200
 TTTTAATGTA ACGGGTGATT TGATTGATGA GGGCGAAGAA ATCAATTTTG 250
 ATAAGCACTG GTCAATTCAT AGAGATCCAC CTCCATTTGA AGAACAAAGT 300
 ACAAAAAGCG AAATCTTTGA AACAGGTATA AAGGTTGTTG ATTTGCTAGC 350
 TCCTTATGCT AAAGGTGGAA AAGTTGGTCT TTTTGGTGGT GCAGGTGTTG 400
 45 GTAAACCCTG TATTATTATG GAATTAATTC ACAATGTTGC ATTTAAACAT 450
 AGCGGATATT CTGTTTTTGC AGGTGTTGGC GAAAGAAGTTC GTGAGGGTAA 500
 TGACCTTTAC AATGAAATGA AAGAAAGTAA TGTATTAGAT AAAGTTGCAT 550
 TGTGTTATGG TCAAATGAAT GAACCACCAG GGGCAAGAAA TCGTATAGCT 600
 TTAACAGGTC TTACTATGGC TGAGTATTTT AGAGATGAAA TGGGACTTGA 650
 50 TGTTTTAATG ATTATTGATA ATATTTTCAG ATTTTCTCAA TCAGGCTCAG 700
 AAATGTCAGC ACTTTTAGGA AGAATTCCTT CAGCTGTTGG TTATCAACCA 750
 ACCTTAGCTA GTGAAATGGG TAAGTTCCAA GAAAGAATTA CTTCAACCAA 800
 GAAAGGATCT ATT 813

2) INFORMATION FOR SEQ ID NO: 1650

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 570 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650

GGTGGGGAAG ACTGTGTTCA TTCAGGAATT GATTGTAAGT TCTGTTATCA 50
 ACTAAAGCCG ACAGCGGTTG CTGATATGCT CTAGAACAAC ATTGCTAAGG 100
 CTCACGGTGG TTA CTCCGTG TTA CTGGTG TCGGTGAGCG TACCCGTGAG 150
 20 GGTAACGATT TGTACCATGA AATGCAAGAG ACCCGTGTCA TTCAACTCGA 200
 CGGAGAGTCC AAGGTCGCTC TTGTCTTCGG TCAAATGAAC GAGCCCCCTG 250
 GTGCCCCGTG CCGTGTGTC CTTACCGGTT TGACCATTGC TGAATACTTC 300
 CGTGACGAGG AAGGCCAAGA CGGTAGGCTT CATGCTTCTA TCGCTAGGGG 350
 CGTGTGATAC AGGAGGCTAA TCGCTTTTCT AGTGCTTCTC TTTATTGACA 400
 25 ACATTTTCCG TTCACTCAA GCTGGTCTG AAGTGTCTGC CTTGCTCGGT 450
 CGTATTCCCT CCGCTGTCGG TTACCAACCT ACTCTCGCCG TCGACATGGG 500
 TGTATGTCAG GAACGTATCA CCACCACCAC CAAGGGATCC ATTACTTCAG 550
 TGCARGCCGT CTACGTCCCC 570

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2) INFORMATION FOR SEQ ID NO: 1651

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 560 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651

TGTCTTCATC CAGGAGTTAA TTGTACGTTT TTTGTCTGCC TACTATAATA 50
 GACGAAGAAA TATTTTGATT TATTTTCTA ATAATTCAA TAGAACAACA 100
 50 TTGCCAAAGC CCACGGTGGT TACTCTGTCT TCACTGGTGT TGGCGAGCGG 150
 ACCCGTGAAG GAAACGATCT GTACCACGAA ATGCAGGAGA CCCGTGTCAT 200
 CCAGCTCGAT GCGGAGTCCA AGGTCGCCCT CGTCTTCGGT CAAATGAACG 250
 AACCCCCCGG AGCCCGTGCC CGTGTTGCC TCACTGGTCT GACCGTTGCT 300

	GAATACTTCC	GTGACGAGGA	AGGTCAAGAT	GGTGCGTATA	TATATATTCC	350
	CCAGTAATTT	GACTCGAAGC	TCCACTCACA	CATATATTAG	TGCTCCTCTT	400
	CATCGACAAC	ATTTTCCGCT	TCACCCAGGC	AGGTTCCGAA	GTGTCCGCCC	450
	TGCTCGGCCG	TATCCCCTCC	GCCGTCGGTT	ACCAGCCCAC	CCTCGCTGTC	500
5	GACATGGGTA	TGATGCAGGA	ACGTATCACC	ACCACCACCA	AGGGCTCCAT	550
	CACCTCCGTG					560

10 2) INFORMATION FOR SEQ ID NO: 1652

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652

25	CCACAAGTGT	ACAGCGCCCT	TGAGGTTAAA	AATGGTGATG	CTCGTCTGGT	50
	GCTGGAAGTT	CAGCAGCAGC	TGGGCGGTGG	CGTGGTTCGT	ACCATCGCCA	100
	TGGGTTCTTC	AGACGGCCTT	AAGCGTGGTC	TGGAAGCCGT	TGACCTTCAG	150
	CACCCAATTG	AAGTACCGGT	AGGTACTGCC	ACACTTGGCC	GTATCATGAA	200
30	CGTGCTGGGT	GAGCCGATCG	ATATGAAAGG	CGACATTGGC	GAAGAAGAGC	250
	GCTGGGCGAT	TCACCGCTCT	GCACCTTCTT	ACGAAGATCA	GTCGAACTCT	300
	CAGGATCTGC	TGGAAACCGG	CATCAAGGTG	ATTGACCTGA	TGTGTCCGTT	350
	CGCCAAGGGC	GGTAAAGTCG	GCTTGTTTCG	TGGTGCGGGC	GTAGGTAAAA	400
	CCGTCAACAT	GATGGAGCTT	ATTCGTAACA	TTGCGGCTGA	GCACTCAGGT	450
35	TTCTCGGTAT	TTGCCGGTGT	GGGTGAGCGT	ACCCGTGAAG	GTAACGACTT	500
	CTACCACGAA	ATGACCGACT	CCAACGTTAT	CGACAAAGTT	TCGCTGGTCT	550
	ATGGTCAGAT	GAACGAGCCA	CCGGGTAACC	GTCTGCGCGT	TGCGCTGACC	600
	GGTCTGACCA	TGGCGGAGAA	GTTCCGTGAC	GAAGGTCGTG	ACGTACTGCT	650
	GTTTATCGAT	AACATCTATC	GTTACACCCT	GGCCGGTACT	GAAGTCTCCG	700
40	CTCTGCTGGG	TCGTATGCCT	TCTGCGGTAG	GTTACCAGCC	AACGCTGGCG	750
	GAAGAGATGG	GCGTTCTGCA	GGAACGTATC			780

45 2) INFORMATION FOR SEQ ID NO: 1653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fonsecaea pedrosoi*
 (B) STRAIN: ATCC 18831

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653

10 TGTGTTTCATT CAGGAGCTGA TTGTGAGTAC CCCGGAGATT TTCCTGCGAT 50
 TGC GCATGAA GCAAGCGCTG ACGTCCATCT AGAACAACAT CGCCAAGGCT 100
 CACGGTGGTT ACTCCGTGTT CTGCGGTGTC GGCGAGCGTA CTCGTGAGGG 150
 TAACGATTTG TACCACGAAA TGCAGGAGAC CGGTGTCATC AACCTCGAGG 200
 GCGAGTCCAA GGTCGCCCTT GTCTTCGGTC AGATGAACGA GCCCCCGGGA 250
 GCCCGTGCCC GTGTCGCCCT TACTGGTCTT ACCGTCGCTG AGTAAGTTTT 300
 GACAACCAGA AGCGAGTATT GCCACAATTA CTGACTAAAA ATCAAGATAT 350
 15 TTCCGTGACG AGGAGGGCCA GGATGTGCTT CTCTTCATTG ACAACATTTT 400
 CCGTTTCACC CAGGCCGGTT CTGAGGTGTC CGCTCTTCTC GGCCGTATTC 450
 CCTCTGCCGT CGGTTACCAG CCCACTCTCG CCGTCGACAT GGGTATGATG 500
 CAGGAGCGTA TCACCACCAC CCAGAAGGGT TCCATCACTT CCGTC 545

20

2) INFORMATION FOR SEQ ID NO: 1654

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 564 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
 (B) STRAIN: WSA-213

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654

40 TGTGTTTATT CAGGAGCTCA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCTGTCTT CACTGGTGTC GGTGAGCGAA CCCGTGAGGG TAACGATCTG 100
 TACCACGAAA TGCAGGAGAC TTCCGTTATT CAGCTTGATG GCGAGTCCAA 150
 GGTGCCCCTG GTTTTCGGTC AGATGAACGA GCCCCCTGGA GCTCGTGCCC 200
 GTGTCGCTCT TACCGGGTAA GTTGATAGAT AGTGCCTTCC CTCCTGTTT 250
 CAACACCTCA ACACCACCAC TCCCCAAGAC ATTGCTACTC ATACTGCACC 300
 ATGATATTAT ATTTACGCCT CTTGGACGCT AGCTAATGTT GTATCGACAG 350
 45 TTTGACTGTT GCTGAGTACT TCAGAGACGA GGAGGGTCAG GACGTGCTGC 400
 TTTTCATTGA CAACATTTTC CGATTCATC AGGCCGGTTC CGAGGTGTCT 450
 GCCCTTCTCG GTCGTATCCC CTCTGCCGTC GGTACCAGC CCACTCTGGC 500
 CGTCGACATG GGTGGTATGC AGGAGCGTAT TACCACCACC ACCAAGGGTT 550
 CCATTACCTC AGTC 564

50

2) INFORMATION FOR SEQ ID NO: 1655

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655

15 CGTACCGCGC GTGTACGAGG CTCTTGAGGT ACAAATGGT AGTGAGAATC 50
 TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATTGT TCGTACCATC 100
 GCCATGGGTT CTTCCGACGG TCTGCGTCGC GGTCTGGAAG TCAAAGACCT 150
 CGAGCATCCG ATCGAAGTCC CGGTAGGTAA AGCAACGCTG GGTCGTATCA 200
 20 TGAACGTACT GGGCCAACCG GTAGACATGA AAGGCGACAT CGGCCAAGAA 250
 GAGCGTTGGG CGATTACCG CGCAGCGCCT TCCTACGAAG AGTTGTCAAA 300
 CTCTCAGGAA CTGCTGGAAA CCGGCATCAA AGTTATCGAC CTGATGTGTC 350
 CGTTTGCGAA GGGCGGTAAA GTTGGTCTGT TCGGTGGTGC GGGTGTAGGT 400
 AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA TCGAGCACTC 450
 25 CGGTTACTCC GTGTTTGCGG GCGTAGGTGA ACGTACTCGT GAGGGTAACG 500
 ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGATAA AGTATCCCTG 550
 GTGTATGGCC AGATGAACGA GCCGCCGGA AACCGTCTGC GCGTTGCGCT 600
 GACCGGCCTG ACCATGGCTG AGAAGTTCCG TGACGAAGGT CGTGACGTTT 650
 TGCTGTTCGT CGATAACATC TATCGTTACA CCCTGGCCGG TACTGAAGTA 700
 30 TCCGCACTGC TGGGTCGTAT GCCTTCAGCG GTAGGTTACC AGCCGACTCT 750
 GGCGGAAGAG ATGGGCGTTC TGCAGG 776

35 2) INFORMATION FOR SEQ ID NO: 1656

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656

50 GTGTTTCATCC AGGAGTTGAT TGTAAGTGAT TATATTCCCC TAGAAAGAAA 50
 TGTTTTGAAC AAAAGTCTCG AATTAGAAAA TTCTTTTCAG ATACTAATTT 100
 ACTATAGAAC AACATTGCCA AGGCTCACGG TGGTTACTCC GTCTTCACCG 150

GTGTCGGAGA GCGAACCCGT GAAGGAAACG ATCTGTACCA TGAAATGCAG 200
 GAAACTCGTG TCATCCAAC T GATGCGGAG TCCAAGGTCG CCCTGGTCTT 250
 CGGTCAGATG AACGAGCCCC CAGGTGCCCG TGCCCGTGTT GCTCTTACTG 300
 GTTTGACCAT TGCTGAGTAC TTCCGTGATG AGGAAGGTCA AGACGGTATG 350
 5 TTCTTTAAAT TAGATATCTT CTGGAGAAAC AGCGTCTAAC AAATTCTTCC 400
 AGTGCTTCTC TTCATCGACA ACATCTTCCG TTTCACCTCAG GCTGGTTCGG 450
 AAGTGTCTGC CCTGCTTGGT CGTATTCCAT CTGCCGTCGG TTACCAACCC 500
 ACTCTTGCCG TCGACATGGG TGGTATGCAG GAACGTATTA CCACCACCAA 550
 GAAGGGATCC ATTACCTCCG TC 572
 10

2) INFORMATION FOR SEQ ID NO: 1657

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Obesumbacterium proteus*
 25 (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657

GCCTAAAGTG TATAACGCAC TTGAGGTGAA AGGCGGTGCC ACTAAACTGG 50
 30 TACTGGAAGT TCAGCAGCAG CTAGGCGGCG GCGTTGTACG CTGTATCGCT 100
 ATGGGTACTT CTGACGGTCT GCGTCGCGGA CTGGACGTTG TTGACCTGGA 150
 GCACCCGATT GAAGTCCCAG TAGGTAAAGC GACCTTAGGC CGCATTATGA 200
 ACGTACTGGG TGAGCCAATT GATATGAAGG GTGATATCGG CGAAGAAGAT 250
 CGCTGGGCTA TTCACCGTGA AGCTCCAAGC TACGAAGAAC TGTCTAACTC 300
 35 GCAAGAACTG CTGGAAACCG GTATCAAGGT AATGGACTTG ATTTGTCCGT 350
 TCGCTAAGGG CGGTAAAGTC GGTCTGTTCC GTGGTGCGGG TGTGTTGTTAA 400
 ACAGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG AGCACTCAGG 450
 TTA CTCTGTA TTTGCCGCGG TGGGTGAACG TACTCGTGAG GGTAACGACT 500
 TCTACCACGA AATGACCGAC TCCAACGTAT TGGACAAAGT ATCACTGGTT 550
 40 TATGGCCAGA TGAACGAGCC ACCAGGAAAC CGTCTGCGCG TTGCGCTGAC 600
 CGGTCTGACT ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT GACGTACTGC 650
 TGTTTCATCGA TAACATCTAC CGTTATACCT TGGCCGGTAC CGAAGTATCT 700
 GCACTGCTGG GTCGTATGCC TTCTGCGGTA GGTATCAGC CAACGCTGGC 750
 GGAAGAGATG GGTGTTCTGC AAGAACGTAT CACCTCTACC 790
 45

2) INFORMATION FOR SEQ ID NO: 1658

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

(B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658

10 TGTCTTCATT CAGGAGCTTA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCCGTCTT CACTGGTGTG GGAGAGCGCA CTCGTGAGGG AAACGACTTG 100
 TATCACGAGA TGCAAGAGAC TTCCGTTATC CAGCTCGAAG GCGAATCCAA 150
 GGTTGCCCTC GTCTTCGGTC AAATGAACGA GCCTCCGGGT GCTCGTGCTC 200
 15 GTGTTGCTCT CACCGGTCGT AAGTGCTCCT TCCCAGATTT CTCTTCCCCA 250
 GTTTCTGGAC CCACTTTTTC CTTCCACCAC CATCTACTG GGTAGGACCA 300
 AGATAGCACT GCCTATTCTG GTGCCTTCCT ACCGCCTACT CTACTGCCTA 350
 TTCCACCACC TTTTCTACCG CCTCTTCTAC TTGCTATTGT ATACTAACTT 400
 ACTCAAACAG TTACTATTGC TGAGTACTTC CGTGACGCTG AGGGCCAGGA 450
 20 TGTGCTTCTC TTCATCGACA ACATTTTCCG TTTCACCCAG GCCGGTTCCTG 500
 AGGTGTCCGC TCTTCTCGGT CGTATCCCCT CCGCCGTCGG TTACCAGCCC 550
 ACCCTTGCCG TCGACATGGG TGGTATGCAG GAGCGTATCA CCACCACCAA 600
 GAAGGGATCC ATTACCTCCG TC 622

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2) INFORMATION FOR SEQ ID NO: 1659

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659

GACGCTGTAC CTCAGGTGTA CGATGCACTG ACAGTTGAGG GTGCTGAGCT 50
 GGTACTGGAA GTGCAGCAGC AGCTGGGTGG TGGTGTGTGTT CGCTGTATCG 100
 45 CGATGGGTGC CTCTGATGGC CTCAAGCGCG GTCTGAAAGC GCACAATACT 150
 GGTGCTCCTA TCACTGTACC GGTGGGTGTG GAAACACTGG GCCGGATCAT 200
 GGATGTGTTG GGTAACCCGA TTGACCAGAA AGGTCCAATC GGTGAACAAG 250
 ATCGCTGGGT GATCCACCGT GAAGCACCAA GCTACGAAGA TCAGGCTAAC 300
 AGCACTGAAC TGCTGGAAAC CGGTATCAAG GTTATCGACC TGGTATGCCC 350
 50 GTTTGCGAAA GGCGGTAAAG TCGGTCTGTT CGGTGGTGCC GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
 GGTTATTCCG TGTTTGCGGG CGTGGGTGAG CGTACCCGTG AAGGTAACGA 500
 CTTCTACCAC GAAATGACAG ACTCCAACGT ACTGGACAAA GTATCCCTGG 550

	TGTACGGTCA	GATGAACGAG	CCGCCAGGTA	ACCGTCTGCG	CGTAGCACTG	600
	ACCGGCCTGA	CCATTGCGGA	GAAATTCCGT	GATGAAGGTC	GTGACGTACT	650
	GCTGTTTCATC	GATAACATCT	ACCGTTATAC	CCTGGCGGGG	ACCGAAGTAT	700
	CGGCACTGCT	GGGCCGTATG	CCTTCTGCGG	TAGGTTATCA	GCCAACGCTG	750
5	GCGGAAGAGA	TGGGTGTACT	GCAAGAGCGT	ATTACCTCTA	CCCG	794

2) INFORMATION FOR SEQ ID NO: 1660

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660

25	AGGTATATGA	CGCTSTGAAG	ATCACAGGTG	AAGGCGCCTG	TAATGGTTTG	50
	GTGCTGGAAG	TTCAGCAACA	GCTAGGCGGT	GGTGTAGTTC	GTACTATCGC	100
	TATGGGTTCT	TCTGATGGTC	TGCGTCGTGG	TCTTGAGGTT	GTAACTCAG	150
	GTTACCTAT	TTCTGTTTCT	GTTGGTACCG	CCACGCTTGG	CCGTATCATG	200
	AACGTATTAG	GTGAGCCTAT	TGATGAAGCG	GGTCCAATCG	GTGAAGAAGA	250
30	GCGTTATGTT	ATTACCGTG	CAGCACCTTC	ATATGAAGAT	CAATCGAACA	300
	CTACTGAAC	GTTAGAGACA	GGTATCAAGG	TTATTGACCT	TGTTTGTCCA	350
	TTCGCTAAGG	GTGGTAAAGT	AGGTCTGTTC	GGTGGTGCGG	GTGTTGGTAA	400
	AACAGTTAAC	ATGATGGAAC	TGATTAACAA	CATCGCTAAA	GCTCACTCGG	450
	GTCTTTCCGGT	GTTCCGCCGT	GTGGGTGAAC	GTACTCGTGA	AGGTAACGAC	500
35	TTCTACTACG	AGATGAAAGA	TTCTGGCGTT	CTCGACAAAG	TGGCCATGGT	550
	TTATGGTCAG	ATGAACGAGC	CACCAGGAAA	CCGTTTACGC	GTAGCACTGT	600
	CAGGTCTGAC	AATGGCTGAG	AAGTTCCGTG	ACGAAGGTCG	TGACGTATTG	650
	TTGTTTCGTTG	ACAACATCTA	CCGTTATACC	TTAGCCGGTA	CTGAAGTATC	700
	TGCACTGTTA	GGCCGTATGC	CTTCTGCGGT	AGGTTATCAA	CCAACATTGG	750
40	CTGAAGAAAT	GGGCGTTCTG	CAAGAGCGTA	TTACTTCAAC	TAAGACGGG	799

2) INFORMATION FOR SEQ ID NO: 1661

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661

TGGGAAGCGA AAATCCTG

18

5.

2) INFORMATION FOR SEQ ID NO: 1662

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 774 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662

	CTATGCCTCA	AACTAGAGAG	CATATCTTGC	TATCTCGCCA	AGTAGGCGTT	50
	CCATATATCG	TTGTATTTAT	GAACAAAGCC	GATATGGTCG	ATGACGCTGA	100
25	GCTTCTTGAG	CTAGTCGAGA	TGGAAATTCG	CGAGCTTCTT	AACGAGTACA	150
	ACTTCCCTGG	CGATGATACT	CCTATCATAT	CAGGTTCTGC	TCTTAAAGCC	200
	CTCGAAGAGG	CTAAAGCAGG	CGTTGATGGC	GAGTGGTCAG	CAAAAGTTCT	250
	TGAGCTTATG	GATAAAGTCG	ATGAGTATAT	CCCAACTCCA	GTTCGTGCTA	300
	CCGATAAAGA	CTTCCTGATG	CCTATCGAAG	ACGTTTTTCTC	TATCTCAGGT	350
30	CGTGGAACGG	TCGTTACTGG	TAGGATCGAA	AAAGGTGTCG	TAAAAGTTGG	400
	CGATACTATC	GAGATCGTTG	GTATCAAACC	TACTCAAAC	ACGACAGTTA	450
	CTGGCGTTGA	GATGTTTAGG	AAAGAGATGG	AACAAGGCGA	GGCCGCTGAT	500
	AACGTAGGTG	TTCTTTTAAG	AGGTACTAAA	AAAGAAGACG	TCGAGCGCGG	550
	CATGGTTCTT	TGTAAGCCAA	AATCAATCAC	TCCTCATACA	AAATTTGAGG	600
35	GTGAGGTTTA	TATCCTAACA	AAAGAGGAAG	GCGGACGCCA	CACTCCATTC	650
	TTTAACAAC	ATAGACCACA	ATTTTATGTA	AGAACAACAG	ACGTTACAGG	700
	TTCTATCACA	CTTCCAGAAG	GAAGTGAAG	GGTTATGCCT	GGAGATAATG	750
	TCAGAATTTC	CGTTGAATC	ATCG			774

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2) INFORMATION FOR SEQ ID NO: 1663

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*

(B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663

5	TTCTGCGGCT	GACGGCCCAA	TGCCACAAAC	TAGAGAGCAC	ATCTTGCTAT	50
	CTCGCCAAGT	AGGCGTTCCG	TATATCGTTG	TTTTTATGAA	CAAAGCCGAT	100
	ATGGTCGATG	ATGCCGAGCT	TCTTGAGCTG	GTTGAGATGG	AGATTTCGCGA	150
	GCTTCTAAAC	GAGTATGATT	TCCCTGGTGA	CGATACTCCA	ATCGTAGCAG	200
	GCTCTGCTCT	TCAAGCTCTT	AATGAAGCCA	AAGCCGGAAC	AGAAGGCGAG	250
10	TGGTCTGCAA	AAATTCTTGA	GCTTATGGCT	AAAGTTGACG	AGTATATCCC	300
	GACTCCGGTT	CGTGCAACGG	ATAAAGACTT	CTTGATGCCT	ATTGAGGACG	350
	TTTTCTCTAT	CTCCGGTCGC	GGCACCGTCG	TTACCGGCAG	AATCGAAAAA	400
	GGTATCGTAA	AAGTCGGTGA	TACTATCGAG	ATCGTAGGTA	TCCGCGATAC	450
	TCAAACAAC	ACCGTTACCG	GCGTTGAGAT	GTTTCAAGAGG	GAGATGGATC	500
15	AAGGCGAAGC	GGGCGATAAC	GTAGGCGTTC	TTCTAAGAGG	CACTAAAAAA	550
	GAAGACGTTG	AGCGCGGTAT	GGTTCCTTTC	AAACCTAAAT	CAATCACTCC	600
	TCACACTAAA	TTTGAGGGAG	AGGTTTATAT	CTTAACTAAA	GAGGAAGGCG	650
	GACGCCATAC	TCCATTCTTT	AATAACTATA	GACCGCAGTT	TTATGTAAGA	700
	ACTACCGACG	TTACCGGTTC	TATCACTCTT	CCGGAAGGAA	CAGAGATGGT	750
20	TATGCCTGGC	GATAACTTAA	AGATAAGCGT	TGAGCTTATC	G	791

2) INFORMATION FOR SEQ ID NO: 1664

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664

40	CGACGGACAG	ATGCCCCAGA	CCAGGGAGCA	CTTGCTCCTC	GCCCCGCCAGG	50
	TCGGTGTC	GCGCATTGTC	GTCTTCGTCA	ACAAGGTCGA	TGCCATTGAG	100
	GACAAGGAGA	TGTTGGAGCT	CGTCGAGATG	GAGATGCGTG	AGCTTCTCTC	150
	CAGCTACGGC	TTCGAGGGTG	ACGACACTCC	CATCGTCATG	GGTTCCGCCC	200
	TTTGCGCCAT	TGAGGGCCGC	GAGCCCCACA	TTGGTGTCGA	GAAGATTGAC	250
45	GAGCTCCTCG	AGCACGTCGA	CACCTGGATC	CCCACCCCCG	AGCGTGACAT	300
	CGCCAAGCCT	TTCCTCATGT	CCGTTGAGGA	CGTCTTCTCC	ATTCCCGGCC	350
	GTGGTACCGT	CGTTCTGGC	CGTGTGAGC	GTGGTGTCCT	GAAGAAGGAT	400
	TCCGAAGTCG	AGCTTGTCGG	CAAGAACAAG	AACCCCATCA	AGACCAAGGT	450
	TACCGACATC	GAGACCTTCA	AGAAGTCTTG	CGACGAGTCC	CGCGCTGGTG	500
50	ACAACCTCCG	TCTCCTTCTC	CGTGGTGTC	AGCGTGACGA	TGTCCTCCGT	550
	GGCATGGTCG	TTGTCCAGCC	CGGCACCACC	AAGGCCACCA	AGAAGTTCCT	600
	TGCCTCCATG	TACGTCTCTA	CCAAGGAGGA	GGGTGGCCGC	CACACTGGTT	650
	TCGCCAACAA	CTACAAGCCC	CAGATGTTCA	TCCGTACCGC	CGATGAGGCC	700

GCCACTCTTA CCTGGCCCGA GGGTACCGAG GAGGACAAGA TGGTCATGCC 750
CGGTGACAAT GTCGAGATGA TCTGCGAGAT CCACAAGCCC ATTGCCGTCG 800
AGCAAGGCCA 810

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2) INFORMATION FOR SEQ ID NO: 1665

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665

20 CAGTACAGGT AGACTTCTG 19

2) INFORMATION FOR SEQ ID NO: 1666

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Microsporium audouinii*
35 (B) STRAIN: ATCC 11347

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666

40 ATGATTGCGA AACCTACTTG CTGTGGAAGA ATTTGGATAT TCTAACATTT 50
CTCTAGGCCT CAAACCAGAG AGCATCTGCT CCTTGCCCGC CAGGTCGGTG 100
TTCAGAAGCT CGTCGTTTTC GTTAACAAGG TCGACGCTGT TGAGGACCCA 150
GAGATGTTGG AACTTGTCGA GCTAGAGATG CGTGAGCTGC TCAGCCACTA 200
TGTTTTCGAG GGTGAGGAGA CCCCAATCAT TTTTGGCTCT GCTCTCTGCG 250
CCCTTGAATC TCGACGACCA GAATTGGGTG TTGAGAAGAT CGATGAGCTA 300
45 TTGAACGCTG TGGATACCTG GATTCCCACC CCAGAGCGTG CCACTGATAA 350
GCCTTTCCTT ATGTCCATTG AGGAAGTTT CTCCATCTCT GGTCGTGGTA 400
CCGTCGTTTC CGGTCGTGTC GAGCGTGGTA TCCTCAAGAA GGA CTCTGAT 450
GTCGAAATTG TGGGTGGATC TGATACACCC ATCAAGACGA AGGTCACCGA 500
CATTGAAACC TTCAAGAAGT CTTGTGACGA ATCCCGAGCT GGTGACAACT 550
50 CCGGTCTACT TCTCCGAGGT GTCAAGCGTG AGGACTTGAG ACGTGGAATG 600
GTTGTTGCTG CTCCCGGATC GACCAAGGCT CATACCGACT TCATGGTCTC 650
CCTTTATGTT CTGACCGAGG CTGAGGGTGG CCGTTCCAAT GGATTCACCC 700
ACAAGTACCG CCCACAGATG TTCATCCGTA CTGCCGGTAT GTAAACCCTT 750

TTTCTACCAT TCACTTTGTT TCACCACTGA CTTGTATACT TTACCGCAGA 800
CGAAGCCGCA TCTTTCAGCT GGCCTGGAGA GGATCAAGAC AAGAAGGCCA 850
TGCCTGGTGA CAATGTCGAG ATGATTTGCA AGACCCTC 888

5

2) INFORMATION FOR SEQ ID NO: 1667

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 793 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Piedraia hortai*
(B) STRAIN: ATCC 24292

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667

ATGCCGCAGA CCCGCGAGCA CTTGCTGCTC GCCCGTCAGG TCGGTGTCCA 50
GAAGATCGTT GTTTTCGTCA ACAAGGTTGA TGCTATCGAC GACCCGGAGA 100
25 TGCTGGAGCT TGTCGAGATG GAGATGCGTG AACTTCTCAG CACATACGGT 150
TTCGAGGGTG ACGAGACCCC TGTTATTATG GGCTCCGCGC TCATGGCTCT 200
CAACAACCAG CGCCCCGAGA TTGGTCAACA GAAGATTGAT GAACTCATGG 250
CCGCTGTCGA CGAGTGGATC CCTACTCCCC AGCGTGACCT CGACAAGCCT 300
TTCCTGATGT CTGTTGAGGA TGTCTTCTCC ATTGCTGGCC GTGGTACCGT 350
30 TGTGTCCGGC CGTGTGGAGC GCGGTACCCT CAAGCGTGAT GAGGAAGTCG 400
AGCTTGTCGG CAAGGGTGTC GACCCCATCA AGACCAAGGT CACCGATATC 450
GAGACTTTCA AGAAGTCCTG CGAGGAGGCT CAGGCTGGTG ACAACTCTGG 500
TCTTCTGATC CGTGGTGTCC GCCGCGAGGA TGTTCTGTCG GGTATGGTTG 550
TCTCCAAGCC CGGCACCGTC AAGTCTCACA CTCAGTTCCT GGCCTCGCTT 600
35 TACGTTCTCA CCAAGGAGGA GGGTGGTCGC CACACTGGTT TCGGCGAGCA 650
CTACCGTCCC CAGCTCTACC TCCGTACCTC AGACGAGTCT GTCGATCTGA 700
CCTTCCCCGA GGGAACTGAG GATCACCCT CCAAGATCGT CATGCCCTGGT 750
GACAACATCG AGATGGTCGT CACGATGACT CACGCCAACG CTA 793

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2) INFORMATION FOR SEQ ID NO: 1668

- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 891 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

- 50 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 KL1699
(C) ACCESSION NUMBER: J01717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668

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5  AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC      50
   TGC GACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC      100
   GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG      150
   GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG TTCGTGAACT      200
10  TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC GTTCGTGGTT      250
   CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG      300
   GAACTGGCTG GCTTCTTGGG TTCTTACATT CCGGAACCAG AGCGTGCGAT      350
   TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC      400
   GTGGTACCGT TGTTACCGGT CGTGTAGAAC GCGGTATCAT CAAAGTTGGT      450
15  GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT CTACCTGTAC      500
   TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT GCTGGTGAGA      550
   ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT      600
   CAGGTAAGTG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC      650
   TGAAGTGTAAT ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT      700
20  TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA CGTGACTGGT      750
   ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG GCGACAACAT      800
   CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC GACGGTCTGC      850
   GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C              891

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25

2) INFORMATION FOR SEQ ID NO: 1669

(i) SEQUENCE CHARACTERISTICS:

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30  (A) LENGTH: 805 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Saksenaea vasiformis
   (B) STRAIN: ATCC 60625

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40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669

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   TCCTCGTGGT CGCCGCCACC GACGGCCCGA TGCCGCAGAC CAAGGAGCAC      50
   GTGCTCCTGG CCCGCCAGGT CGGCGTTCCG TACATCGTCG TCGCCCTCAA      100
45  CAAGGCCGAC ATGGTGACG ACGAGGAGAT CCTGGAGCTC GTCGAGCTCG      150
   AGGTCCGTGA GCTCCTCTCC GAGTACGAGT TCCCGGGCGA CGACGTTCCC      200
   GTCGTCAAGG TCTCCGCTCT GAAGGCCCTC GAGGGCGACA AGGAGTGGGG      250
   CAACTCGGTT CTCGAGCTCA TGAACGCCGT CGACACGGCG ATCCCCGAGC      300
   CCGAGCGTGA CGTCGACAAG CCGTTCTCTA TGCCGATCGA GGACGTCTTC      350
50  ACGATCACCG GTCGCGGTAC GGTGCTCACC GGCCGTATCG AGCGTGGTGT      400
   CCTGAAGGTC AACGAGACCG TCGACATCAT CGGCATCAAG ACCGAGAAGA      450
   CCACCACCAC GGTCAACGGC ATCGAGATGT TCCGGAAGCT CCTCGACGAG      500
   GGCCAGGCCG GTGAGAACGT CGGTCTGCTC CTCCGTGGCA TCAAGCGCGA      550

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GGACGTCGAG CGCGGCCAGG TCATCATCAA GCCGGGCTCG GTCACGCCGC 600
 ACACGGAGTT CGAGGCGCAG GCCTACATCC TGTCCAAGGA CGAGGGTGGC 650
 CGCCACACGC CGTTCTTCAA CAACTACCGC CCGCAGTTCT ACTTCCGTAC 700
 GACGGACGTG ACCGGCGTGG TGACCCTCCC CGAGGGCACC GAGATGGTCA 750
 5 TGCCGGGTGA CAACACCGAG ATGAAGGTGG AGCTCATCCA GCCCGTCGCC 800
 ATGGA 805

10 2) INFORMATION FOR SEQ ID NO: 1670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 935 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670

25 GCTTCTGACG GTCAAATGTA ATTGAATGCC CGCCCAGACA GATGAAAGGA 50
 TTTGACGTTT CTAACATCAG TCTAGGCCTC AGACCAGAGA ACATTTGCTC 100
 CTTGCCCCGC AGGTCGGTGT CCAGAAGCTG GTCGTTTTTCG TTAACAAGGT 150
 CGATGCCGTT GAGGACCCAG AGATGTTGGA GCTTGTGCGAA CTTGAAATGC 200
 30 GTGAACCTCT CAGCCACTAC GGTTTCGAGG GTGAGGAGAC CCCCATCATT 250
 TTTGGCTCTG CTCTCTGTGC CCTCGAGTCC CGTCGACCTG AGCTTGGTGT 300
 CGAGAAGATT GACGAGCTAT TGAACGCCGT CGACACCTGG ATCCCCACCC 350
 CAGAGCGCGC CACTGATAAG CCTTTCCTCA TGTCCATTGA GGAAGTGTTT 400
 TCTATCTCTG GTCGTGGTAC CGTCGTCTCC GGTCTGTGTTG AGCGTGGTAT 450
 35 CCTCAAGAAG GATTCGGACG TCGAAATTGT TGGTGGCTCT ACCACCCCTA 500
 TCAAGACCAA GGTCACCGAT ATCGAAACCT TCAAGAAGTC CTGCGATGAA 550
 TCTCGAGCTG GTGACAACCT TGGTCTCCTT CTCCGAGGTA TCAAGCGTGA 600
 GGAATTGAAG CGTGGAATGG TTGTTGCTGC CCCCAGATCC ACCAAGGCTC 650
 ACACCGACTT CATGGTCTCC CTCTACGTCC TGACTGAGGC TGAGGGTGGT 700
 40 CGTTCCAACG GCTTCACCCA CAAGTACCGC CCCCAAATGT TCATCCGTAC 750
 TGCTGGTATG TAACCCAAGT TTCCGCTATT TACTAAGTAG ATCATTGCTA 800
 ACTTGATTTT CCTTCCGTAG ACGAAGCCGC ATCTTTCAGC TGGCCTGGAG 850
 AAGACCAAGA CAAGAAGGCT ATGCCTGGTG ACAACGTCGA GATGATTTGC 900
 AAGACCCTCC ACCCCATTGC TGCCGAGGCT GGCCA 935
 45

2) INFORMATION FOR SEQ ID NO: 1671

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter aerogenes*

(B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671

10
 ACGATGCCCT TGAGGTACAG AATGGTAATG AGAGCCTGGT GCTGGAAGTT 50
 CAGCAGCAGC TCGGCGGTGG CGTAGTCCGT GCTATCGCCA TGGGTTCTTC 100
 CGACGGTCTG CGTCGTGGTC TGGAAGTTAA AGACCTTGAG CACCCGATCG 150
 AAGTCCCGGT AGGTAAAGCG ACTCTGGGCC GTATCATGAA CGTCCTGGGT 200
 15 CAGCCGATCG ACATGAAAGG CGACATCGGC GAAGAAGAAC GTTGGGCTAT 250
 CCACCGCGCG GCGCCTTCCT ATGAAGAGCT GTCCAGCTCT CAGGAAGTGC 300
 TGGAAACCGG CATCAAAGTT ATCGACTTGA TGTGTCCGTT CGCTAAGGGC 350
 GGTAAAGTTG GTCTGTTCGG TGGTGCGGGT GTAGGTAAAA CCGTAAACAT 400
 GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT TACTCCGTGT 450
 20 TTGCGGGCGT TGGTGAGCGT ACTCGTGAGG GTAACGACTT CTATCACGAA 500
 ATGACCGACT CCAACGTTCT GGATAAAGTA TCCCTGGTTT ACGGCCAGAT 550
 GAACGAGCCG CCGGGAAACC GTCTGCGCGT TGCCTGACC GGCCTGACCA 600
 TGGCTGAGAA ATTCCGTGAC GAAGGTCGTG ACGTTCTGCT GTTCGTGAT 650
 AACATCTATC GTTACACCCT GGCCGGTACT GAAGTATCTG CACTGCTGGG 700
 25 CCGTATGCCT TCAGCGGTAG GTTATCAGCC GACTCTGGCG GAAGAGATGG 750
 GCGTTCTGCA GGAACGTATC AC 772

30 2) INFORMATION FOR SEQ ID NO: 1672

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1401 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bordetella pertussis*

(B) STRAIN: Tohama 1

(C) ACCESSION NUMBER: Genome project

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1672

ATGAGCAACG GAACCATCGT TCAGTGCATC GGCGCCGTGG TGGATATTCA 50
 GTTCCCCCGC GATAACATGC CCAAGATCTA CGAAGCGCTC ACCCTGGTGC 100
 ACGAGGGTTC CTCGTTCCGC GAGAAGGGCT TGACGCTGGA AGTGCAACAA 150
 50 CAGCTGGGCG ACGGCGTGGT GCGTACCATC GCGCTGGGTT CCAGCGACGG 200
 GCTGCGCCGC GGCATGCAAG TGGCCGGCAC CGGCGCACCG ATCTCGGTGC 250
 CCGTGGGCCA CGGCACCCTG GGCCGCATCA TGGACGTGCT GGGCCGTCCC 300
 ATCGACGAAG CCGGTCCCAT CGCCTCCGAC GAGAAGCGCG CCATCCACCA 350

GCGGCGCGCC CGTTTCGACG AGCTGTCGCC GTCGGTCGAG CTGCTGGAAA 400
 CCGGCATCAA GGTATCGAC CTGGTGTGCC CGTTCGCCAA GGGCGGCAAG 450
 GTCGGCCTGT TCGGCGGCGC CGGCGTGGGC AAGACCGTCA ACATGATGGA 500
 ACTGATCAAC AACATCGCCA AGCAGCACAG CGGCTTGTCG GTGTTGCGCCG 550
 5 GCGTGGGCGA GCGTACCCGC GAAGGCAACG ACTTCTACCA CGAAATGGAA 600
 GAGTCGAACG TTCTGGACAA GGTGGCCATG GTGTTGCGCC AGATGAACGA 650
 GCGGCGGCGC AACCGCCTGC GCGTGGCGCT GACCGGCCTG ACCATGGCCG 700
 AGAAGTTCCG CGACGAAGGC CGTGACATCC TGTTCTTCGT CGACAACATC 750
 TACCGCTACA CCCTGGCCGG TACCGAAGTG TCGGCGCTGC TGGGCCGTAT 800
 10 GCCGTCGGCG GTGGGCTACC AGCCTACGCT GGCCGAGGAA ATGGGCGTGC 850
 TGCAAGAGCG CATCACCTCG ACCAAGACCG GTTCGATCAC CTCGATCCAG 900
 GCCGTGTACG TGCCTGCCGA CGACTTGACC GACCCGTCGC CCGCCACGAC 950
 CTTCCAGCAC TTGGACTCGA CCGTCGTGCT GTCGCGTGAC ATCGCTGCGC 1000
 TGGGCATCTA TCCCGCCGTG GACCCGCTGG ATTCTCCAG CCGCCAGCTC 1050
 15 GACCCGCAAG TCGTGGGCGA AGAGCACTAC CAGGTGGCCC GTGGCGTGCA 1100
 GCAGACGCTG CAGCGCTACA AGGAACTGCG CGACATCATC GCGATTCTGG 1150
 GCATGGACGA ACTGTCGCCG GAAGACAAGC AGGCCGTGGC CCGCGCGCGC 1200
 AAGATCCAGC GCTTCCTGTC GCAGCCCTTC TACGTGGCCG AAGTGTTAC 1250
 CGGCTCGCCG GGCAAGTACG TGTCGCTGGC CGAAACGATC CGTGGCTTCA 1300
 20 AGATGATCGT CGACGGCGAG TGCGACGCGC TGCCCGAGCA GGCGTTCTAC 1350
 ATGGTCGGCA CGATCGACGA GGCCTTCGAG AAGGCCAAGA AACTCCAATA 1400
 A 1401

25

2) INFORMATION FOR SEQ ID NO: 1673

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 797 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 35
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Arcanobacterium haemolyticum*
 (B) STRAIN: ATCC 9345

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673

CAGCTACCGA CGGTCCAATG GCTCAGACCC GCGAGCACGT TCTTCTTGCT 50
 CGCCAGGTTG GCGTTCCACA GATCATCGTT GCTCTCAACA AGGCTGACAT 100
 GGTTGACGAC GAGGAAATCC TCGAACTCGT CGAAATGGAA GTTCGTGAGC 150
 45 TTCTCTCTTC CCAGGAGTAC CCAGGTGACG ACCTCCCAGT CGTCAAGATC 200
 TCGGCACTCA AGGCTCTCGA AGGCGATGCC GAATGGAGCA AGGCAATCGA 250
 AGATCTCATG GAAGCTGTCT ATACCTACTT CGACGATCCA GTGCGTGACC 300
 TCGATAAGCC ATTCTCATG CCAATCGAAG ACGTCTTCAC CATCACCGGT 350
 CGTGGCACCG TTGTTACCGG CCGTGCAGAG CGCGGTATGC TCAACTTGAA 400
 50 CGAAGAAGTT GAAATCCTCG GTATCCGTGC ACCACAGAAG ACAACCGTTA 450
 CCGGTATCGA AATGTTCCAC AAGTCGATGG ATCACGCAGA TGCAGGCGAA 500
 AACTGTGGTC TTCTCCTCCG TGGCACCAAG CGCGAAGATG TTGAACGTGG 550
 TCAGGTTGTT GCCAAGCCAG GCACCATCAC CCCACACACC AACTTCGAAG 600

CTCAGGTCTA	CGTGCTCGGT	AAGGAAGAAG	GTGGCCGTCA	CAACCCATTC	650
TTCTCCAACT	ACCGTCCACA	GTTCTACTTC	CGTACCACGG	ATGTTACCGG	700
CGTGATCACC	CTTCCAGAGG	GCACCGAAAT	GGTTATGCCA	GGCGACAACA	750
CCGACATGAC	AGTTGAGCTC	ATCCAGCCAA	TCGCTATGGA	AGAGGGC	797

5

2) INFORMATION FOR SEQ ID NO: 1674

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Butyrivibrio fibrisolvens*
- (B) STRAIN: ATCC 19171

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674

CTGATGGTCC	TATGCCACAG	ACCCGTGAGC	ACATCCTATT	AGCACGTCAG	50
GTAGGCGTAC	CATACATCAT	CGTATTCCTA	AACAAGTGCG	ATATGGTTGA	100
CGACGAGGAA	TTATTAGAGT	TAGTTGAGAT	GGACGTACGT	GATCTATTAA	150
ATCAGTACCA	GTTCCCAGGC	GACGACACTC	CAATCATCCG	TGGTTCAGCA	200
CTAGGTGCAT	TAAACGGCGA	AGAGAAGTGG	AAAGAGGCAA	TCTATCAGTT	250
AGCAGACACT	CTAGATTCAT	ACATTCCAGA	GCCAAAGCGT	GATATCGATG	300
ATCCATTCCT	ATTACCAATC	GAAGATATCT	TCTCAATCTC	AGGTCGTGGT	350
ACTGTAGTAA	CCGGCCGTGT	AGAGCGTGGT	ATTGTACACG	TAGGTGACGA	400
AGTTGAAATC	GTTGGTATTC	GTCCAACCAC	CAAGACCACT	GTAACGGCG	450
TTGAAATGTT	CCGTAAGTTA	CTAGACGAAG	GTCGTGCAGG	TGATAACGTT	500
GGTGTTCTAC	TACGTGGTAC	CAAGCGTGAT	GAGGTTGAGC	GTGGTCAGGT	550
TCTAGCTGCT	CCAGGCACAA	TCACTCCACA	CACCAAGTTC	ACTGGTCAGG	600
TTTACGTACT	AAGCAAGGAT	GAAGGTGGTC	GTCACACTCC	ATTCTTCAAG	650
GGCTACCGTC	CACAGTTCTT	CTTCCGTACA	ACCGATATTA	CCGGTTCTAT	700
CGATCTGAAA	GAGGGCCTAG	AGATGGTAAT	GCCAGGTGAT	AACACCGACA	750
TGACCGTAAC	CCTAATCCAC	CCAGTAGCTA	TGGCT		785

40

2) INFORMATION FOR SEQ ID NO: 1675

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*

(B) STRAIN: ATCC 49349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675

5
 TGGGGCGATC TTGGTTGTTT CTGCTGCAGA TGGTCCTATG CCACAAACTA 50
 GAGAGCACAT TCTTCTTTCT CGTCAAGTAG GCGTTCCATA TATTGTTGTT 100
 TTTATGAATA AAGCAGATAT GGTGATGAT GCTGAGCTTT TAGAGTTAGT 150
 TGAAATGGAA ATTAGAGAAT TATTAAGCTC TTATGATTTC CCAGGCGATG 200
 10 ATACACCTAT TATTTCTGGT TCTGCTTTAA AAGCTCTTGA AGAAGCTAAA 250
 GCTGGACAAG ATGGTGAATG GTCAGCAAAA ATTATGGATC TTATGGCTGC 300
 AGTTGATAGT TATATTCCAA CTCCAACCTCG TGATACTGAA AAAGACTTCT 350
 TGATGCCAAT TGAAGACGTT TTCTCAATTT CAGGTCGTGG TACTGTTGTT 400
 ACAGGTAGAA TTGAAAAAGG TGTTGTAAAA GTAGGTGATA CTATCGAAAT 450
 15 CGTTGGTATT AAAGACACTC AAACAACAAC TGTAACAGGT GTTGAAATGT 500
 TCAGAAAAGA AATGGATCAA GCGGAGGCAG GAGATAACGT AGGTGTTCTT 550
 CTTCTGGTGA CTAAAAAGA AGAAGTTATT CGCGGTATGG TTCTTGCTAA 600
 ACCAAAATCA ATTACTCCAC AACTGACTT CGAAGCTGAA GTTTATATCT 650
 TAAATAAGA TGAAGGTGGT AGACATACTC CATTCTTTAA CAACTATAGA 700
 20 CCACAGTTTT ATGTAAGAAC AACTGATGTT ACAGGTTCGA TTAAATTAGC 750
 TGATGGTGTT GAAATGGTTA TGCCAGGTGA AAATGTGAGA ATTACTGTAA 800
 GCTTGATCGC TCCAGTAGCA CTTGAAGAAG GAACT 835

25

2) INFORMATION FOR SEQ ID NO: 1676

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter lari*

(B) STRAIN: ATCC 43675

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676

TTCTGCAGCA GACGGCCCTA TGCCACAAAC TAGAGAGCAT ATCTTACTTT 50
 CTCGTCAAGT AGGTGTACCA TATATTGTTG TTTTCATGAA CAAAGCTGAT 100
 ATGGTTGATG ATGCAGAATT ATTAGAATTA GTTGAAATGG AAATTAGAGA 150
 45 ATTACTAAGC TCTTATGATT TCCCAGGAGA TGATACTCCA ATTATTTTCAG 200
 GTTCAGCATT ACAAGCTCTT GAAGAAGCAA AAGCTGGTCA AGATGGTGAA 250
 TGGTCTAAAA AAATCTTAGA TCTTATGGCT GCAGTTGATG ATTATATTCC 300
 AACTCCGGCT CGTGATACAG ATAAAGATTT CTTGATGCCA ATCGAAGATG 350
 TTTTCTCAAT CTCAGGTCGT GGAAGTGTG TTACCGGTAG AATTGAAAAA 400
 50 GGTGTTGTAA AAGTTGGTGA TACTATAGAA ATCGTTGGTA TTAGAGACAC 450
 TCAAACAACC ACAGTTACTG GTGTTGAAAT GTTTAGAAAA GAAATGGATC 500
 AAGGTGAAGC TGGTGATAAT GTTGGTGTAT TACTTCGTGG AACTAAAAAA 550
 GAAGATGTTG AACGTGCTAT GGTTCCTGCT AAACCAAAT CAATCACTCC 600

	ACATACTGAT	TTTGAAGCAG	AAGTTTATAT	CTTAAATAAA	GATGAAGGTG	650
	GTCGTCATAC	TCCATTCTTT	AATAATTATA	GACCGCAATT	TTATGTAAGA	700
	ACAACTGATG	TTACAGGTGC	TATTAACTT	GCAGAAGGCG	TTGAGATGGT	750
	TATGCCAGGC	GATAATGATA	GAATTACTGT	AAGTCTTATT	GCTCCAGTTG	800
5	CACTTGAGGA	AG				812

2) INFORMATION FOR SEQ ID NO: 1677

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*
 (B) STRAIN: ATCC 35980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677

25	GCTATTCTTG	TATGTTTCAGC	TGCAGATGGT	CCAATGCCAC	AGACTAGAGA	50
	GCATATTCTA	CTATCAAGAC	AAGTTGGTGT	TCCATACATA	GTTGTTTTCT	100
	TAAATAAAGA	AGATATGGTT	GATGATGCTG	AGCTTATAGA	GTTGGTTGAA	150
	GTTGAGGTTA	GAGATTTATT	AAATGAATAT	GATTTCCCTG	GAGATGATAC	200
	TCCAATCGTA	ATAGGTTCTG	CTCTTAAAGC	TTTAGAAGAA	GCAAAAGCTG	250
30	GAACAGAGGG	TGAATGGTCT	GCTAAAATTA	TGAAACTTAT	GGATGCTGTT	300
	GATAGCTATA	TCCCAACTCC	AACAAGAGAT	ACAGATAAAG	ATTCCTTAT	350
	GCCAATCGAA	GATATCTTCT	CAATTTCTGG	TCGTGGTACA	GTTGTAACAG	400
	GTAGAATTGA	AAAAGGTGTA	GTAAAAGTTG	GCGAGACTAT	TGAGATAGTT	450
	GGTATTAGAC	CTACTCAAAC	AACAACAGTT	ACTGGTGTTG	AAATGTTTAG	500
35	AAAAGAGCTA	GATCAAGGTG	AAGCTGGAGA	TAATGTTGGT	ATCTTGTTAA	550
	GAGGTACAAA	AAAAGAAGAT	GTTGAAAGAG	GTATGGTTTT	ATGTAAACCA	600
	AAATCAATCA	CTCCTCACAA	GAAATTTGAA	GGCGAAGTTT	ATATTCTTAC	650
	AAAAGATGAA	GGTGGTAGAC	ATACTCCTTT	CTTTAGTAAC	TATAGACCAC	700
	AATTTTATGT	TAGAACAACA	GATGTAACAG	GTTCTATATC	TCTTCCTGAG	750
40	GGAACAGAGA	TGGATATGCC	TGGTGATAAT	GTAAAACTTA	CAGTTGAACT	800
	TATAAACCCA	ATTGCTCTTG	AGCAAGGA			828

45 2) INFORMATION FOR SEQ ID NO: 1678

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter upsaliensis*

(B) STRAIN: ATCC 49815

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678

```

CGATTTTGGT TGTTCCTGCT GCTGATGGTC CTATGCCACA AACTAGAGAG      50
CACATTTTGC TTTCTCGTCA AGTGGGTGTT CCTTATATCG TAGTTTTTAT      100
10 GAATAAGGCT GATATGGTTG ATGATGCAGA GCTTTTAGAA TTGGTTGAAA      150
TGGAAATTAG AGAACTTTTA AGCTCTTATG ATTTCCCGGG CGATGACACT      200
CCTATCATTT CAGGCTCTGC TCTTCAAGCC TTAGAAGAGG CTAAGGCGGG      250
ACAAGATGGC GAGTGGTCAG CTAAGATTTT AGAGCTTATG AAGGCAGTTG      300
ATGAGTATAT CCCAACTCCT GTTCGCGATA CTGAAAAGA TTTCTTGATG      350
15 CCTATTGAAG ATGTTTTTTC AATTTCTGGT CGTGGAAGT TTGTAACAGG      400
TAGAATTGAA AAAGGTGTGG TTAAAGTCGG CGATACTATT GAGATAGTAG      450
GTATCAAAGA TACTCAAAC ACAACAGTTA CAGGCGTTGA GATGTTTAGA      500
AAAGAAATGG ATCAAGGTGA GGCTGGCGAT AATGTCGGTG TGCTTTTAAG      550
AGGAACAAAA AAAGAAGATG TTCTTCGTGG TATGGTTCTT GCAAAGCCTA      600
20 AATCTATCAC TCCTCATACT GATTTTGAAG CAGAAAGTTA TATTCTAAAT      650
AAAGATGAGG GCGGTCGCCA TACTCCTTTC TTAAACAATT ATCGTCCGCA      700
GTTTTATGTA AGAACGACTG ATGTAAGTGG TTCTATTAAA TTAGCTGATG      750
GTGTTGAGAT GGTTATGCCG GGTGAAAATG TAAGAATTAC AGTTAGCCTT      800
ATCGCTCCAG TTGCACTTGA      820
25

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2) INFORMATION FOR SEQ ID NO: 1679

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Globicatella sanguis*

40 (B) STRAIN: ATCC 51173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679

```

CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACATAT CTTATTATCA      50
45 CGTCAAGTAG GTGTTCCCTTA CATGGTTGTC TTCTTAAACA AAGTTGACAT      100
GGTTGACGAT GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGATT      150
TATTATCTGA ATACGAATTC CCTGGAGACG ACGTTCCAGT AATCGCTGGT      200
TCAGCTTTAA AAGCTTTAGA AGGCGAAGAA CAATATGAAG CAAAAGTATT      250
AGAATTAATG GAAGCTGTAG ATACATACAT TCCAGAACCA GTTCGTGATA      300
50 CTGAAAAACC ATTCATGATG CCAGTTGAAG ATGTGTTCTC AATCACAGGT      350
CGTGGTACAG TTGCTACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG      400
TGACGAAGTT GAAATCGTTG GTATTGCTGA AGAAATTAGC AAAACAAGT      450
TAACTGGTGT TGAAATGTTC CGTAAATTAT TAGATTACGC TGAAGCTGGA      500

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GATAACATTG GTGCGTTATT ACGTGGTGTT ACACGTGAAC AAATCCAACG 550
 TGGTCAAGTA TTAGCAAAAC CAGGAACAAT TACACCTCAT ACTAAATTCG 600
 AGGCGGAAGT TTACGTATTA TCAAAAGAAG AAGGTGGACG TCATACTCCA 650
 TTCTTCGCTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CTGACGTTAC 700
 5 AGGTGTTGTA GAATTACCAG AAGGTACAGA AATGGTAATG CCTGGAGATA 750
 ACGTATCAAT GACAGTTGAA TTAATTCACC CAA 783

10 2) INFORMATION FOR SEQ ID NO: 1680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus acidophilus*
 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680

25 GCTATCTTAG TTGTTGCTGC AACTGATGGT CCTATGCCAC AAATCTCGTGA 50
 ACACATTTTG CTTGCTCGTC AAGTTGGTGT TAACTACATC GTAGTATTCT 100
 TGAACAAGTG CGATTTAGTT GACGACCCAG AATTGATCGA CTTGGTTGAA 150
 ATGGAAGTTC GTGACTTGTT GACTGAATAC GATTACCCTG GTGATGATAT 200
 30 TCCAGTTGTT CGTGGTTCAG CATTAAAGGC TTTACAAGGT GACAAGGAAG 250
 CTCAAGACCA AATCATGAAG TTGATGGACA TTGTTGATGA ATACATCCCA 300
 ACTCCAGAAC GTCAAACCTGA CAAGCCATTC TTGATGCCAG TTGAAGACGT 350
 ATTCACTATC ACTGGTTCGTG GTACTGTTGC TTCAGGTCGT ATCGACCGTG 400
 GTACTGTAA GGTCCGTGAC GAAGTTGAAA TCGTTGGTTT GGTAGATAAA 450
 35 GTTCTTAAGT CAGTTGTTAC TGGTTTGGA ATGTTCCACA AGACTTTGGA 500
 CTTAGGTGAA GCCGGCGATA ACGTTGGTGT ATTGCTTCGT GGTGTTGACC 550
 GTGATCAAGT TGTTCTGTGGT CAAGTATTGG CTGCACCCGG CTCAATCCAA 600
 ACTCATAAGA AGTTTAAGGC ACAAGTTTAT GTTTTGAAGA AGGACGAAGG 650
 TGGTCGTCAC ACTCCATTCT TCTCAGACTA CCGTCCACAA TTCTACTTCC 700
 40 ACACCACTGA TATTACTGGT GAAATTGAAT TGCCAGAAGG TACTGAAATG 750
 GTTATGCCTG GTGATAACAC TGAATTCAC GTTACTTTGA TCAAGCCAGC 800
 TGCCATCGAA AAGGGTACTA AGT 823

45

2) INFORMATION FOR SEQ ID NO: 1681

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leuconostoc mesenteroides* subsp.
dextranicum
 (B) STRAIN: ATCC 19255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681

```

10 GCTGCAACTG ATGGTCCTAT GCCACAAACA CGTGAACACA TCTTGTTGGC      50
   ACGTCAAGTT GGTGTTGACT ACTTGTTGTG CTTCTTGAAC AAGACTGATT      100
   TGGTTGATGA TGAAGAATTA GTTGAATTGG TTGAAATGGA AGTTCGTGAA      150
   TTGTTGTCAG AATATGACTT CCCAGGTGAC GATATTCCTG TACTTAAGGG      200
   TTCAGCTTTG AAGGCTTTGG AAGGTGATCC TGAACAAGTT AAGGTTATCG      250
15 AAGAATTGAT GGATACTGTT GATTCATACA TTCCAGAACC AGCACGTGAA      300
   ACAGACAAGC CATTCTTGAT GCCTGTCGAA GACGTCCTCA CAATCACTGG      350
   TCGTGGTACA GTTGCTTCTG GTCGTGTTGA CCGTGGTGTA TTGACTACAG      400
   GAACTGAAAT TGAAATCGTT GGTTTGAAGG ACGAAGTTCA AAAGACTACT      450
   GTTACAGGTA TCGAAATGTT CCGTAAGACT TTGGAAGAAG CTCAAGCGGG      500
20 TGATAACATT GGTGCATTGT TGC GTGGTGT TGATCGTAGC AACATTGAAC      550
   GTGGTCAAGT TTTGGCAAAG CCAGGTTCAA TTAAGACACA CAAGAAGTTC      600
   AAGGCTGAAG TTTATGTCTT GACAAAGGAA GAAGGTGGTC GTCATACACC      650
   ATTCTTCACT AACTACCGTC CACAATTCTA CTTCCACACA ACTGATGTTA      700
   CAGGTGTTGT TGAATTGCCA GCCGGTGTG AAATGGTTAT GCCTGGTGAC      750
25 CAAGTGACAT TCGAAATCGA ATTGATCTCA CCAGTTGCCA TCG              793

```

2) INFORMATION FOR SEQ ID NO: 1682

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 796 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Prevotella buccalis*
 (B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682

```

45 TATCCTTGTA GTTGCTGCTA CTGATGGTCC TATGCCACAG ACACGTGAGC      50
   ACGTGCTTTT GGCTCGTCAG GTAAACGTTT CTCGTTTGGT TGTGTTTCATG      100
   AACAAGTGTG ACTTGGTAGA AGACGAAGAG ATGCTTGAAC TCGTTGAAAT      150
   GGAGTTGCGC GAACTTCTTG AGCAATACGA ATTCGAAGAG GATACTCCAA      200
   TCGTTTCGTG TTCTGCACTG GGTGCATTGA ATGGTGTTGA CAAGTGGGTT      250
50 GACAGCGTGA TGACGTTGAT GGACACTGTT GACGAGTGGA TTCAAGAGCC      300
   AGAGCGTGAC CTTGACAAAC CTTTCTTGAT GCCAGTAGAG GACGTGTTCT      350
   CTATCACAGG TCGTGGTACC GTTGTAACAG GACGTATTGA GACTGGTAAG      400
   GTAAAGGTTG GCGACGAGAT TCAGTTGCTC GGTCTTGGTG AGGACAAGAA      450

```


GTCTGTTGTA ACAGGCGTTG AAATGTTCCG TAAGATTCTT TCTGAAGGTG 500
 AAGCAGGTGA TAACGTAGGA CTTTGTGCTC GCGGTATCGA TAAGGATGAA 550
 GTAAAGCGTG GTATGGTTGT TGTACACCCA GGTGCCATCA CTCCTCACGA 600
 TCACTTCAAG GCTTCCATCT ATGTATTGAA GAAGGAAGAG GGTGGACGTC 650
 5 ATACTCCATT CGGAAACAAG TATCGTCCTC AGTTCTATCT CCGTACAATG 700
 GACTGTACAG GTGAGATCAC TTTGCCAGAA GCGGTAGAGA TGGTGATGCC 750
 TGGTGACAAC GTAGAGATTG AGGTTACCTT GATTTACAAG GTTGCC 796

10

2) INFORMATION FOR SEQ ID NO: 1683

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ruminococcus bromii*
 (B) STRAIN: ATCC 27255

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683

GGTGCTGCT ACTGACGGCC CGATGCCTCA GACTCGTGAG CACGTTCTGC 50
 TCGCTCGTCA GGTGGGTGTG CCCGCCATCG TCGTCGCCCT CAACAAGTGC 100
 GACATGGTTG ACGATGAGGA GCTCATTGAG CTTGTGAGGA TGGAGGTCCG 150
 30 CGAGCTGCTG ACCTCGCAGG AGTTCGACGG CGACAAGTGC CCTGTGCTTC 200
 GCATCTCCGC CTTCCAGGCC CTCCAGGGTG ACGAGAAGTG GACCCAGTCG 250
 ATCCTCGACC TCATGGACGC CGTGGACGAG TACATCCCGC AGCCTGAGCG 300
 CGATCTCGAC AAGCCCTTCC TTATGCCGAT CGAGGACGTC TTCACCATCA 350
 CCGGCCGTGG CACCGTTGTC ACCGGTCGTG TCGAGCGTGG TGTCGTCAAG 400
 35 ACTGGCGAAG AGGTCGAGAT CGTCGGTATC CACGAGAAGA CCCAGAAGAC 450
 CACCGTTACC GGTGTCGAGA TGTTCCGTAA GATCCTCGAC GAGGGCCGCG 500
 CTGGTGAGAA CGTCGGCGTT CTGCTCCGTG GCACCAAGAA GGAGGACGTC 550
 GTTCGCGGCA TGGTCCTCTC CAAGCCTGGT TCCACCACCC CCCACACCGA 600
 CTTGAGGGC CAGGTCTACG TCCTCAAGAA GGATGAGGGT GGCCGCCACA 650
 40 AGCCGTTCTT CTCCCATTAC AGCCCCAGT TCTACTTCCG TACCACGGAC 700
 GTGACTGGCA CTGTTGAGCT CCCCAGGGC ACCGAGATGG TCATGCCTGG 750
 CGACAACACC GACATGACTG TGCACCTGAT TCACCCGTT GCCATGGAGG 800

45

2) INFORMATION FOR SEQ ID NO: 1684

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 5 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684

```

10 TGTCTTTATT CAGGAACTGA TTGTATGTTT CTTCTCGTTT ATATATAACA      50
   TACCTTCTAT ATTTTCATGTG TTTCTAACGA ACTCATAGAA CAACATTGCC      100
   AAGGCTCACG GTGGTTACTC CGTGTTCACC GGTGTCGGTG AGCGTACCCG      150
   TGAAGGAAAC GATCTGTACC ACGAAATGCA GGAAACCCGC GTCATCCAGC      200
   TGGACGGCGA GTCCAAAGTC GCCCTCGTCT TCGGCCAGAT GAACGAGCCC      250
   CCCGGAGCCC GTGCCCCTGT TGCCCTGACC GGTCTGACCA TCGCTGAATA      300
15 CTTCCGTGAC GAAGAAGGCC AAGATGGTAC GTTCCCCCAT TCCATATATG      350
   TTTCTTGTGC GCTTTGCCAA CTAAACACCA CCTAGTGCTC CTCTTCATCG      400
   ACAATATCTT CCGCTTCACC CAAGCCGGTT CCGAAGTGTC CGCCCTGCTA      450
   GGCCGCATCC CCTCCGCCGT CGGCTATCAA CCCACCCTCG CCGTCGACAT      500
   GGGTGGTATG CAGGAGCGCA TCACAACCTAC AACAAAAGGC TCCAT          545
20

```

2) INFORMATION FOR SEQ ID NO: 1685

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*
 35 (B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685

```

40 GATATCGCTT TATGGAAATT CGAAACTCCA AAATTCCACG TTACYGTTAT      50
   CGATGCTCCA GGTACACAGAG ATTTTCATCAA GAATATGATT ACYGGTACCT      100
   CCCAAGCTGA TTGTGCTATT TTAATCATTG CTGGTGGTGT TGGTGAATTC      150
   GAAGCTGGTA TCTCAAAGA TGGTCAAACC AGAGAACACG CTTTGTTAGC      200
   TTTCACCTTA GGTGTAAAC AATTGATTGT TGCCGTTAAC AAAATGGACT      250
   CTGTCAAATG GGATCAATCC CGTTTCGAAG AAATCGTCAA GGAAGCTTCC      300
45 GGTTCATCA AGAAAGTTGG TTACAACCCA AAGACTGTTC CATTCGTTCC      350
   AATCTCTGGT TGAATGGTG ACAACATGAT TGAAGTYTCW GCTAACGCYC      400
   CATGGTACAA AGGTTGGGAA AAGGAAACCA AAGCYGGTGT CGTTAAAGGT      450
   AAAACTTTAT TAGAAGCCAT TGATGCTATT GAACCACCTT CAAGACCAAC      500
   TGAAAAACCA TTGAGATTGC CATTGCAAGA TGTCTACAAG ATTGGTGGTA      550
50 TCGGAACCGT ACCAGTCGGT ARAGTTGAAA CCGGTGTCAT TAAACCAGGT      600
   ATGATTGTTA CTTTCGCCCC AGCCGGTGT ACTACTGAAG TCAAATCTGT      650
   TGAAATGCAT CACGAACAAT TAGAAGCTGG TTACCCAGGT GACAATGTTG      700
   GTTTC AACGT CAAGAATGTT TCAGTTAAAG AAATCAGAAG AGGTAHGTG      750

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	GCTGGTGA	CT	CAAGAACGA	TCCACCAAAA	GGTGCTGAAT	CTTTCAACGC	800
	TCAAGTTATT	GTCTTGAACC	ATCCAGGTCA	AATCTYTGCT	GGTTACTYTC		850
	CAGTTTTTGA	TTGTCACACT	GCCCACATTG	CTTGTAAT	CGATGAAATC		900
	TTGGAAAAGA	TTGACAGAAG	ATCCGGTAAG	AAATTGGAAG	AAAATCCAAA		950
5	ATTCATCAAA	TCTGGTGACG	CTGCTAWTGT	CAAATTTGTT	CCATWTAAAC		1000
	CATRTGTGT	TGAAGCTTTC					1020

10 2) INFORMATION FOR SEQ ID NO: 1686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 929 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686

25	TGCTGCTTCC	GATGGTCAAA	TGTACGATTG	ATATTCCTTC	CAGCCAGTCA	50
	GGATAACAGC	TGATAACAGT	TGCAATAGG	CCCCAGACTC	GTGAGCACTT	100
	GTTGCTTGCC	CGTCAGGTTG	GTGTCCAGAA	GATCGTTGTC	TTCGTCAACA	150
	AGGTTGACGC	TGTCGATGAC	CCTGAGATGT	TGGAGCTTGT	TGAGCTCGAG	200
30	ATGCGTGAGC	TCCTCAACAC	TTACGGTTTC	GAGGGAGAGG	AGACCCCTAT	250
	CATCTTCGGT	TCCGCCCTGT	GCGCTCTCGA	AGGCCGCCGC	GAGGACATTG	300
	GTA	CTCAGC	G	CCGTTGACAC	TTGGATCCCT	350
	ACCCCCAGC	GTGACTTGGA	CAAGCCCTTC	CTGATGTCCA	TTGAGGAAGT	400
	TTTCTCCATT	GGTGGTCGTG	GTACCGTCGC	CTCTGGTCGT	GTCGAGCGTG	450
35	GTCTCCTCAA	GAAGGATACC	GAAGTTGAAA	TTCACGGTGC	TGATGGTATT	500
	CTGAAGACCA	AGGTCACCGA	CATTGAGACC	TTCAAGAAGA	GCTGCGATGA	550
	GTCTCGTGCT	GGTGACA	ACT	CCGGTCTTCT	CCTCCGTGGT	600
	AGGATGTTTC	TCGTGGTATG	GTCATCGCTG	CCCCTGGCTC	CATCAAGGCC	650
	TCCAAGAAGT	TCATGGTCTC	CATGTACGTC	TTGACTGAGG	CTGAAGGTGG	700
40	CCGCAAGAAC	GGCTTCGGTG	CCA	ACTACCG	CCCCCAGGCT	750
	CTGCTGGTAA	GTTTCGAACT	ATTTGATTCA	TTGATCACGT	CCCTAACTGT	800
	TACTTTAGAC	GAGGCTTGCG	ACCTTCATTT	CCCTGATGAG	GCCGACAAGG	850
	ACCGCCACGT	CATGCCCGGT	GACAACGTCG	AAATGGTCCT	CAACCTCAAC	900
45	AACCCCGTTG	CTGCTGAGGC	TGGACAGCG			929

2) INFORMATION FOR SEQ ID NO: 1687

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus terreus*

(B) STRAIN: WSA-174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687

```

10 TGCCGCTTCC GATGGTCAGA TGTACGCTCA AGCCCCAGTT TCCATATAAA      50
   CATAAACGAT CTATCATCAG CACAACGCTG ACTTCTTCGC TTCCAGGCCC      100
   CAGACCCGTG AGCACTTGCT GTTGGCCCGT CAGGTCGGTG TCCAGAAGAT      150
   CGTGGTCTTC GTCAACAAGG TCGATGCCGT TGATGACCCG GAGATGTTGG      200
15 AGCTCGTTGA GCTGGAAATG CGCGAGCTCC TGACCAGCTA CGGATTTCGAG      250
   GGTGAAGAGA CCCCCATCAT CTTCGGTTCT GCTCTCTGCG CTCTTGAGGG      300
   CCGCCGTCCT GAGATTGGTA CTGAGAAGAT TGACGAGCTG ATGCACGCCG      350
   TCGACACCTG GATCCCCACC CCCCAGCGTG ACCTCGACAA GCCCTTCCTG      400
   ATGTCCGTCG AGGAAGTCTT CTCCATTGCT GGTCTGGTGA CCGTCGCTTC      450
20 CGGCCGTGTC GAGCGTGGTA TTCTGAAGAA GGATAGCGAA GTCGAGATCA      500
   TCGGTGGTGC TTTGACGCC ACGAAGACCA AGGTCACTGA CATCGAGACC      550
   TTCAAGAAGT CTTGCGACGA GTCTCGCGCT GGTGACAACT CTGGTCTCCT      600
   CCTCCGTGGT ATCCGTCGTG AGGATGTTTC GCGTGGTATG GTCATTGCTG      650
   CTCCTGGCAG CACCAAGGCC CACGACAAGT TCCTTGCTCT TATGTACGTC      700
25 CTCACTGAGG CTGAGGGTGG CCGTCGTACC GGATTTCGTA CCAACTACCG      750
   CCCCCAGGTC TTCATCCGTA CTGCCGGTAA GTGTTCCCTG AAGAGGCTTT      800
   GAGCCTATAT AGGATCTCGG ATAATTACT AATCCACCAT ATAGATGAGG      850
   CCGCTGACCT CAGCTTCCCC GACAACGATG ACTCCCGCCG TGTGATGCCC      900
   GGTGACAACG TTGAGATGGT CCTGAAGACC CACCGCCCCG TGGCTGCTGA      950
30 G

```

2) INFORMATION FOR SEQ ID NO: 1688

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Candida norvegica*

(B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688

```

50 CGTTGCCGCT ACCGATGGTC AAATGCCTCA AACTAGAGAA CATTTGCTAT      50
   TGGCTAGACA GGTTGGTGTT CAACACATTG TCGTGTTTGT TAACAAGGTT      100
   GACACTATTG ATGATCCAGA AATGTTGGAA TTGGTTGAAA TGGAAATGAG      150
   AGAGTTGATT GCCACTTATG GTTTCGATGG TGATAACACC CCAGTTATCA      200

```

TGGGTTCTGC TCTATGTGCT TTGGAAGGTC GTGAACCTGA AATCGGTGCT 250
 CAATCAATCG ACAGATTGTT GGAAGCCGTT GATGAATACA TTCCAACCTCC 300
 AACTAGAGAT TTGGAAAAAC CATTCTTGAT GGGTGTGAA GATGTCTTCT 350
 CCATTTCTGG TAGAGGTACC GTCTGTACCG GTCGTGTTGA AAGAGGTAAC 400
 5 TTGAAGAAAG GTGATGAAAT CGAAATTGTC GGCTACAACA AGACTCCAAT 450
 CAAAACCAACC GTCACCGGTA TTGAGATGTT CAAAAAGGAA TTAGACCAAG 500
 CTATGGCTGG TGATAACTGT GGTATCTTAT TACGTGGTGT TAAGAGAGAT 550
 GATATCAAGA GAGGTATGGT TATCTCTAAA GTCAACACCG TTTCCGCACA 600
 CACCAAATTC TTGGCCTCTT TATACGTCTT GACTAAAGAA GAAGGTGGTC 650
 10 GTCATTCAGG TTTTGTGTA AACTACAGAC CTCAATTGTT CATCAGAACC 700
 GGTGATGTCA CTGTTACTTT AACCTTCCCA GAAGATGCTG ATCACTCTCA 750
 GCAAGTCTTA CCAGGTGACA ACGTTGAAAT GGAATGTACC TTGGTTCATC 800
 CAACTGCTCT TGAAACCGGT CAA 823

15

2) INFORMATION FOR SEQ ID NO: 1689

- (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 201076
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689

GCTGCTACTG ACGGTCAAAT GCCTCAAAC AGGGAACATA TGTGTTGGC 50
 GAGACAAGTT GGTATCCAAA ACTTGTTGT TTTTGTTAAC AAAGTTGATA 100
 35 CCATTGATGA CCCAGAAATG TTGGAATTGG TTGAAATGGA AATGAGGGAA 150
 TTATTGAGCT CTTATGGGTT TGATGGTGAA AACACTCCAG TTATCATGGG 200
 ATCAGCCTTG TGTGCTTTAG AAGGTAAACA ACCAGAAATC GGTGTTCAAG 250
 CCATTCAAAA ATTATTGGAT GCTGTTGATG AATATATTCC AACTCCAGAA 300
 AGAGATGCTG ACCAACCATT TTTGATGCCA GTGGAAGATG TGTTTTCTAT 350
 40 TTCAGGTAGA GGAACCGTTG TCACCGGAAG AGTTGAAAGA GGTATGTTGA 400
 AGAAAGGTGA AGAAGTAKAA GTCATTGGTG AAAACTCATT TAAGGCTACT 450
 TCCACGGGTA TTGAGATGTT CAAAAAGGAA TTGGATGCCG CTATGGCCGG 500
 TGACAACTGT GGTATTTTGT TGAGAGGTGT CAAGAGAGAC GAAGTCAAGA 550
 GGGGTATGGT TTTGGCCAAA CCAGGTACCA CCACCCACA CCAAAAGTTT 600
 45 TTGGCTTCCA TTTATATCTT GACTGCTGAA GAAGGTGGAC GTAGTACCCC 650
 TTTCAGTGAA GGATACAAAC CACAATGTTT CTTTAGAACT AGTGATGTTA 700
 CCACGACATT TACTTTCCCA GAAGGTGAAG GTGTTGACCA CTCACAAATG 750
 GTTATGCCAG GAGRCAATGT TGAAATGGTG GGAACCTTAA TCAAGAAAGC 800
 TCC 803
 50

2) INFORMATION FOR SEQ ID NO: 1690

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690

CAGGTCCTGT TGCGACTGAA GAA

23

15

2) INFORMATION FOR SEQ ID NO: 1691

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691

CACAGATAAA CCTGAGTGTG CTTTC

25

30

2) INFORMATION FOR SEQ ID NO: 1692

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692

GGTGAGAACT GTGGTATCTT ACTT

24

45

2) INFORMATION FOR SEQ ID NO: 1693

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693

CATTTCACG CCTTCTTTCA ACTG

24

10

2) INFORMATION FOR SEQ ID NO: 1694

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694

AAGGCAAGGA TGACAACGGC

20

25

2) INFORMATION FOR SEQ ID NO: 1695

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695

ACGATTTCCTTCTTCCTG G

21

40

2) INFORMATION FOR SEQ ID NO: 1696

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696

ATGTTCTGT AGTTGCTGGA

20

5

2) INFORMATION FOR SEQ ID NO: 1697

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697

TTTCTTCAGC AATACCAACA AC

22

20

2) INFORMATION FOR SEQ ID NO: 1698

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698

35 GGAATCAACA GATGGTTTAC AAA

23

2) INFORMATION FOR SEQ ID NO: 1699

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699

50

GCATCTTCTG GGAAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1700

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700

AAGATGCGGA AAGAAGCGAA

20

15

2) INFORMATION FOR SEQ ID NO: 1701

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701

30 ATTATGGATC AGTTCTTGGA TCA

23

2) INFORMATION FOR SEQ ID NO: 1702

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: Challis V288
 (C) ACCESSION NUMBER: L20574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702

50

TTCATAGACG	CTGAGCACGC	TTTGGATCCA	TCTTACGCGG	CTGCTCTAGG	50
TGTAAATATT	GATGAGCTGT	TGCTATCTCA	ACCAGATTCT	GGTGAGCAAG	100
GTTTAGAAAT	TGCAGGAAAA	TTGATTGACT	CTGGGGCAGT	TGATTTAGTT	150

GTCATCGACT	CTGTTGCAGC	TCTTGTACCA	CGTGCGGAAA	TCGATGGAGA	200
TATCGGTGAT	AGC				213

5

2) INFORMATION FOR SEQ ID NO: 1703

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: strain GS-5
 (C) ACCESSION NUMBER: M61897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703

GGGCCGGAAT	CTTCTGGTAA	GACAACTGTC	GCTCTTCATG	CTGCTGCTCA	50
GGCGCAAAAA	GATGGCGGTA	TTGCCGCTTT	CATTGATGCA	GAACATGCCC	100
TTGATCCAGC	CTATGCTGCT	GCTCTTGCGC	TTAATATTGA	TGAGCTTTTG	150
CTTTCACAAC	CAGATTCAGG	AGAACAGGGT	CTTGAAATTG	CAGGGAAATT	200
GATTGATTCT	GGCGCTGTTG	ATTTAGTTGT	TGTTGACTCA	GTGGCAGCTT	250
TAGTACCACG	TGCGGAGATT	GACGGAGATA	TTGGTAATAG	TCATGTTGGC	300
TTACAAGCAC	GCATGATGAG	TCAAGCGATG	CGTAAATTAT	CAGCTTCAAT	350
CAATAAAACA	AAAACCATTG	CTATTTTAT	TAATCAATTG	CGGGAAAAAG	400
TTGGTATTAT	GTTTGGTAAT	CCAGAAACAA	CCCCTGGCGG	GCGTGCCTTG	450
AAGTTTTATT	CTTCTGTGCG	TCTTGATGTC	CGCGGCAATA	CTCAAATTAA	500
AGGAACCGGG	GAACAAAAAG	ACAGCAATAT	TGGTAAAGAG	ACCAAAATTA	550
AAGTTGTAA	AAATAAAGTT	GCTCCACCAT	TTAAGGAAGC	TTTTGTAGAA	600
ATTATATATG	GTGAAGGCAT	TTCTCGTACA	GGTGAATTAG	TTAAGATTGC	650
CAGTGATTTG	GGAATTATCC	AAAAAGCTGG	AGCTTGGTAC	TC	692

40 2) INFORMATION FOR SEQ ID NO: 1704

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (C) ACCESSION NUMBER: Z17307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704

	ATGGCGAAAA	AACCAAAAAA	ATTAGAAGAA	ATTTCAAAAA	AATTTGGGGC	50
	AGAACGTGAA	AAGGCCTTGA	ATGACGCTCT	TAAATTGATT	GAGAAAGACT	100
5	TTGGTAAAGG	ATCAATCATG	CGTTTGGGTG	AACGTGCGGA	GCAAAAAGTG	150
	CAAGTGATGA	GCTCAGGTTC	TTTAGCTCTT	GACATTGCCC	TTGGCTCAGG	200
	TGGTTATCCT	AAGGGACGTA	TCATCGAAAT	CTATGGCCCA	GAGTCATCTG	250
	GTAAGACAAC	GGTTGCCCTT	CATGCAGTTG	CACAAGCGCA	AAAAGAAGGT	300
	GGGATTGCTG	CCTTTATCGA	TGCGGAACAT	GCCCTTGATC	CAGCTTATGC	350
10	TGCGGCCCTT	GGTGTCAATA	TTGACGAATT	GCTCTTGTCT	CAACCAGACT	400
	CAGGAGAGCA	AGGTCTTGAG	ATTGCGGGAA	AATTGATTGA	CTCAGGTGCA	450
	GTTGATCTTG	TCGTAGTCGA	CTCAGTTGCT	GCCCTTGTTT	CTCGTGCGGA	500
	AATTGATGGA	GATATCGGAG	ATAGCCATGT	TGGTTTGCAG	GCTCGTATGA	550
	TGAGCCAGGC	CATGCGTAAA	CTTGGCGCCT	CTATCAATAA	AACCAAAACA	600
15	ATTGCCATTT	TTATCAACCA	ATTGCGTGAA	AAAGTTGGAG	TGATGTTTGG	650
	AAATCCAGAA	ACAACACCGG	GCGGACGTGC	TTTGAAATTC	TATGCTTCAG	700
	TCCGCTTGGA	TGTTCGTGGT	AATACACAAA	TTAAGGGAAC	TGGTGATCAA	750
	AAAGAAACCA	ATGTCGGTAA	AGAAACTAAG	ATTAAGGTTG	TAAAAAATAA	800
	GGTAGCTCCA	CCGTTTAAGG	AAGCCGTAGT	TGAAATTATG	TACGGAGAAG	850
20	GAATTTCTAA	GACTGGTGAG	CTTTTGAAGA	TTGCAAGCGA	TTTGGATATT	900
	ATCAAAAAAG	CAGGGGCTTG	GTATTCTTAC	AAAGATGAAA	AAATTGGGCA	950
	AGGTTCTGAG	AATGCTAAGA	AATACTTGGC	AGAGCACCCA	GAAATCTTTG	1000
	ATGAAATTGA	TAAGCAAGTC	CGTTCTAAAT	TTGGCTTGAT	TGATGGAGAA	1050
	GAAGTTTCAG	AACAAGATAC	TGAAAACAAA	AAAGATGAGC	CAAAGAAAGA	1100
25	AGAAGCAGTG	AATGAAGAAG	TTCCGCTTGA	CTTAGGCGAT	GAAGTTGAAA	1150
	TCGAAATTGA	AGAATAAGCT	GTAAAGCAG	TGGAGAAATC	CGCTACTTTT	1200
	TCGA					1204

30.

2) INFORMATION FOR SEQ ID NO: 1705

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 981 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: NZ131
- (C) ACCESSION NUMBER: U21934

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705

	ATGCGTTCAG	GAAGTCTAGC	TCTTGATATT	GCTTGGATAG	CTGGTGGTTA	50
	TCCTAAAGGA	CGTATCATCG	AAATCTATGG	TCCAGAGTCT	TCCGGTAAAA	100
50	CGACTGTGGC	TTTACATGCT	GTAGCACAAG	CTCAAAAAGA	AGGTGGAATC	150
	GCAGCCTTTA	TCGATGCCGA	GCATGCGCTT	GATCCAGCTT	ATGCTGCTGC	200
	GCTTGGGGTT	AATATTGATG	AACCTCTCTT	GTCTCAACCA	GATTCTGGAG	250
	AACAAGGACT	TGAAATTGCA	GGTAAATTGA	TTGATTCTGG	TGCGGTTGAC	300

	CTGGTTGTTG	TCGATTCAGT	AGCAGCTTTA	GTGCCACGTG	CTGAAATTGA	350
	TGGTGATATT	GGCGATAGCC	ATGTCGGATT	GCAAGCACGT	ATGATGAGTC	400
	AGGCCATGCG	TAAATTATCA	GCTTCTATTA	ATAAAACAAA	AACTATCGCA	450
	ATCTTTATCA	ACCAATTGCG	TGAAAAAGTT	GGTGTGATGT	TTGGAAATCC	500
5	TGAAACAACA	CCAGGTGGTC	GAGCTTTGAA	ATTCTATGCT	TCTGTTGCGC	550
	TGGATGTGCG	TGGAACAAC	CAAATTAAAG	GAAGTGGTGA	CCAAAAGATA	600
	GCCAGCATTG	GTAAGGAGAC	CAAATCAAG	GTTGTTAAAA	ACAAGGTCGC	650
	TCCGCCATTT	AAGGTAGCAG	AAGTTGAAAT	CATGTATGGG	GAAGGTATTT	700
	CTCGTACAGG	GGAGCTTGTG	AAAATTGCTT	CTGATTTGGA	CATTATCCAA	750
10	AAAGCAGGTG	CTTGTTCTC	TTATAATGGT	GAGAAGATTG	GCCAAGGTTT	800
	TGAAATGCT	AAGCGTTATT	TGGCCGATCA	TCCACAATTG	TTTGATGAAA	850
	TCGACCGTAA	AGTACGTGTT	AAATTTGGTT	TGCTTGAAGA	AAGCGAAGAA	900
	GAATCTGCTA	TGGCAGTAGC	ATCAGAAGAA	ACCGATGATC	TTGCTTTAGA	950
	TTTAGATAAT	GGTATTGAAA	TTGAAGATTA	A		981
15						

2) INFORMATION FOR SEQ ID NO: 1706

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus salivarius* subsp. *thermophilus*
 - (C) ACCESSION NUMBER: M94062
- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706

35	GCGTATGCAC	GAGCTCTAGG	TGTTAATATC	GATGAGCTTC	TTTTGTGCGA	50
	GCCTGATTCT	GGTGAGCAAG	GTCTCGAAAT	TGCAGGTAAG	CTGATTGACT	100
	CTGGTGCACT	GGATTTAGTT	GTTGTTGACT	CAGTTGCGGC	CTTCGTACCA	150
	CGTGACAGAAA	TTGATGGAGA	TAGTGGTGAC	AGTCATGTAG	GACTTCAAGC	200
	GCGTATGATG	AGTCAAGCCA	TGCGTAAACT	TTCTGCATCT	ATTAATAAAA	250
40	CAAAAACGAT	TGCTATCTTT	ATTAACCACT	TGCGTGAAAA	AGTTGGTATC	300
	ATGTTTGTA	AC				312

45 2) INFORMATION FOR SEQ ID NO: 1707

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 831 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 50
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: J02967

5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707

	ATGAAAAACA	CAATACATAT	CAACTTCGCT	ATTTTTTTTAA	TAATTGCAAA	50
	TATTATCTAC	AGCAGCGCCA	GTGCATCAAC	AGATATCTCT	ACTGTTGCAT	100
10	CTCCATTATT	TGAAGGAACT	GAAGGTTGTT	TTTTACTTTA	CGATGCATCC	150
	ACAAACGCTG	AAATTGCTCA	ATTCAATAAA	GCAAAGTGTG	CAACGCAAAT	200
	GGCACCAGAT	TCAACTTTCA	AGATCGCATT	ATCACTTATG	GCATTTGATG	250
	CGGAAATAAT	AGATCAGAAA	ACCATATTCA	AATGGGATAA	AACCCCCAAA	300
	GGAATGGAGA	TCTGGAACAG	CAATCATACA	CCAAAGACGT	GGATGCAATT	350
15	TTCTGTTGTT	TGGGTTTCGC	AAGAAATAAC	CCAAAAAATT	AGATTAAATA	400
	AAATCAAGAA	TTATCTCAAA	GATTTTGATT	ATGGAAATCA	AGACTTCTCT	450
	GGAGATAAAG	AAAGAAACAA	CGGATTAACA	GAAGCATGGC	TCGAAAGTAG	500
	CTTAAAAATT	TCACCAGAAG	AACAAATTCA	ATTCCTGCGT	AAAATTATTA	550
	ATCACAATCT	CCCAGTTAAA	AACTCAGCCA	TAGAAAACAC	CATAGAGAAC	600
20	ATGTATCTAC	AAGATCTGGA	TAATAGTACA	AAACTGTATG	GGAAAACCTGG	650
	TGCAGGATTC	ACAGCAAATA	GAACCTTACA	AAACGGATGG	TTTGAAGGGT	700
	TTATTATAAG	CAAATCAGGA	CATAAATATG	TTTTTGTGTC	CGCACTTACA	750
	GGAAACTTGG	GGTCGAATTT	AACATCAAGC	ATAAAAGCCA	AGAAAAATGC	800
	GATCACCATT	CTAAACACAC	TAAATTTATA	A		831

25.

2) INFORMATION FOR SEQ ID NO: 1708

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

40 (B) STRAIN: HH22

(C) ACCESSION NUMBER: M60253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708

45	TTGAAAAAGT	TAATATTTTT	AATTGTAATT	GCTTTAGTTT	TAAGTGCATG	50
	TAATTCAAAC	AGTTCACATG	CCAAAGAGTT	AAATGATTTA	GAAAAAAAAT	100
	ATAATGCTCA	TATTGGTGTT	TATGCTTTAG	ATACTAAAAG	TGGTAAGGAA	150
	GTAATAATTTA	ATTCAGATAA	GAGATTTGCC	TATGCTTCAA	CTTCAAAAGC	200
	GATAAATAGT	GCTATTTTGT	TAGAACAAGT	ACCTTATAAT	AAGTTAAATA	250
50	AAAAAGTACA	TATTAACAAA	GATGATATAG	TTGCTTATTC	TCCTATTTTA	300
	GAAAAATATG	TAGGAAAAGA	TATCACTTTA	AAAGCACTTA	TTGAGGCTTC	350
	AATGACATAT	AGTGATAATA	CAGCAAACAA	TAAAATTATA	AAAGAAATCG	400
	GTGAATCAA	AAAAGTTAAA	CAACGTCTAA	AAGAAGTAGG	AGATAAAGTA	450

	ACAAATCCAG	TTAGATATGA	GATAGAATTA	AATTACTATT	CACCAAAGAG	500
	CAAAAAAGAT	ACTTCAACAC	CTGCTGCTTT	CGGTAAGACT	TTAAATAAAC	550
	TTATCGCAAA	TGGAAAATTA	AGCAAAGAAA	ACAAAAAATT	CTTACTTGAT	600
	TTAATGTAA	ATAATAAAAG	CGGAGATACT	TTAATTAAAG	ACGGTGTTC	650
5	AAAAGACTAT	AAGGTTGCTG	ATAAAAGTGG	TCAAGCAATA	ACATATGCTT	700
	CTAGAAATGA	TGTTGCTTTT	GTTTATCCTA	AGGGCCAATC	TGAACCTATT	750
	GTTTTAGTCA	TTTTTACGAA	TAAAGACAAT	AAAAGTGATA	AGCCAAATGA	800
	TAAGTTGATA	AGTGAAACCG	CCAAGAGTGT	AATGAAGGAA	TTTTAA	846

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2) INFORMATION FOR SEQ ID NO: 1709

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 555 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: M29695

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709

	ATGTCCGCGA	GCACCCCCC	CATAACTCTT	CGCCTCATGA	CCGAGCGCGA	50
	CCTGCCGATG	CTCCATGACT	GGCTCAACCG	GCCGCACATC	GTTGAGTGGT	100
30	GGGGTGGCGA	CGAAGAGCGA	CCGACTCTTG	ATGAAGTGCT	GGAACACTAC	150
	CTGCCCAGAG	CGATGGCGGA	AGAGTCCGTA	ACACCGTACA	TCGCAATGCT	200
	GGGCGAGGAA	CCGATCGGCT	ATGCTCAGTC	GTACGTCGCG	CTCGGAAGCG	250
	GTGATGGCTG	GTGGGAAGAT	GAAACTGATC	CAGGAGTGCG	AGGAATAGAC	300
	CAGTCTCTGG	CTGACCCGAC	ACAGTTGAAC	AAAGGCCTAG	GAACAAGGCT	350
35	TGTCCGCGCT	CTCGTTGAAC	TACTGTTCTC	GGACCCCACC	GTGACGAAGA	400
	TTCAGACCGA	CCCAGACTCCG	AACAACCATC	GAGCCATACG	CTGCTATGAG	450
	AAGGCAGGAT	TCGTGCGGGA	GAAGATCATC	ACCACGCCTG	ACGGGCCGGC	500
	GGTTTACATG	GTTCAAACAC	GACAAGCCTT	CGAGAGAAAG	CGCGGTGTTG	550
	CCTAA					555

40

2) INFORMATION FOR SEQ ID NO: 1710

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: K02987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710

5
 ATGAACCAGA AAAACCCTAA AGACACGCAA AATTTTATTA CTTCTAAAAA 50
 GCATGTAAAA GAAATATTGA ATCACACGAA TATCAGTAAA CAAGACAACG 100
 TAATAGAAAT CGGATCAGGA AAAGGACATT TTACCAAAGA GCTAGTCAAA 150
 ATGAGTCGAT CAGTTACTGC TATAGAAATT GATGGAGGCT TATGTCAAGT 200
 10 GACTAAAGAA GCGGTAAACC CCTCTGAGAA TATAAAAGTG ATTCAAACGG 250
 ATATTCTAAA ATTTTCCTTC CCAAAACATA TAAACTATAA GATATATGGT 300
 AATATTCCTT ATAACATCAG TACGGATATT GTCAAAAGAA TTACCTTTGA 350
 AAGTCAGGCT AAATATAGCT ATCTTATCGT TGAGAAGGGA TTTGCGAAAA 400
 GATTGCAAAA TCTGCAACGA GCTTTGGGTT TACTATTAAT GGTGGAGATG 450
 15 GATATAAAAA TGCTCAAAAA AGTACCACCA CTATATTTTC ATCCTAAGCC 500
 AAGTG TAGAC TCTGTATTGA TTGTTCTTGA ACGACATCAA CCATTGATTT 550
 CAAAGAAGGA CTACAAAAAG TATCGATCTT TTGTTTATAA GTGGGTAAAC 600
 CGTGAATATC GTGTTCTTTT CACTAAAAAC CAATTCCGAC AGGCTTTGAA 650
 GCATGCAAAT GTCATAATA TTAATAAACT ATCGAAGGAA CAATTTCTTT 700
 20 CTATTTTCAA TAGTTACAAA TTGTTTCACT AA 732

2) INFORMATION FOR SEQ ID NO: 1711

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Escherichia coli*

(B) STRAIN: BM2570

(C) ACCESSION NUMBER: M19270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711

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ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTTAACGA GTGAAAAAGT 50
 ACTCAACCAA ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT 100
 ACGAAATTGG AACAGGTAAA GGGCATTTAA CGACGAAACT GGCTAAAATA 150
 AGTAAACAGG TAACGTCTAT TGAATTAGAC AGTCATCTAT TCAACTTATC 200
 45 GTCAGAAAAA TTA AAATCGA ATACTCGTGT CACTTTAATT CACCAAGATA 250
 TTCTACAGTT TCAATTCCCT AACAAACAGA GGTATAAAAT TGTTGGGAAT 300
 ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGTAAAG 350
 CCATGCGTCT GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA 400
 CCTTGGATAT TCACCGAACA CTAGGGTTGC TCTTGACAC TCAAGTCTCG 450
 50 ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA TGCTTTCATC CTAAACCAAG 500
 AGTAAACAGT GTCTTAATAA AACTTACCGG CCATACCACA GATGTTCCAG 550
 ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAAATG GGTCAATCGA 600
 GAATATCGTC AACTGTTTAC TAAAAATCAG TTTCATCAAG CAATGAAACA 650

CGCCAAAGTA	AACAATTTAA	GTACCGTTAC	TTATGAGCAA	GTATTGTCTA	700
TTTTTAATAG	TTATCTATTA	TTTAACGGGA	GGAAATAA		738

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2) INFORMATION FOR SEQ ID NO: 1712

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: RN451
 (C) ACCESSION NUMBER: M17990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712

ATGAACGAGA	AAAATATAAA	ACACAGTCAA	AACTTTATTA	CTTCAAAACA	50
TAATATAGAT	AAAATAATGA	CAAATATAAG	ATTAAATGAA	CATGATAATA	100
TCTTTGAAAT	CGGCTCAGGA	AAAGGGCATT	TTACCCTTGA	ATTAGTACAG	150
AGGTGTAATT	TCGTAAGTGC	CATTGAAATA	GACCATAAAT	TATGCAAAAC	200
TACAGAAAAT	AAACTTGTTG	ATCACGATAA	TTTCCAAGTT	TTAAACAAGG	250
ATATATTGCA	GTTTAAATTT	CCTAAAAACC	AATCCTATAA	AATATTTGGT	300
AATATACCTT	ATAACATAAG	TACGGATATA	ATACGCAAAA	TTGTTTTTGA	350
TAGTATAGCT	GATGAGATTT	ATTTAATCGT	GGAATACGGG	TTTGCTAAAA	400
GATTATTAAA	TACAAAACGC	TCATTGGCAT	TATTTTAAAT	GGCAGAAGTT	450
GATATTTCTA	TATTAAGTAT	GGTTCCAAGA	GAATATTTTC	ATCCTAAACC	500
TAGAGTGAAT	AGCTCACTTA	TCAGATTAAA	TAGAAAAAAA	TCAAGAATAT	550
CACACAAAGA	TAAACAGAAG	TATAATTATT	TCGTTATGAA	ATGGGTAAAC	600
AAAGAATACA	AGAAAATATT	TACAAAAAAT	CAATTTAACA	ATTCTTTAAA	650
ACATGCAGGA	ATTGACGATT	TAAACAATAT	TAGCTTTGAA	CAATTCCTAT	700
CTCTTTTCAA	TAGCTATAAA	TTATTTAATA	AGTAA		735

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2) INFORMATION FOR SEQ ID NO: 1713

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

(C) ACCESSION NUMBER: U00456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713

5	ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
	TGATGTGTCTG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
	AAAAATTCTGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
	CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
	ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
10	AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCCGTTTT	GCATGGCAAA	300
	TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
	CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTG CATG	GACAAATCAC	400
	TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
	ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
15	CTTTGTGAAG	CCGGCACGGT	CAGGTTCTGC	CTTTGGCGTA	ACCAAAGTAA	550
	ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
	GGAAAAATCT	TAATTGAGCA	AGCGATTTCT	GGCTGTGAGG	TCGGCTGCGC	650
	GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
	GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
20	GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTGCGAGGA	800
	ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
	GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
	GTTCTAAACG	AGGTCAATAC	CCTGCCCCGT	TTTACATCGT	ACAGCCGCTA	950
	TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
25	GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 1714

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714

45	GCACAGGTTT	AGTTGGGCTT	GATCTTGCTT	TAGGTATAGG	CGGTGTTCCA	50
	AAAGGAAGAA	TTATAGAAAT	TTATGGRCTT	GAAAGTTCAG	GTAAAACCAC	100
	TCTAACTCTA	CACATTATCG	CAGAATGCCA	AAAAGCAGGT	GGRGTTTGTG	150
	CTTTTATCGA	TGCAGAACAT	GCRCTTGATG	TRAAATATGC	TAAAAATTTG	200
	GGTGTAATA	CAGATGATTT	GTATGTTTCT	CAGCCTGATT	TTGGAGARCA	250
50	AGCCTTAGAA	ATTGTAGAAA	CTATAGCAAG	AAGTGGCGCA	G TAGATCTTA	300
	TCGTAGTAGA	TAGCGTTGCA	GCGCTTACCC	CAAAAGCAGA	AATTGAAGGC	350
	GATATGGGTG	ATCAACATGT	AGGACTTCAA	GCAAGACTTA	TGTCTCAAGC	400
	TCTAAGAAAA	CTTACAGGTA	TAGTTCATAA	AATGAATACC	ACAGTAATTT	450

	TYATCAACCA	AATTCGTATG	AAAATCGGTG	CTATGGGTTA	TGGTACTCCT	500
	GAAACCACAA	CAGGTGGAAA	TGCATTAAAA	TTTTATGCTT	CTGTGCGTTT	550
	AGATGTTAGA	AAAGTAGCAA	CCTTAAACA	AAACGAAGAA	CCTATAGGAA	600
	ACCGCGTTAA	AGTAAAAGTA	GTTAAAAATA	AAGTTGCTCC	TCCATTGAGA	650
5	CAAGCTGAAT	TTGATGTGAT	GTTTGGAGAG	GGTTTAAGCC	GTGAAGGTGA	700
	ATTGATCGAT	TATGGTGTAA	AACTTGATAT	CGTAGATAAA	AGTGGTGCCT	750
	GGTTTTCTTA	TAAAGATAAA	AACTTGGAC	AAGGTAGAGA	AAATTCAAAA	800
	GCTTTCTTAA	AAGAAAAC				818

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2) INFORMATION FOR SEQ ID NO: 1715

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 809 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Abiotrophia adiacens*
(B) STRAIN: ATCC 49175
25 (C) ACCESSION NUMBER: AF124224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715

	TGGTGCTATC	TTAGTAGTAT	CTGCAGCTGA	TGGTCCAATG	CCTCAAACAC	50
30	GTGAACACAT	CTTATTATCA	CGTCAAGTAG	GTGTTCCCTA	CATCGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
	ACACTCCAGT	TGTTGCAGGT	TCTGCTTTAC	GCGCTTTAGA	AGGCGACGCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ACGAATACAT	300
35	TCCAACCTCA	GAACGYGACG	TTGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATCACAGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGTGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTTTCAGA	450
	AGAAACTTCA	AAAACAACTG	TAAGTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGG	GATAACATTG	GTACATTATT	ACGTGGTGTT	550
40	ACACGTGACA	ACATCGAACG	TGGACAAGTT	CTTGCTAAAC	CAGGAACAAT	600
	CACTCCACAT	ACTAAATTCA	AAGCTGAAGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CAGACATCAC	TGGTGTGTTG	GTGTTACCAG	AAGGCGTTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATTCACC	800
45	CAGTAGCGA					809

2) INFORMATION FOR SEQ ID NO: 1716

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*
(B) STRAIN: ATCC 49176
(C) ACCESSION NUMBER: AF124225

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716

	CGGCGCGATC	CTCGTTGTAT	CTGCTGCTGA	CGGCCCAATG	CCACAAACTC	50
	GTGAACACAT	CCTCTTGTCT	CGTCAAGTTG	GTGTTCCCTA	CATCGTAGTA	100
15	TTCTTGAACA	AAGTTGACAT	GGTTGACGAC	GAAGAATTGC	TCGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACC	TCTTGTCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	AACTACGAAG	CTAAAGTTTT	AGAATTGATG	GAACAAGTTG	ATGCTTACAT	300
	TCCAGAACCA	GAACGTGACA	CTGACAAGCC	ATTCATGATG	CCAGTCGAAG	350
20	ACGTATTCTC	TATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGTCAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCGAAGA	450
	AGAAACTTCT	AAGACTACCG	TTACCGGTGT	TGAAATGTTT	CGTAAGTTAT	500
	TGGATTACGC	TGAAGCTGGG	GACAACGTTG	GTACCTTGTT	ACGTGGTGTA	550
	ACTCGTGACC	AAATCCAACG	TGGTCAAGTA	TTATCTAAAC	CAGGTTCAAT	600
25	CACTCCGYAC	ACTAAGTTCG	AAGCTGAAGT	GTACGTATTG	TCTAAAGAAG	650
	AAGGTGGTCG	TCACACTCCA	TTCTTCTCTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCAGGCGACA	ACGTACAAAT	GGTTGTTGAA	TTGATCCACC	800
	CAATCGCGAT	CGAAGAA				817

30

2) INFORMATION FOR SEQ ID NO: 1717

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium accolens*
(B) STRAIN: ATCC 49725

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717

	CGGCGCTATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
50	GCGAGCACGT	TCTGCTTGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTCGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAAATCA	TCGAGCTCGT	150
	GGAGATGGAG	ATCTCCGAGC	TGCTCGCAGA	GCAGGACTAC	GATGAGGAAG	200
	CTCCTATCGT	TCACATCTCC	GCTCTGAAGG	CACTCGAGGG	TGACGAGAAG	250

	TGGGTACAGT	CCATCGTTGA	CCTGATGGAT	GCCTGCGACA	ACTCCATCCC	300
	TGATCCGGAG	CGCGCTACCG	ATCAGCCGTT	CTTGATGCCT	ATCGAGGACA	350
	TCTTCACCAT	TACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGTCGTCTGA	ACGTCAACGA	GGACGTTGAG	ATCATCGGTA	TCCAGGAGAA	450
5	GTCCCAGAAC	ACCACCGTTA	CCGGTATCGA	GATGTTCCGC	AAGATGATGG	500
	ACTACACCGA	GGCTGGCGAC	AACTGTGGTC	TGCTTCTGCG	TGGTACCAAG	550
	CGTGAGGACG	TTGAGCGTGG	CCAGGTTGTT	ATCAAGCCGG	GCGCTTACAC	600
	CCCTCACACC	AAGTTCGAGG	GTTCCGTCTA	CGTCCTGAAG	AAGGAAGAGG	650
	GCGGCCGCCA	CACCCCGYTC	ATGAACAAC	ACCGTCCTCA	GTTCTACTTC	700
10	CGCACCACCG	ACGTTACCGG	TGTTGTGAAC	CTGCCTGAGG	GCACCAGAT	750
	GGTTATGCCT	GGCGACAACG	TTGAGATGTC	TGTTGAGCTC	ATCCAGCCTG	800
	TTGCTATGGA	CGAG				814

15

2) INFORMATION FOR SEQ ID NO: 1718

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*
 (B) STRAIN: ATCC 33031

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718

	CGGCGCCATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GTGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTAGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAGCTGC	TGGAGCTCGT	150
35	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CACCTGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
	TGGGCTAAGC	AGATCCTGGA	GCTCATGGAG	GCTTGCGACA	ACTCCATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGRGGACA	350
	TCTTCACCAT	TACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
40	GGCGTCCTGA	ACCTGAACGA	CGAGGTCGAG	ATCCTGGGCA	TCCGCGAGAA	450
	GTCCACCAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
	ACACCGCAGA	GGCTGGCGAC	AACGCCGCAC	TGCTGCTGCG	TGGCCTGAAG	550
	CGCGAAGATG	TTGAGCGTGG	TCAGATCGTT	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
45	GTGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTATTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCGGAGG	GCACCGAGAT	750
	GGTTATGCCG	GGCGACAACG	TTGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

50

2) INFORMATION FOR SEQ ID NO: 1719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*
 (B) STRAIN: ATCC 43216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719

15	CGGCGCCATC	CTGGTTGTTG	CCGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GCGAGCACGT	TCTGCTGGCY	CGCCAGGTTG	GCGTTCCGTA	CATCCTGGTT	100
	GCACTGAACA	AGTGTGACAT	GGTTGACGAT	GAGGAGCTGC	TGGAGCTCGT	150
	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CTCCGGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
20	TGGGCTAACC	AGATTCTCGA	GCTGATGCAG	GCTTGCGACG	AGTCTATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGWGGACA	350
	TCTTCACCAT	TACCGGTCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGCATCCTGA	ACCTGAACGA	CGAGGTTGAG	ATCCTGGGTA	TCCGCGAGAA	450
	GTCCGAGAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
25	ACACCGCAGA	GGCTGGCRAC	AACGCTGCAC	TGCTGCTGCG	TGGTCTGAAG	550
	CGCGAGGACG	TTGAGCGTGG	CCAGATCATC	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCTGAGG	GCACCGAGAT	750
30	GGTTATGCCG	GGCGACAACG	TYGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

35 2) INFORMATION FOR SEQ ID NO: 1720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720

50	CGGCGCTATC	TTGGTTGTTG	CAGCTACCGA	CGGCCCAATG	CCACAGACTC	50
	GCGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTGGTT	100
	GCACTAAACA	AGTGCGACAT	GGTTGACGAC	GAGGAAATCC	TCGAGCTCGT	150

	CGAGATGGAG	ATCCGCGAAT	TGCTGGCTGA	CCAGGAATTC	GACGAAGAAG	200
	CTCCAATCGT	TCACATCTCC	GCAGTCGGCG	CCTTGGAAGG	CGAAGAGAGG	250
	TGGGTAAACG	CCATCGTTGA	ACTGATGGAT	GCTTGTGACG	AGTCGATCCC	300
	TGATCCAGAC	CGTGCTACCG	ACAAGCCATT	CCTGATGCCT	ATCGAGGACA	350
5	TCTTCACCAT	TACCGGTCGT	GGCACCGTTG	TTACGGGTCG	TGTTGAGCGT	400
	GGTTCCCTGA	AGGTCAACGA	AGAAGTCGAG	ATCATCGGCA	TCAAGGAAAA	450
	GTCCCAGAAG	ACCACCATCA	CCGGTATCGA	AATGTTCCGC	AAGATGCTGG	500
	ACTACACCGA	GGCCGGCGAC	AACGCTGGTC	TGCTGCTTCG	CGGTACCAAG	550
	CGTGAAGACG	TTGAGCGTGG	ACAGGTTATC	GTTGCTCCAG	GTGCTTACAG	600
10	CACCCACAAG	AAGTTCGAAG	GTTCCGTCTA	CGTTCTTTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCTCTA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTTACC	CTGCCTGAGG	GCACCGAG	748

15

2) INFORMATION FOR SEQ ID NO: 1721

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium striatum*
 (B) STRAIN: ATCC 6940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721

	GGCGCTATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCGRTGC	CGCAGACCCG	50
	CGAGCACGTT	CTTCTGGCTC	GCCAGGTGCG	CGTTCCTTAC	ATCCTCGTTG	100
	CACTGAACAA	GTGCGACATG	GTTGACGACG	AGGAAATTAT	CGAGCTCGTC	150
35	GAGATGGAGA	TCCGCGAACT	GCTCGCAGAG	CAGGACTACG	ATGAGGAAGC	200
	TCCGATCGTT	CACATCTCTG	CTCTGAAGGC	TCTTGAGGGC	GRCGAGAAGT	250
	GGGTACAGGC	TATCGTTGAC	CTGATGCAGG	CTTGCGATGA	CTCCATCCCG	300
	GATCCGGAGC	GCGAGCTGGA	CAAGCCGTTC	CTGATGCCAA	TCGAGGACAT	350
	CTTCAACATC	ACCGGCCGCG	GTACCGTTGT	TACTGGCCGT	GTTGAGCGTG	400
40	GCTCCCTGAA	CGTCAACGAG	GACGTTGAGA	TCATCGGTAT	CCAGGACARG	450
	TCCATCTCCA	CCACCGTTAC	CGGTATCGAG	ATGYTCCGCA	AGATGATGGA	500
	CTACACCGAG	GCTGGCGACA	ACTGTGGTCT	GCTTCTGCGT	GGTACCAAGC	550
	GTGAAGAGGT	TGAGCGCGGC	CAGGTTGTTA	TTAAGCCGGG	CGCTTACACC	600
	CCTCACACCC	AGTTCGAGGG	TTCCGTCTAC	GTCCTGAAGA	AGGAAGAGGG	650
45	CGGCCGCCAC	ACCCCGTTCA	TGGACAAC	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTTACCGGC	GTCATCAAGC	TGCCTGAGGG	CACCGAGATG	750
	GTTATGCCTG	GCGACAACGT	CGAGATGTCY	GTCGAGCTGA	TCCAGCCGGT	800
	CGCTATGGAC	GAG				813

50

2) INFORMATION FOR SEQ ID NO: 1722

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025
 (C) ACCESSION NUMBER: AF124220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722

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15  CGGAGCTATC  TTAGTAGTAT  CTGCTGCTGA  TGGCCCTATG  CCTCAAAC TC      50
    GTGAACACAT  CTTGTTATCT  CGTAACGTTG  GTGTTCCCTA  CATCGTTGTA      100
    TTCTTAAACA  AAATGGATAT  GGTTGACGAT  GAAGAATTAC  TTGAATTAGT      150
    TGAAATGGAA  GTTCGTGACT  TATTAAC TGA  ATACGACTTC  CCAGGCGACG      200
20  ACACTCCAGT  TATCGCAGGT  TCAGCGTTGA  AAGCTTTAGA  AGGCGACGCT      250
    TCATACGAAG  AAAAAATCTT  AGAATTAATG  GCTGCTGTTG  ACGAATATAT      300
    CCCAACACCA  GTTCGTGATA  CTGACAAACC  ATTCATGATG  CCAGTCGAAG      350
    ACGTATTCTC  AATCACTGGT  CGTGGTACTG  TTGCAACTGG  TCGTGTG TAA      400
    CGTGGACAAG  TTCGCGTTGG  TGACGAAGTT  GAAATCGTAG  GTATCGCTGA      450
25  CGAAACTGCT  AAAACAACTG  TTACAGGTGT  TGAAATGTTC  CGTAAATTGT      500
    TAGACTACGC  TGAAGCAGGT  GACAACATCG  GTGCTTTGTT  ACGTGGTGT T      550
    GCACGTGAAG  ATATCCAACG  TGGACAAGTA  TTGGCTAAAC  CAGCTTCAAT      600
    CACTCCACAT  ACAA AATTCT  CTGCAGAAGT  TTATGTTCTA  ACTAAAGAAG      650
    AAGGTGGACG  TCATACTCCA  TTCTTCACTA  ACTACCGTCC  TCAGTTCTAC      700
30  TTCCGTACAA  CTGACGTAA C  TGGTGTAGTT  GATCTACCAG  AAGGTACTGA      750
    AATGGTWATG  CCTGGGGATA  ACGTAACTAT  GGAAGTTGAA  TTGATYCACC      800
    CAATYCGGGT  AGAAGAC                                817
  
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35

2) INFORMATION FOR SEQ ID NO: 1723

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
 (B) STRAIN: ATCC 14018

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723

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    TGGCGCAATC  CTCGTGGTTG  CTGCTACCGA  CGGTCCAATG  GCTCAGACCC      50
    GTGAACACGT  CTTGCTTGCT  AAGCAGGTCG  GCGTTCCAAA  AATTCTTGTT      100
  
```

	GCTTTGAACA	AGTGCGATAT	GGTTGACGAC	GAAGAGCTTA	TCGATCTCGT	150
	TGAAGAAGAG	GTCCGTGACC	TCCTCGAAGA	AAACGGCTTC	GATCGCGATT	200
	GCCCAGTCYT	CCGTACTTCC	GCTTACGGCG	CTTTGCATGA	TGACGCTCCA	250
	GACCACGACA	AGTGGGTAGA	GACCGTCAAG	GAACTCATGA	AGGCTGTTGA	300
5	CGAGTACATC	CCAACCCCAA	CTCACGATCT	TGACAAGCCA	TTCTTGATGC	350
	CAATCGAAGA	TGTGTTCCACC	ATCTCCGGTC	GTGGTYCCGT	TGTCACCGGT	400
	CGTGTTGAGC	GTGGTAAGCT	CCCAATCAAC	ACCCAGTTG	AGATCGTTGG	450
	TTTGCGCGAT	ACCCAGACCA	CCACCGTCAC	CTCTATCGAG	ACCTTCCACA	500
	AGCAGATGGA	TGAGGCAGAG	GCTGGCGATA	ACACTGGTCT	TCTTCTCCGC	550
10	GGTATCAACC	GTACCGACGT	TGAGCGTGGT	CAGGTGTGG	CTGCTCCAGG	600
	TTCTGTGACT	CCACACACCA	AGTTCGAAGG	CGAAGTTTAC	GTCTTGACCA	650
	AGGACGAAGG	TGGCCGTCAC	TCGCCATTCT	TCTCCAATA	CCGTCCACAG	700
	TTCTACTTCC	GTACCACCGA	TGTTACTGGC	GTTATCACCT	TGCCAGACGG	750
	CATCGAAATG	GTTCAGCCAG	GCGATCACGC	AACCTTCACT	GTTGAGTTGA	800
15	TCCAGGCTAT	CGCAATGGAA	GAG			823

2) INFORMATION FOR SEQ ID NO: 1724

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Listeria innocua*
- (B) STRAIN: ATCC 33090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
40	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGAACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTT	CGTAAATTAC	500
45	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTAA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
50	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1725

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACATAT	TCTTACTTTC	ACGTCAAGTT	GGTGTTCAT	ACATCGTTGT	100
	ATTCATGAAC	AAATGTGACA	TGGTTGACGA	TGAAGAATTA	CTTGAATTAG	150
20	TTGAAATGGA	AATTCGTGAT	CTATTAAGTG	AATATGAATT	CCCTGGCGAC	200
	GACATTCCTG	TAATCAAAGG	TTCAGCTCTT	AAAGCACTTC	AAGGTGAAGC	250
	TGATTGGGAA	GCTAAAATTG	ACGAGTTAAT	GGAAGCTGTA	GATTCTTACA	300
	TTCCAAGTCC	AGAACGTGAT	ACTGACAAAC	CATTTCATGAT	GCCAGTTGAG	350
	GATGTATTCT	CAATCACTGG	TCGTGGAACA	GTTGCAACTG	GACGTGTTGA	400
25	ACGTGGACAA	GTTAAAGTTG	GTGACGAAGT	AGAAGTTATC	GGTATTGAAG	450
	AAGAAAGCAA	AAAAGTAGTA	GTAAGTGGAG	TAGAAATGTT	CCGTAAATTA	500
	CTAGACTACG	CTGAAGCTGG	CGACAACATT	GGCGCACTTC	TACGTGGTGT	550
	TGCTCGTGAA	GATATCCAAC	GTGGTCAAGT	ATTAGCTAAA	CCAGGTTCGA	600
	TTACTCCACA	TACTAACTTC	AAAGCTGAAA	CTTATGTTTT	AACTAAAGAA	650
30	GAAGGTGGAC	GTCATACTCC	ATTCTTCAAC	AACTACCGCC	CACAATTCTA	700
	TTTCCGTACT	ACTGACGTAA	CTGGTATTGT	TACACTTCCA	GAAGGTACTG	750
	AAATGGTAAT	GCCTGGTGAT	AACATTGAGC	TTGCAGTTGA	ACTAATTGCA	800
	CCAATCGCTA	TCGAAGAC				818

35

2) INFORMATION FOR SEQ ID NO: 1726

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: LSPQ 5093202

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
5	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCCW	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATCGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTT	CGTAAATTAC	500
10	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACR	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
15	AATGGTAAYG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1727

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria seeligeri*
 (B) STRAIN: ATCC 35967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGTGATG	200
40	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCC	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
45	AGAAAGCAAA	AAAGTAATAG	TAAGTGGAGT	AGAAATGTTT	CGTAAATTAC	500
	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAT	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
50	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1728

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 25923

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728

	CGGTGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
20	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAR	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTARTG	GAAGCTGTAG	ATACTTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGCTACTG	TTGCTACAGG	CCGTGTTGAA	400
25	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
	CACATCTAAA	ACAACTGTTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	650
30	GTGGACGTCA	CACTCCATTC	TTCTCAAAC	ATCGTCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACGTG	TGTTGTTCAC	TTACCAGAAG	GTACTGAAAT	750
	GGTAATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCAA	800
	TCGCGATTGA	AGAC				814

35

2) INFORMATION FOR SEQ ID NO: 1729

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 15305

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACACAT	TCTTTTATCA	CGTRACGTTG	GTGYTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAY	GAAGAATTAT	TAGAATTRGT	150
	AGAAATGGAA	GTTCGTGRCT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACGCT	250
5	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTYCAT	300
	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAATC	GARATCATCG	GTATGCAAGA	450
	AGAATCAAGC	AAAACAACCTG	TTACTGGTGT	AGAAATGTTT	CGTAAATTAT	500
10	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCATTATT	ACGTGGTGTG	550
	TCACGTGATG	ATGTACAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTACTAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGATGT	TTACGTTTTA	TCTAAAGATG	650
	AAGGTGGTCG	TCATACGCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTTACTA	CTGACGTAAC	TGGTGTTGTT	AACTTACCAG	AAGGTACTGA	750
15	AATGGTTATG	CCTGGCGATA	ACGTTGAAAT	GGATGTTGAA	TTAATTTCTC	800
	CAATCGCTAT	TGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1730

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus simulans*
 (B) STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730

35	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
40	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
45	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGTG	550
	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
50	TTCCGTTACTA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTGATCGCTC	800
	CAATCGCGAT	TGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1731

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591
 (C) ACCESSION NUMBER:

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731

	CGGAGCTATC	CTTGTAAGTTG	CTTCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTA	100
20	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTTCAGA	ATACGACTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCACTTGA	AGGCGACGAA	250
	AAATACGAAG	ACATCATCAT	GGAATTGATG	AGCACTGTTG	ATGAGTACAT	300
	TCCAGAACCA	GAACGTGATA	CTGACAAACC	TTTACTTCTT	CCAGTTGAAG	350
25	ATGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTCGTGTCAA	CGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
	AGATATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTT	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
30	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAATTCCAG	CAGGAACAGA	750
	AATGGTTATG	CCTGGTGATA	ACGTTACTAT	CGAAGTTGAA	TTGATTACAC	800
35	CAATCGCCGT	AGAACAA				817

2) INFORMATION FOR SEQ ID NO: 1732

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732

	CGGAGCTATC	CTTGTAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TATTGTCAGA	ATACGACTTC	CCAGGTGACG	200
5	ATCTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATACGAAG	ACATCGTTAT	GGAATTGATG	AACACAGTTG	ATGAGTATAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTATCG	TTAAAGTCAA	CGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
10	AGAAACTCRA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTAG	GTGTCCTTCT	TCGTGGTGT	550
	CAACGTGATG	AAATCGAACG	TGGACAAGTT	ATCGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	CTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
15	TTCCGTACTA	CTGACGTTAC	AGGTTCAATC	GAACTTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTGACAAT	CGACGTTGAG	TTGATTCCACC	800
	CAATCGCCGT	AGAACAA				817

20

2) INFORMATION FOR SEQ ID NO: 1733

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733

	CGGTGCGATC	CTTGTAGTAG	CATCTACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TTCTTTTCAGA	ATACGATTTT	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGATTCT	250
	AAATACGAAG	ACATCATCAT	GGACTTGATG	AACACTGTTG	ACGAATACAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGTTGCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTGTTG	TTCGTGTCAA	TGACGAAGTT	GAAATCGTTG	GTCTTAAAGA	450
	AGACATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGRAGG	TATTGCCGGA	GATAACGTCG	GTGTTCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTGCAC	CTGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAACTTCCTG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAA				817

2) INFORMATION FOR SEQ ID NO: 1734

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Agrobacterium tumefaciens*
 (C) ACCESSION NUMBER: x99673
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734

	AACATGATCA	CCGGTGCTGC	CGAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
	GGCTGCCGAC	GGCCCCGATGC	CACAGACCCG	CGAGCACATC	CTGCTTGCCC	100
	GTCAGGTGGG	CGTTCCGGCC	ATCGTCGTGT	TCCTCAACAA	GGTCGACCAG	150
20	GTTGACGACG	CCGAGCTTCT	CGAGCTCGTC	GAGCTTGAAG	TTCGCGAACT	200
	TCTGTTCGTCC	TACGACTTCC	CGGGCGACGA	TATCCCGATC	ATCAAGGGTT	250
	CGGCACTTGC	TGCTCTTGAA	GATTCTGACA	AGAAGATCGG	TGAAGACGCG	300
	ATCCGCGAGC	TGATGGCTGC	TGTCGACGCC	TACATCCCGA	CGCCTGAGCG	350
	TCCGATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
25	CGGGTTCGTGG	TACGGTTGTG	ACGGGTCGCG	TTGAGCGCGG	TATCGTCAAG	450
	GTTGGTGAAG	AAGTCGAAAT	CGTCGGCATC	CGTCCGACCT	CGAAGACGAC	500
	TGTTACCGGC	GTTGAAATGT	TCCGCAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACAT	CGGTGCACTC	GTTGCGGGCG	TTACCCGTGA	CGGCGTCGAG	600
	CGTGGTCAGA	TCCTGTGCAA	GCCGGGTTTCG	GTCAAGCCGC	ACAAGAAGTT	650
30	CATGGCAGAA	GCCTACATCC	TGACGAAGGA	AGAAGGCGGC	CGTCATACGC	700
	CGTTCTTCAC	GAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACTGACGTT	750
	ACCGGTATCG	TTTCGCTTCC	TGAAGGCACG	GAAATGGTTA	TGCCTGGCGA	800
	CAACGTCACT	GTTGAAGTCG	AGCTGATCGT	TCCGATCGCG	ATGGAAGAAA	850
35	AGCTGCGCTT	CGCTATCCGC	GAAGGCGGCC	GTACCGTCGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1735

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 885 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus subtilis*
 (B) STRAIN: 168
 (C) ACCESSION NUMBER: Z99104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735

	ATGATCACTG	GTGCTGCGCA	AATGGACGGA	GCTATCCTTG	TAGTATCTGC	50
	TGCTGATGGC	CCAATGCCAC	AAACTCGTGA	GCACATCCTT	CTTTCTAAAA	100
	ACGTTGGTGT	ACCATACATC	GTTGTATTCT	TAAACAAATG	CGACATGGTA	150
5	GACGACGAAG	AGCTTCTTGA	ACTAGTTGAA	ATGGAAGTTC	GCGATCTTCT	200
	TAGCGAATAC	GACTTCCCTG	GTGATGATGT	ACCAGTTGTT	AAAGGTTCTG	250
	CTCTTAAAGC	TCTTGAAGGA	GACGCTGAGT	GGGAAGCTAA	AATCTTCGAA	300
	CTTATGGATG	CGGTTGATGA	GTACATCCCA	ACTCCAGAAC	GCGACACTGA	350
	AAAACCATTC	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	400
10	GTACAGTTGC	TACTGGCCGT	GTAGAACGCG	GACAAGTTAA	AGTCGGTGAC	450
	GAAGTTGAAA	TCATCGGTCT	TCAAGAAGAG	AACAAGAAAA	CAACTGTTAC	500
	AGGTGTTGAA	ATGTTCCGTA	AGCTTCTTGA	TTACGCTGAA	GCTGGTGACA	550
	ACATTGGTGC	CCTTCTTCGC	GGTGTATCTC	GTGAAGAAAT	CCAACGTGGT	600
	CAAGTACTTG	CTAAACCAGG	TACAATCACT	CCACACAGCA	AATTCAAAGC	650
15	TGAAGTTTAC	GTTCTTTCTA	AAGAAGAGGG	TGGACGTCAT	ACTCCATTCT	700
	TCTCTAACTA	CCGTCCTCAG	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	750
	ATCATCCATC	TTCCAGAAGG	CGTAGAAATG	GTTATGCCTG	GAGATAACAC	800
	TGAAATGAAC	GTTGAACTTA	TTTCTACAAT	CGCTATCGAA	GAAGGAACTC	850
	GTTTCTCTAT	TCGTGAAGGC	GGACGTACTG	TTGGT		885
20.						

2) INFORMATION FOR SEQ ID NO: 1736

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*
 (B) STRAIN: DSM 2151
 (C) ACCESSION NUMBER: P33165

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736

40	ATGGTTACTG	GTGCTGCTCA	GATGGACGGT	GCTATCATTG	TAGTTGCTGC	50
	TACTGATGGT	CCGATGCCTC	AGACTCGTGA	GCACATCCTT	TTGGCTCGTC	100
	AGGTAAACGT	TCCGAAGCTG	GTTGTATTCA	TGAACAAGTG	CGATATGGTT	150
	GAAGATGCTG	AGATGTTGGA	ACTTGTTGAA	ATGGAAATGA	GAGAATTGCT	200
	TTCATTCTAT	GATTTTCGACG	GTGACAATAC	TCCGATCATT	CAGGGTTCTG	250
45	CTCTTGGTGC	ATTGAACGGC	GTAGAAAAAT	GGGAAGACAA	AGTAATGGAA	300
	CTGATGGAAG	CTGTTGATAC	TTGGATTCCA	CTGCCTCCGC	GCGATGTTGA	350
	TAAACCTTTC	TTGATGCCGG	TAGAAGACGT	GTTCTCTATC	ACAGGTCGTG	400
	GTAAGTGTAGC	TACAGGTCGT	ATCGAAACTG	GTGTTATCCA	TGTAGGTGAT	450
	GAAATCGAAA	TCCTCGGTTT	GGGTGAAGAT	AAGAAATCAG	TTGTAACAGG	500
50	TGTTGAAATG	TTCCGCAAAC	TTCTGGATCA	GGGTGAAGCT	GGTGACAACG	550
	TAGGTCTGTT	GCTTCGTGGT	GTTGACAAGA	ACGAAATCAA	ACGTGGTATG	600
	GTTCTTTGTA	AACCGGGTCA	GATTAAACCT	CACTCTAAAT	TCAAAGCAGA	650
	GGTTTATATC	CTGAAGAAAG	AAGAAGGTGG	TCGTCACACT	CCATTCCATA	700

ACAAATATCG	TCCTCAGTTC	TACCTGCGTA	CTATGGACTG	TACAGGTGAA	750
ATCACTCTTC	CGGAAGGAAC	TGAAATGGTA	ATGCCGGGTG	ATAACGTAAC	800
TATCACTGTA	GAGTTGATCT	ATCCGGTTGC	ACTGAACATC	GGTCTTCGTT	850
TCGCTATCCG	CGAAGGTGGA	CGTACAGTAG	GT		882

5

2) INFORMATION FOR SEQ ID NO: 1737

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
 (B) STRAIN: U78183
 (C) ACCESSION NUMBER: U78183

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737

25	AATATGATTA	CAGGAGCAGC	TCAAATGGAT	GCAGCGATAC	TTTtagTTGC	50
	TGCTGATAGT	GGTGCTGAGC	CTCAAACAAA	AGAGCATTTG	CTTCTTGCTC	100
	AAAGAATGGG	AATAAAGAAA	ATAATAGTTT	TTTTAAATAA	ATTGGACTTA	150
	GCAGATCCTG	AACTTGTTGA	GCTTGTTGAA	GTTGAAGTTT	TAGAACTTGT	200
	TGAAAAATAT	GGCTTTTCAG	CTGATACTCC	AATAATCAAA	GGTTCAGCTT	250
30	TTGGGGCTAT	GTCAAATCCA	GAAGATCCTG	AATCTACAAA	ATGCGTTAAA	300
	GAAGTTCTTG	AATCTATGGA	TAATTATTTT	GATCTTCCAG	AAAGAGATAT	350
	TGACAAGCCA	TTTTTGCTTG	CTGTTGAAGA	TGTATTTTCT	ATTCAGGAA	400
	GAGGCACTGT	TGCTACTGGG	CGTATTGAAA	GAGGTATTAT	TAAAGTTGGT	450
	CAAGAAGTTG	AAATAGTTGG	AATTAAAGAA	ACCAGAAAAA	CTACTGTTAC	500
35	TGGTGTTGAA	ATGTTCCAGA	AAATTCTTGA	GCAAGGTCAA	GCAGGGGATA	550
	ATGTTGGTCT	TCTTTTGAGA	GGCGTTGATA	AAAAAGACAT	TGAGAGGGGG	600
	CAAGTTTGTG	CAGCTCCAGG	TACAATTACT	CCACACAAGA	AATTTAAAGC	650
	TTCAATTTAT	TGTTTGACTA	AAGAAGAAGG	CGGTAGGCAC	AAGCCATTTT	700
	TCCCAGGGTA	TAGACCACAG	TTCTTTTTTA	GAACAACCGA	TGTTACTGGA	750
40	GTTGTTGCTT	TAGAGGGCAA	AGAAATGGTT	ATGCCTGGTG	ATAATGTTGA	800
	TATTATTGTT	GAGCTGATCT	CTTCAATAGC	TATGGATAAG	AATGTAGAAT	850
	TTGCTGTTCG	AGAAGGTGGA	AGAACCGTTG	CTTCAGGA		888

45

2) INFORMATION FOR SEQ ID NO: 1738

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Brevibacterium linens*
 (B) STRAIN: DSM 20425
 (C) ACCESSION NUMBER: X76863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738

10	AACATGATCA	CCGGTGCCGC	TCAGATGGAC	GGTGCGATCC	TCGTCGTCGC	50
	CGCTACCGAC	GGACCGATGC	CCCAGACCCG	TGAGCACGTG	CTGCTCGCGC	100
	GTCAGGTCGG	CGTTCCCTAC	ATCGTCGTGG	CTCTGAACAA	GTCCGACATG	150
	GTCGATGACG	AGGAGCTCCT	CGAGCTCGTC	GAATTCGAGG	TCCGCGACCT	200
	GCTCTCGAGC	CAGGACTTCG	ACGGAGACAA	CGTCCGGTC	ATTCCGGTGT	250
15	CCGCTCTCAA	GGCGCTGGAA	GGCGACGAGA	AGTGGGTCAA	GAGCGTTCAG	300
	GATCTCATGG	CTGCCGTCGA	TGACAACGTT	CCGGAGCCGG	AGCGCGATGT	350
	CGACAAGCCG	TTCCTCATGC	CCGTCGAGGA	CGTCTTCACG	ATCACCCGGTC	400
	GTGGAACCGT	CGTCACCGGT	CGTGTCGAGC	GCGGCGTGCT	CCTGCCTAAC	450
	GACGAAATCG	AAATCGTCCG	CATCAAGGAG	AAGTCGTCCA	AGACGACTGT	500
20	CACCGCTATC	GAGATGTTCC	GCAAGACCCT	GCCGGATGCC	CGTGCAGGTG	550
	AGAACGTCGG	TCTGCTCCTC	CGCGGCACCA	AGCGCGAGGA	TGTTGAGCGC	600
	GGTCAGGTCA	TCGTGAAGCC	GGGTTCGATC	ACCCCGCACA	CCAAGTTCGA	650
	GGCTCAGGTC	TACATCCTGA	GCAAGGACGA	GGGCGGACGT	CACAACCCGT	700
	TCTACTCGAA	CTACCGTCCG	CAGTTCTACT	TCCGGACCAC	GGACGTCACC	750
25	GGTGTTCATCA	CGCTGCCCGA	GGGCACCGAG	ATGGTCATGC	CCGGCGACAA	800
	CACCGATATG	TCGGTCGAGC	TCATCCAGCC	GATCGCTATG	GAGGACCGCC	850
	TCCGCTTCGC	AATCCGCGAA	GGTGGCCGCA	CCGTCGGCGC	CGGT	894

30

2) INFORMATION FOR SEQ ID NO: 1739

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: F/IC-Cal-13
 (C) ACCESSION NUMBER: L22216

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739

	ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
	AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
50	AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
	GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
	CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGCGGATC	300

	ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
	AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	AGCGCGGCAT	CGTGAAGGTC	450
	GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
5	CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
	GGCCAGGTTT	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
10	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
	CGTGTGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
	TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCCGC		888

15

2) INFORMATION FOR SEQ ID NO: 1740

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*
 (B) STRAIN: S85
 (C) ACCESSION NUMBER: X76866

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740

	AACATGGTGA	CTGGTGCTGC	TCAGATGGAC	GGCGCTATCC	TCGTTGTTGC	50
	CGCTACTGAC	GGTCCGATGC	CGCAGACTCG	CGAACACATC	CTTCTCGCTC	100
35	ACCAGGTTGG	CGTGCCGAAG	ATCGTCGTGT	TCATGAACAA	GTGCGACATG	150
	GTTGACGATG	CTGAAATTCT	CGACCTCGTC	GAAATGGAAG	TTCGCGAACT	200
	CCTCTCCAAG	TATGACTTCG	ACGGTGACAA	CACCCCGATC	ATCCGTGGTT	250
	CCGCTCTCAA	GGCCCTCGAA	GGCGATCCGG	AATACCAGGA	CAAGGTCATG	300
	GAATCATGA	ACGCTTGCGA	CGAATACATC	CCGCTCCCGC	AGCGCGATAC	350
40	CGACAAGCCG	TTCTTCATGC	CGATCGAAGA	CGTGTTACG	ATTACTGGCC	400
	GCGGCACTGT	CGCTACTGGC	CGTATCGAAC	GCGGTGTCGT	TCGCTTGAAC	450
	GACAAGGTTG	AACGTATCGG	TCTCGGTGAA	ACCACCGAAT	ACGTCATCAC	500
	CGGTGTTGAA	ATGTTCCGTA	AGCTCCTCGA	CGACGCTCAG	GCAGGTGACA	550
	ACGTTGGTCT	CCTCCTCCGT	GGTGCTGAAA	AGAAGGACAT	CGTCCGTGGC	600
45	ATGGTTCTCG	CAGCTCCGAA	GTCTGTCACT	CCGCACACCG	AATTTAAGGC	650
	TGAAATCTAC	GTTCTCACGA	AGGACGAAGG	TGGCCGTCAC	ACGCCGTTCA	700
	TGAATGGCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTTACTGGT	750
	ACGATCCAGC	TCCCGGAAGG	TGTCGAAATG	GTTACTCCGG	GTGACACGGT	800
	CACGATCCAC	GTGAACCTCA	TCGCTCCGAT	CGCTATGGAA	AAGCAGCTCC	850
50	GCTTCGCTAT	CCGTGAAGGT	GGACGTACTG	TTGGTGCTGG	C	891

2) INFORMATION FOR SEQ ID NO: 1741

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Flavobacterium ferrugineum*
 (B) STRAIN: DSM 13524
 (C) ACCESSION NUMBER: X76867

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741

	AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGTGCTATCT	TAGTTGTGGC	50
	TGCATCAGAC	GGTCCTATGC	CTCAACAAA	AGAACACATC	CTGCTTGCTG	100
20	CCCAGGTAGG	TGTACCTAAA	ATGGTTGTGT	TTCTGAATAA	AGTTGACCTC	150
	GTTGACGACG	AAGAGCTCCT	GGAGCTGGTT	GAGATCGAGG	TTCGCGAAGA	200
	ACTGACTAAA	CGCGGTTTCG	ACGGCGACAA	CACTCCAATC	ATCAAAGGTT	250
	CCGCTACAGG	CGCCCTCGCT	GGTGAAGAAA	AGTGGGTAA	AGAAATTGAA	300
	AACCTGATGG	ACGCTGTTGA	CAGCTACATC	CCACTGCCTC	CTCGTCCGGT	350
25	TGATCTGCCG	TTCCTGATGA	GCGTAGAGGA	CGTATTCTCT	ATCACTGGTC	400
	GTGGTACTGT	TGCTACCGGT	CGTATCGAGC	GTGGCCGTAT	CAAAGTTGGT	450
	GAGCCTGTTG	AGATCGTAGG	TCTGCAGGAG	TCTCCCTGA	ACTCTACCGT	500
	TACAGGTGTT	GAGATGTTCC	GCAAATCCT	CGACGAAGGT	GAAGCTGGTG	550
	ATAACGCCGG	TCTCCTCCTC	CGTGGTGTG	AAAAAACACA	GATCCGTCGC	600
30	GGTATGGTAA	TCGTTAAACC	CGGTTCCATC	ACTCCGCACA	CGGACTTCAA	650
	AGGCGAAGTT	TACGTACTGA	GCAAAGACGA	AGGTGGCCGT	CACACTCCAT	700
	TCTTCAACAA	ATACCGTCCT	CAATTCTACT	TCCGTACAAC	TGACGTTACA	750
	GGTGAAGTAG	AACTGAACGC	AGGAACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CACCAACCTG	ACCGTTAAAC	TGATCCAACC	GATCGCTATG	GAAAAAGGTC	850
35	TGAAATTTCG	GATCCGCGAA	GGTGGCCGTA	CCGTAGGTGC	AGGA	894

2) INFORMATION FOR SEQ ID NO: 1742

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: 26695
 (C) ACCESSION NUMBER: AE000626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742

	AACATGATCA	CCGGTGCGGC	GCAAATGGAC	GGAGCGATTT	TGGTTGTTTC	50
	TGCAGCTGAT	GGCCCTATGC	CTCAAAC TAG	GGAGCATATC	TTATTGTCTC	100
5	GTC AAGTAGG	CGTGCCTCAC	ATCGTTGTTT	TCTTAAACAA	ACAAGACATG	150
	G TAGATGACC	AAGAATTGTT	AGAACTTGTA	GAAATGGAAG	TGCGCGAATT	200
	GTTGAGCGCG	TATGAATTTT	CTGGCGATGA	CACTCCTATC	G TAGCGGGTT	250
	CAGCTTTAAG	AGCTTTAGAA	GAAGCAAAGG	CTGGTAATGT	GGGTGAATGG	300
	GGTGAAAAAG	TGCTTAAACT	TATGGCTGAA	GTGGATGCCT	ATATCCCTAC	350
10	TCCAGAAAGA	GACACTGAAA	AACTTTCTT	GATGCCGGTT	GAAGATGTGT	400
	TCTCTATTGC	GGGTAGAGGG	ACTGTGGTTA	CAGGTAGGAT	TGAAAGAGGC	450
	GTGGTGAAAG	TAGGCGATGA	AGTGGAATC	GTTGGTATCA	GACCTACACA	500
	AAAAACGACT	GTAACCGGTG	TAGAAATGTT	TAGGAAAGAG	TTGGAAAAAG	550
	GTGAAGCCGG	CGATAATGTG	GGCGTGCTTT	TGAGAGGAAC	TAAAAAAGAA	600
15	GAAGTGGAAC	GCGGTATGGT	TCTATGCAAA	CCAGGTTCTA	TCACTCCGCA	650
	CAAGAAATTT	GAGGGAGAAA	TTTATGTCCT	TTCTAAAGAA	GAAGGCGGGA	700
	GACACACTCC	ATTCTTCACC	AATTACCGCC	CGCAATTCTA	TGTGCGCACA	750
	ACTGATGTGA	CTGGCTCTAT	CACCCTTCCT	GAAGGCGTAG	AAATGGTTAT	800
	GCCTGGCGAT	AATGTGAAAA	TCACTGTAGA	GTTGATTAGC	CCTGTTGCGT	850
20	TAGAGTTGGG	AACTAAATTT	GCGATTCTGT	AAGGCGGTAG	GACCGTTGGT	900
	GCTGGT					906

25 2) INFORMATION FOR SEQ ID NO: 1743

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*
 (B) STRAIN: IFO 3333
 (C) ACCESSION NUMBER: M17788

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743

	AACATGATCA	CCGGCGCCGC	TCAGATGGAC	GGCGCGATCC	TCGTGGTCGC	50
	CGCTACCGAC	GGCCCGATGG	CCCAGACCCG	TGAGCACGTG	CTCCTGGCCC	100
	GCCAGGTCGG	CGTGCCGGCC	CTGCTCGTGG	CCCTGAACAA	GTCGGACATG	150
45	GTGGAGGACG	AGGAGCTCCT	CGAGCGTGTC	GAGATGGAGG	TCCGGCAGCT	200
	GCTGTCCTCC	AGGAGCTTCG	ACGTCGACGA	GGCCCCGGTC	ATCCGCACCT	250
	CCGCTCTGAA	GGCCCTCGAG	GGCGACCCCC	AGTGGGTCAA	GTCCGTCTGAG	300
	GACCTCATGG	ATGCCGTGGA	CGAGTACATC	CCGGACCCGG	TGCGCGACAA	350
	GGACAAGCCG	TTCCTGATGC	CGATCGAGGA	CGTCTTCACG	ATCACCGGCC	400
50	GTGGCACCGT	GGTGACCGGT	CGCGCCGAGC	GCGGCACCCT	GAAGATCAAC	450
	TCCGAGGTCG	AGATCGTCGG	CATCCGCGAC	GTGCAGAAGA	CCACTGTCAC	500
	CGGCATCGAG	ATGTTCCACA	AGCAGCTCGA	CGAGGCCTGG	GCCGGCGAGA	550
	ACTGCGGTCT	GCTCGTGCGC	GGTCTGAAGC	GCGACGACGT	CGAGCGCGGC	600

	CAGGTGCTGG	TGGAGCCGGG	CTCCATCACC	CCGCACACCA	ACTTCGAGGC	650
	GAACGTCTAC	ATCCTGTCCA	AGGACGAGGG	TGGGCGTCAC	ACCCCGTTCT	700
	ACTCGAACTA	CCGCGCGCAG	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	750
	GTCATCACGC	TGCCCCGAGGG	CACCGAGATG	GTCATGCCCCG	GCGACACCAC	800
5	CGAGATGTCG	GTCGAGCTCA	TCCAGCCGAT	CGCCATGGAG	GAGGGCCTCG	850
	GCTTCGCCAT	CCGCGAGGGT	GGCCGCACCG	TGGGCTCCGG	C	891

10 2) INFORMATION FOR SEQ ID NO: 1744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: Erdmann
 (C) ACCESSION NUMBER: X63539

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744

	AACATGATCA	CCGGCGCCGC	GCAGATGGAC	GGTGCGATCC	TGGTGGTCGC	50
	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	CGAGCACGTT	CTGCTGGCGC	100
	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	CGCTGAACAA	GGCCGACGCA	150
30	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	GAGATGGAGG	TCCGCGAGCT	200
	GCTGGCTGCC	CAGGAATTCT	ACGAGGACGC	CCCGGTTGTG	CGGGTCTCGG	250
	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	GGGTTGCCTC	TGTCGAGGAA	300
	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	GACCCGGTCC	GCGAGACCGA	350
	CAAGCCGTTC	CTGATGCCGG	TCGAGGACGT	CTTCACCATT	ACCGGCCGCG	400
35	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	GCGTGATCAA	CGTGAACGAG	450
	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	ACCACCAAGA	CCACCGTCAC	500
	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	CCAGGGCCAG	GCGGGCGACA	550
	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	GCGAGGACGT	CGAGCGTGGC	600
	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	CCGCACACCG	AGTTCGAAGG	650
40	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	CGGCCGGCAC	ACGCCGTTCT	700
	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTGACCGGT	750
	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	GTGATGCCCCG	GTGACAACAC	800
	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	CGCCATGGAC	GAAGGTCTGC	850
45	GTTTCGCGAT	CCGCGAGGGT	GGCCGCACCG	TGGGCGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1745

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(B) STRAIN: G37

(C) ACCESSION NUMBER: U39732

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745

	AATATGATCA	CAGGTGCTGC	ACAAATGGAT	GGAGCTATTC	TAGTTGTTTC	50
	AGCAACTGAT	AGTGTGATGC	CCCAAACCCG	CGAGCACATC	TTACTTGCCC	100
	GCCAAGTAGG	GGTTCCTAAA	ATGGTAGTTT	TTCTAAACAA	GTGTGATATT	150
15	GCTAGTGATG	AAGAGGTACA	AGAACTTGTT	GCTGAAGAAG	TACGTGATCT	200
	GTTAACTTCC	TATGGTTTTG	ATGGTAAGAA	CACTCCTATT	ATTTATGGCT	250
	CAGCTTTAAA	AGCATTGGAA	GGTGATCCAA	AGTGGGAGGC	TAAGATCCAT	300
	GATTTGATTA	AAGCAGTTGA	TGAATGGATT	CCAACTCCTA	CACGTGAAGT	350
	AGATAAACCT	TTCTTATTAG	CAATTGAAGA	TACGATGACC	ATTACTGGTA	400
20	GAGGTACAGT	TGTTACAGGA	AGAGTTGAAA	GAGGTGAACT	CAAAGTAGGT	450
	CAAGAAGTTG	AAATTGTTGG	TTTAAAACCA	ATTAGAAAAG	CAGTTGTTAC	500
	TGGAATTGAA	ATGTTCAAAA	AGGAACCTGA	TTCAGCAATG	GCTGGTGACA	550
	ATGCTGGGGT	ATTATTACGT	GGTGTGTAAC	GTAAAGAAGT	TGAAAGAGGT	600
	CAAGTTTTAG	CAAACCAGG	CTCTATTAAA	CCGCACAAGA	AATTTAAAGC	650
25	TGAGATCTAT	GCTTTAAAGA	AAGAAGAAGG	TGGTAGACAC	ACTGGTTTTT	700
	TAAACGGTTA	CCGTCCTCAA	TTCTATTTCC	GTACCACTGA	TGTAACGGT	750
	TCTATTGCTT	TAGCTGAAAA	TACTGAAATG	GTTCTACCTG	GTGATAATGC	800
	TTCTATTACT	GTTGAGTTAA	TTGCTCCTAT	CGCTTGTGAA	AAAGGTAGTA	850
	AGTTCTCAAT	TCGTGAAGGT	GGTAGAACTG	TAGGGGCAGG	C	891

30

2) INFORMATION FOR SEQ ID NO: 1746

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

45 (B) STRAIN: MS11

(C) ACCESSION NUMBER: L36380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746

50	AACATGATTA	CCGGCGCCGC	ACAAATGGAC	GGTGCAATCC	TGGTATGTTC	50
	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	CGAACACATC	CTGCTGGCCC	100
	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	TCATGAACAA	ATGCGACATG	150
	GTCGACGATG	CCGAGCTGTT	CCAACCTGGT	GAAATGGAAA	TCCGCGACCT	200

	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	CTGCCCCGATC	GTACAAGGTT	250
	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	CTTACGAAGA	AAAAATCTTC	300
	GAAGTGGCTA	CCGCATTGGA	CAGATACATC	CCGACTCCCG	AGCGTGCCGT	350
	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	CGTGTCTCTC	ATTTCGGGCC	400
5	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	GAGGTATCAT	CCACGTTGGT	450
	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	ACCCAAAAAA	CCACCTGTAC	500
	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAG	GCGGGCGACA	550
	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	GTGAAGACGT	AGAACGCGGT	600
	CAGGTATTGG	CCAAACGGGG	TACTATCACT	CCTCACACCA	AGTTCAAAGC	650
10	AGAAGTGATC	GTATTGAGCA	AAGAAGAGGG	CGGCCCCCAT	ACCCCGTTTT	700
	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	GTACCACTGA	CGTAACCGGC	750
	ACGATTACTT	TGGAAAAAGG	TGTGGAAATG	GTAATGCCGG	GTGAGAACGT	800
	AACCATTACT	GTAGAAGTGA	TTGCGCCTAT	CGCTATGGAA	GAAGGTCTGC	850
	GCTTTGCGAT	TCGCGAAGGC	GGCCGTACCG	TGGGTGCCGG	C	891
15						

2) INFORMATION FOR SEQ ID NO: 1747

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*
 (B) STRAIN: Madrid E
 (C) ACCESSION NUMBER: Z54170

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747

35	AATATGATAA	CTGGTGCCGC	TCAGATGGAT	GGTGCTATAT	TAGTAGTTTC	50
	TGCTGCTGAT	GGTCCTATGC	CTCAAACCTAG	AGAACATATA	TTACTGGCAA	100
	AACAGGTAGG	TGTACCTGCT	ATGGTAGTAT	TTTTGAATAA	AGTAGATATG	150
	GTAGATGATC	CTGACCTATT	AGAATTAGTT	GAGATGGAAG	TAAGAGAATT	200
	ATTATCAAAA	TATGGTTTCC	CTGGTAATGA	AATACCTATT	ATTAAAGGTT	250
40	CTGCACTTCA	AGCTTTAGAA	GGAAAACCTG	AAGGTGAAAA	AGCTATTAAT	300
	GAGTTAATGA	ATGCAGTAGA	TACGTATATA	CCTCAGCCTA	TAGAGCTACA	350
	AGATAAACCT	TTTTTAATGC	CAATAGAGGA	TGTATTTTCT	ATTTCAAGCA	400
	GAGGTACCGT	TGTAAGTGGT	AGAGTGGAGT	CAGGCATAAT	TAAGGTGGGT	450
	GAAGAAATTG	AAATAGTAGG	TCTAAAAAAT	ACGCAAAAAA	CGACTTGTAC	500
45	AGGTGTAGAA	ATGTTTCAGAA	AATTACTTGA	TGAAGGACAA	TCTGGAGATA	550
	ATGTCGGTAT	ATTACTACGT	GGTACAAAAA	GAGAAGAAGT	AGAAAGAGGA	600
	CAAGTACTTG	CAAAACCTGG	GAGCATAAAA	CCGCATGATA	AATTTGAAGC	650
	TGAAGTGTAT	GTGCTTAGTA	AAGAGGAAGG	TGGACGTCAT	ACCCCATTTA	700
	CTAATGATTA	TCGCCCACAG	TTCTATTTTA	GAACAACAGA	TGTTACCGGC	750
50	ACAATAAAAT	TGCCTTCTGA	TAAGCAGATG	GTTATGCCTG	GAGATAATGC	800
	TACTTTTTCA	GTAGAATTAA	TTAAGCCGAT	TGCTATGCAA	GAAGGGTTAA	850
	AATTCTCTAT	ACGTGAAGGT	GGTAGAACAG	TAGGAGCCGG	T	891

2) INFORMATION FOR SEQ ID NO: 1748

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: LT2 trpE91
 15 (C) ACCESSION NUMBER: X55116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748

20	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	GGCGCGATCC	TGGTTGTTGC	50
	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	TGAGCACATC	CTGCTGGGTC	100
	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	ATGCGACATG	150
	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	TTCGCGAACT	200
	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	GTTCGTGGTT	250
	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	GAAAATCATC	300
25	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	CCGGAACCAG	AGCGTGCGAT	350
	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	ATCTCCGGTC	400
	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	CAAAGTGGGC	450
	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	CTACCTGTAC	500
	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	GCCGGTGAGA	550
30	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	CGAACGTGGT	600
	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	AGTTCGAATC	650
	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	ACTCCGTTCT	700
	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	CGTGACTGGT	750
	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	800
35	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	GACGGTCTGC	850
	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	TTGGCGCGGG	C	891

40 2) INFORMATION FOR SEQ ID NO: 1749

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 881 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
 (B) STRAIN: DSM 50426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749

	ATGATCACTG	GTGCTGCACA	GATGGACGGC	GCGATTCTGG	TAGTCGCTTC	50
	AACAGACGGT	CCAATGCCAC	AGACTCGTGA	GCACATCCTG	CTTTCTCGTC	100
5	AGGTTGGCGT	ACCATTTCATC	ATCGTATTCA	TGAACAAATG	TGACATGGTA	150
	GATGACGAAG	AGCTGTTAGA	GCTAGTTGAG	ATGGAAGTGC	GTGAACTGTT	200
	ATCAGAATAC	GATTTCCCAG	GTGATGACTT	ACCGGTAATC	CAAGGTTTCAG	250
	CTCTGAAAGC	GCTAGAAGGC	GAGCCAGAGT	GGGAAGCAAA	AATCCTTGAA	300
	TTAGCAGCGG	CGCTGGATTG	TTACATTCCA	GAACCACAAC	GTGACATCGA	350
10	TAAGCCGTTT	CTACTGCCAA	TCGAAGACGT	ATTCTCAATT	TCAGGCCGTG	400
	GTACAGTAGT	AACAGGTCGT	GTTGAGCGTG	GTATTGTACG	CGTAGGCGAC	450
	GAAGTTGAAA	TCGTTGGTGT	ACGTGCGACA	ACTAAGACAA	CGTGTACTGG	500
	TGTAGAAATG	TTCCGTAAAC	TGCTTGACGA	AGGTCGTGCA	GGTGAGAACT	550
	GTGGTATTTT	GTTACGTGGT	ACTAAGCGTG	ATGACGTAGA	ACGTGGTCAA	600
15	GTATTAGCGA	AGCCAGGTTT	AATCAACCCA	CACACTACTT	TTGAATCAGA	650
	AGTTTACGTA	CTGTCAAAAG	AAGAAGGTGG	TCGTCACACG	CCATTCTTCA	700
	AAGGCTACCG	TCCACAGTTC	TACTTCCGTA	CAACTGACGT	AACCGGTACT	750
	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	ATGCCAGGCG	ATAACATCAA	800
	GATGGTAGTG	ACACTGATTT	GCCCAATCGC	GATGGACGAA	GGTTTACGCT	850
20	TCGCAATCCG	TGAAGGCGGT	CGTACAGTGG	T		881

2) INFORMATION FOR SEQ ID NO: 1750

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Stigmatella aurantiaca*
- (B) STRAIN: DW4
- (C) ACCESSION NUMBER: X82820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750

40

	AACATGATCA	CGGGCGCGGC	GCAGATGGAC	GGAGCGATTG	TGGTGGTGTC	50
	CGCGGCCGAC	GGCCCGATGC	CCCAGACGCG	TGAGCACATC	CTGCTGGCCA	100
	GGCAGGTGGG	CGTGCCCTAC	ATCGTCGTCT	TCCTGAACAA	GGTGGACATG	150
	CTGGACGATC	CGGAGCTGCG	CGAGCTGGTG	GAGATGGAGG	TGCGCGACCT	200
45	GCTCAAGAAG	TACGAGTTCC	CGGGCGACAG	CATCCCCATC	ATCCCTGGCA	250
	GCGCGCTCAA	GGCGCTGGAG	GGAGACACCA	GCGACATCGG	CGAGGGAGCG	300
	ATCCTGAAGC	TGATGGCGGC	GGTGGACGAG	TACATCCCGA	CGCCGCAGCG	350
	TGCGACGGAC	AAGCCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCCATCG	400
	CAGGCCGAGG	AACGGTGGCG	ACGGGCCGAG	TGGAGCGCGG	CAAGATCAAG	450
50	GTGGGCGAGG	AAGTGGAGAT	CGTGGGGATC	CGTCCGACGC	AGAAGACGGT	500
	CATCACGGGG	GTGGAGATGT	TCCGCAAGCT	GCTGGACGAG	GGCATGGCGG	550
	GAGACAACAT	CGGAGCGCTG	CTGCGAGGCC	TGAAGCGCGA	GGACCTGGAG	600
	CGTGGGCGAG	TGCTGGCGAA	CTGGGGGAGC	ATCAACCCGC	ACACGAAGTT	650

	CAAGGCGCAG	GTGTACGTGC	TGTCGAAGGA	AGAGGGAGGG	CGGCACACGC	700
	CGTTCTTCAA	GGGATACCGG	CCGCAGTTCT	ACTTCCGGAC	GACGGACGTG	750
	ACCGGAACGG	TGAAGCTGCC	GGACAACGTG	GAGATGGTGA	TGCCGGGAGA	800
	CAACATCGCC	ATCGAGGTGG	AGCTCATTAC	TCCGGTCGCC	ATGGAGAAGG	850
5	AGCTGCCGTT	CGCCATCCGT	GAGGGTGGCC	GCACGGTGGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1751

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Thiomonas cuprina*
 (B) STRAIN: Hoe5
 (C) ACCESSION NUMBER: x76871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1751

25

	AACATGATCA	CCGGTGCGGC	CCAGATGGAC	GGCGCCATCC	TGGTCGTGTC	50
	CGCCGCCGAC	GGCCCCATGC	CCCAAACCCG	CGAGCACATC	CTGCTGGCGC	100
	GTCAGGTGGG	CGTGCCCTAC	ATCATCGTGT	TCCTCAACAA	GTGCGACATG	150
	GTCGACGACG	CCGAGCTGCT	CGAACTCGTC	GAGATGGAAG	TGCGCGAGCT	200
30	GCTGTCCAAG	TACGACTTCC	CCGGTGACGA	CACCCCCATC	ATCAAGGGCT	250
	CGGCCAAGCT	GGCCCTCGAA	GGCGACAAGG	GCGAACTGGG	CGAAGGCGCC	300
	ATTCTCAAGC	TGGCCGAGGC	CCTGGACACC	TACATCCCCA	CGCCCGAGCG	350
	GGCCGTCGAC	GGCGCGTTCC	TCATGCCCGT	GGAAGACGTG	TTCTCCATCT	400
	CCGGGCGCGG	CACGGTGGTC	ACCGGGCGTG	TGGAGCGCGG	CATCATCAAG	450
35	GTCGGCGAGG	AAATCGAGAT	TGTCGGCCTC	AAGCCCACCC	TCAAGACCAC	500
	CTGCACCGGC	GTGGAAATGT	TCAGGAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACGT	CGGCATCTTG	CTGCGCGGCA	CCAAGCGCGA	GGAAGTCGAG	600
	CGCGGCCAGG	TGCTGTGCAA	ACCGGGCTCG	ATCAAGCCCC	ACACCCACTT	650
	CACCGCCGAG	GTGTACGTGC	TGAGCAAGGA	CGAGGGCGGC	CGCCACACCC	700
40	CCTTCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGCAC	CACCGACGTC	750
	ACCGGCGCCA	TCGAACTGCC	CAAGGACAAG	GAAATGGTCA	TGCCCGGCGA	800
	TAATGTGAGC	ATCACCGTCA	AGCTCATCGC	CCCCATCGCC	ATGGAAGAAG	850
	GCCTGCGCTT	CGCCATCCGC	GAAGGCGGCC	GCACCGTCGG	CGCCGGC	897

45

2) INFORMATION FOR SEQ ID NO: 1752

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: AE001202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752

```

10 AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC      50
   TGC GCCTGAC GGC GTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC      100
   GTCAGGTTGG TGTTCCCTCC ATCATTGTTT TTTTGAACAA GGTTGATTTG      150
   GTTGATGATC CTGAGTTGCT AGAGCTGGTG GAAGAAGAGG TCGGTGATGC      200
15 GCTTGCTGGA TATGGGTTT CGCGTGAGAC GCCTATCGTC AAGGGGTCTG      250
   CGTTTAAAGC TCTGCAGGAT GGC GCTTCCC CGGAGGATGC AGCTTGATT      300
   GAGGAACTGC TTGCGGCCAT GGATTCCCTAC TTTGAAGACC CAGTGCGTGA      350
   CGACGCAAGA CCTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTCTG      400
   GGC GTGGTAC CGTTGTCACG GGGCGCATCG AATGTGGGGT AATTAGTCTG      450
20 AATGAAGAGG TCGAGATCGT CGGGATTAAG CCCACTAAGA AAACAGTGGT      500
   TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA ATTGCAGGTG      550
   ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAAGA GGTTGAGCGC      600
   GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA      650
   GGC GCAGATC TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCTT      700
25 TTTTTCAAGG TTATCGTCCG CAGTTTTATT TTAGA ACTAC TGACATTACC      750
   GGTACGATTT CTCTTCCTGA AGGGGTAGAC ATGGTGAAGC CGGGGGATAA      800
   CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG GACAAGGGTC      850
   TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT          894

```

30

2) INFORMATION FOR SEQ ID NO: 1753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ureaplasma urealyticum*
 (B) STRAIN: ATCC 33697
 45 (C) ACCESSION NUMBER: Z34275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753

```

50 AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC      50
   TGCATCTGAT GGG GTTATGG CTCAA ACTAA AGAACATATT TTATTAGCAC      100
   GTCAAGTTGG TGTTCCAAAA ATCGTTGTTT TCTTAAACAA ATGTGATTTC      150
   ATGACAGATC CAGATATGCA AGATCTTGTT GAAATGGAAG TTCGTGAATT      200
   ATTATCTAAA TATGGATTG ATGGCGATAA CACACCAGTT ATTCGTGGTT      250

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	CAGGTCTTAA	GGCTTTAGAA	GGAGATCCAG	TTTGAGAAGC	AAAAATTGAT	300
	GAATTAATGG	ACGCAGTTGA	TTCATGAATT	CCATTACCAG	AACGTAGTAC	350
	TGACAAACCA	TTCTTATTAG	CAATTGAAGA	TGTATTACACA	ATTCAGGAC	400
	GTGGTACAGT	AGTAACTGGA	CGTGTTGAAC	GTGGTGTATT	AAAAGTTAAT	450
5	GATGAGGTTG	AAATTGTTGG	TCTAAAAGAC	ACTCAAAAAA	CTGTTGTTAC	500
	AGGAATTGAA	ATGTTTAGAA	AATCATTAGA	TCAAGCTGAA	GCTGGTGATA	550
	ATGCTGGTAT	TTTATTACGT	GGTATTAAAA	AAGAAGATGT	TGAACGTGGT	600
	CAAGTACTTG	TAAAACCAGG	ATCAATTAAA	CCTCACCGTA	CTTTTACTGC	650
	TAAAGTTTAT	ATTCTTAAAA	AAGAAGAAGG	TGGACGTCAT	ACACCTATTG	700
10	TTTCAGGATA	CCGTCCACAA	TTCTATTTTA	GAACAACAGA	TGTAACAGGT	750
	GCTATTTTCAT	TACCTGCTGG	TGTTGATTTG	GTTATGCCAG	GTGATGACGT	800
	TGAAATGACT	GTAGAATTAA	TTGCTCCAGT	TGCGATTGAA	GATGGATCTA	850
	AATTCTCAAT	CCGTGAAGGT	GGTAAACTG	TAGGTCATGG	T	891

15

2) INFORMATION FOR SEQ ID NO: 1754

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 909 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wolinella succinogenes*
 (B) STRAIN: DSM 1740
 30 (C) ACCESSION NUMBER: X76862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754

	AACATGATTA	CAGGTGCTGC	TCAAATGGAT	GGCGCGATTC	TTGTTGTTTC	50
35	TGCGGCGGAT	GGCCCCATGC	CCCAAAC TAG	GGAGCACATT	CTTCTTTCTC	100
	GACAAGTAGG	CGTTCCTTAC	ATCGTGGTTT	TCTTGAACAA	AGAAGATATG	150
	GTTGATGACG	CTGAGCTTCT	TGAGCTTGTT	GAAATGGAAG	TTAGAGAACT	200
	TCTTAGCAAC	TACGACTTCC	CTGGAGATGA	CACTCCTATC	GTTGCAGGTT	250
	CCGCTCTTAA	AGCTCTTGAA	GAGGCTAACG	ACCAGGAAAA	TGTTGGCGAG	300
40	TGGGGCGAGA	AAGTATTGAA	GCTTATGGCT	GAGGTTGACC	GATATATTCC	350
	TACGCCTGAG	CGAGATGTGG	ATAAGCCTTT	CCTTATGCCT	GTTGAAGACG	400
	TATTCTCCAT	CGCGGGTCGT	GGAACCGTTG	TGACAGGAAG	AATTGAAAGA	450
	GGCGTGTTTA	AAGTCGGTGA	CGAAGTAGAA	ATCGTTGGTA	TCCGAAACAC	500
	ACAAAAACA	ACCGTAACTG	GCGTTGAGAT	GTTCCGAAAA	GAGCTCGACA	550
45	AGGGTGAGGC	GGGTGACAAC	GTTGGTGTTT	TTTTGAGAGG	CACCAAGAAA	600
	GAAGATGTTG	AGAGAGGTAT	GGTTCTTTGT	AAAATAGGTT	CTATCACTCC	650
	TCACACTAAC	TTTGAAGGTG	AAGTTTACGT	TCTTTCCAAA	GAGGAAGGCG	700
	GACGACACAC	TCCATTCTTC	AATGGATACC	GACCTCAGTT	CTATGTTAGA	750
	ACTACAGACG	TTACCGGTTT	TATCTCTCTT	CCTGAGGGCG	TAGAGATGGT	800
50	TATGCCTGGT	GACAACGTTA	AGATCAATGT	TGAGCTTATC	GCTCCTGTAG	850
	CCCTCGAAGA	GGGAACACGA	TTCGCGATCC	GTGAAGGTGG	TCGAACCGTT	900
	GGTGCGGGT					909

2) INFORMATION FOR SEQ ID NO: 1755

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755

15

ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
AGGTTGGTGT	TCCGTACATC	ATCGTGTTC	TGAACAAGTG	CGACAGTGTG	150
GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
20 GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300
ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	AGCGCGGCAT	CGTGAAGGTC	450
25 GGC GAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
30 TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
CGTGTGCATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCTGGC		888

35

2) INFORMATION FOR SEQ ID NO: 1756

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756

TGAAAGTTCA GGTAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50

AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 5 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1757

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: ATCC 4229

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757

TGAAAGTTCA GGTAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 30 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

35

2) INFORMATION FOR SEQ ID NO: 1758

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 45 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 50 (B) STRAIN: ATCC 7064
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758

5 TGAAAGTTCA GGTAAAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388
 10

2) INFORMATION FOR SEQ ID NO: 1759

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- 25 (B) STRAIN: ATCC 13472
- (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759

30 TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC 50
 AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT 100
 CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC 150
 ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 35 CCGAAAGCAG AGATTGAAGG TGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA 350
 AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT 388

40

2) INFORMATION FOR SEQ ID NO: 1760

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 bases
- 45 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
- (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760

```

5  AAACGACAGT TTCATTACAT GCAATTGCAG AAGTACAACG TCAAGGTGGA      50
   CAAGCAGCAT TCATCGATGC GGAGCACGCA ATGGATCCTG TATATGCACA      100
   AAAATTAGGC GTTAACATAG ATGAATTACT ATTATCACAG CCTGATACAG      150
   GGGAGCAAGG ATTAGAAATC GCAGAAGCAC TTGTACGAAG TGGTGCGGTT      200
   GACATTATCG TAATTGACTC TGTAGCAGCT CTTGTACCGA AAGCAGAGAT      250
   TGAAGGAGAC ATGGGTGACT CACACGTAGG TTTACAAGCA CGTTTAATGT      300
10  CACAAGCACT TCGTAAGCTT TCAGGAGCAA TCAACAAATC AAAAACAATT      350
   GCAATCTTTA TTAACCAAAT TCGT                                374

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15 2) INFORMATION FOR SEQ ID NO: 1761

(i) SEQUENCE CHARACTERISTICS:

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20  (A) LENGTH: 381 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Bacillus pseudomycoides
    (B) STRAIN: NRRL BD-10

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761

```

30  GGAAAGTTCA GGTAAAACAA CGGTTTCCTT ACATGCGATT GCAGAAGTGC      50
   AACGTCAAGG TGGACAAGCG GCATTTATTG ATGCGGAGCA TGCGATGGAT      100
   CCTGTATATG CACAAAAGTT AGGTGTTAAT ATTGATGAGT TACTATTATC      150
   GCAGCCTGAT ACAGGAGAAC AAGGTTTAGA AATCGCAGAA GCATTAGTAC      200
35  GAAGCGGTGC GATTGATATC ATTGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CCAAAGCAG AAATCGAAGG GGAAATGGGT GACTCCACG TTGGTTTACA      300
   AGCGCGTTTA ATGTCACAAG CACTTCGTAA GCTTTCTGGT GCGATTAACA      350
   AATCAAAAAC AATTGCAATC TTCATTAACC A                                381

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40

2) INFORMATION FOR SEQ ID NO: 1762

(i) SEQUENCE CHARACTERISTICS:

```

45  (A) LENGTH: 388 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Bacillus thuringiensis

```

(B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762

5	TGAAAGTTCA	GGTAAAACGA	CAGTTTCATT	ACATGCAATT	GCAGAAGTAC	50
	AACGTCAAGG	TGGACAAGCA	GCATTCATCG	ATGCGGAGCA	CGCAATGGAT	100
	CCTGTATATG	CACAAAAATT	AGGCGTTAAC	ATAGATGAAT	TACTATTATC	150
	ACAGCCTGAT	ACAGGGGAGC	AAGGATTAGA	AATCGCGGAA	GCACTTGTAC	200
	GAAGTGGTGC	GGTTGACATT	ATCGTAATTG	ACTCTGTAGC	AGCTCTTGTA	250
10	CCGAAAGCAG	AGATTGAAGG	CGACATGGGT	GACTCACACG	TAGGTTTACA	300
	AGCACGTTTA	ATGTCACAAG	CAC TTCGTAA	GCTTTCAGGA	GCAATCAACA	350
	AATCAAAAAC	AATTGCAATC	TTTATTAACC	AAATTCGT		388

15

2) INFORMATION FOR SEQ ID NO: 1763

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 388 bases
20	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Bacillus thuringiensis</i>
	(B) STRAIN: HER 1418

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763

	TGAAAGTTCA	GGTAAAACGA	CAGTTTCATT	ACATGCAATT	GCAGAAGTAC	50
	AACGTCAAGG	TGGACAAGCA	GCATTCATTG	ATGCGGAGCA	CGCAATGGAT	100
	CCTGTATATG	CACAAAAATT	AGGCGTTAAC	ATAGATGAAT	TACTATTATC	150
35	ACAGCCTGAT	ACAGGGGAGC	AAGGATTGGA	AATCGCGGAA	GCACTTGTAC	200
	GAAGTGGTGC	GGTTGACATT	ATCGTAATTG	ACTCTGTAGC	AGCTCTTGTA	250
	CCGAAAGCAG	AGATTGAAGG	CGATATGGGT	GACTCACACG	TAGGTTTACA	300
	AGCACGTTTA	ATGTCACAAG	CAC TTCGTAA	GCTTTCAGGA	GCAATCAACA	350
	AATCAAAAAC	AATTGCAATC	TTTATTAACC	AAATTCGT		388

40

2) INFORMATION FOR SEQ ID NO: 1764

(i) SEQUENCE CHARACTERISTICS:

45	(A) LENGTH: 358 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764

5 CTCCTATCTG GATTATGCGA TGTCGGTCAT TGTTGGCCGT GCGCTGCCGG 50
 ATGTCCGAGA TGGCCTGAAG CCGGTACACC GTCGCGTACT ATACGCCATG 100
 AACGTATTGG GCAATGACTG GAACAAAGCC TATAAAAAAT CTGCCCCGTGT 150
 CGTGGGTGAC GTCATCGGTA AATACCACCC TCATGGTGAT ACTGCCGTAT 200
 10 ACGACACCAT TGTACGTATG GCGCAGCCCT TCTCCCTGCG TTACATGCTG 250
 GTAGATGGCC AGGGTAACTT TGGTTCGGTC GACGGCGACT CCGCCGCAGC 300
 GATGCGTTAT ACGGAAATCC GTATGTCGAA GATCGCCCAT GAACTGATGG 350
 CCGACCTC 358

15

2) INFORMATION FOR SEQ ID NO: 1765

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 365 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*

(B) STRAIN: ATCC 11296

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765

TTAAGAACTC TTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG 50
 CTGCCGGATG TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTTTA 100
 35 CGCCATGAAC GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCAG 150
 CCCGTGTCTG TGGTGACGTA ATCGGTAAAT ACCACCCGCA CGGCGACTCC 200
 GCGGTATACG ACACCATCGT GCGTATGGCG CAGCCGTTCT CGCTGCGTTA 250
 CATGCTGGTG GACGGCCAGG GTAACCTTGG TTCCATCGAC GGCGACTCCG 300
 CCGCGGCGAT GCGTTATACC GAAATTCGTC TGGCGAAAAT CGCTCATGAG 350
 40 CTGATGGCCG ATCTT 365

2) INFORMATION FOR SEQ ID NO: 1766

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766

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AAGAGCTCGT ATCTGGATTA TCGCATGTCG GTCATTGTTG GCCGTGCGCT      50
GCCGGATGTC CGAGATGGCC TGAAACCGGT ACACCGTCGC GTACTTTACG      100
CCATGAACGT ATTGGGCAAT GACTGGAACA AAGCCTATAA AAAATCCGCC      150
10 CGTGTCTGTTG GTGACGTAAT CGGTAAATAC CACCCTCATG GTGATACCGC      200
CGTTTATGAC ACCATTGTAC GTATGGCACA GCCATTCTCC TTGCGTTATA      250
TGCTGGTCGA TGGCCAGGGT AACTTCGGTT CTGTTCGATGG CGACTCCGCC      300
GCAGCGATGC GTTATACGGA AATCCGTATG TCGAAAATCG CCCA          344

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15

2) INFORMATION FOR SEQ ID NO: 1767

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 345 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767

```

AACTCTTATC TGGATTATGC GATGTCGGTC ATTGTTGGCC GTGCGCTGCC      50
GGATGTCCGA GATGGCCTGA AGCCGGTACA CCGTCGCGTA CTTTACGCCA      100
35 TGAACGTATT GGGCAATGAC TGGAACAAAG CCTATAAAAA ATCAGCCCGT      150
GTCGTTGGTG ACGTAATCGG TAAATACCAC CCGCACGGCG ACTCCGCGGT      200
ATACGACACC ATCGTTCGTA TGGCGCAGCC GTTCTCGCTG CGTTACATGC      250
TGGTGGACGG CCAGGGTAAC TTTGGTTCCA TCGACGGCGA CTCCGCCGCG      300
GCGATGCGTT ATACCGAAAT TCGTCTGGCG AAAATCGCTC ATGAG          345

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2) INFORMATION FOR SEQ ID NO: 1768

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 356 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768

5 CTTATCTGGA TTATGCGATG TCGGTCATTG TTGGCCGTGC GCTGCCGGAT 50
 GTCCGAGATG GCCTGAAGCC GGTACACCGT CGCGTACTTT ACGCCATGAA 100
 CGTATTGGGC AATGACTGGA ACAAAGCCTA TAAAAAATCA GCCCGTGTCTG 150
 TTGGTGACGT AATCGGTAAA TACCACCCGC ACGGCGACTC CGCGGTATAC 200
 10 GACACCATCG TCGGTATGGC GCAGCCGTTT TCGCTGCGTT ACATGCTGGT 250
 GGACGGCCAG GGTAACCTTG GTTCCATCGA CGGCGACTCC GCCGCGGCGA 300
 TCGGTTATAC CGAAATTCGT CTGGCGAAAA TCGCTCATGA GCTGATGGCC 350
 GATCTT 356

15

2) INFORMATION FOR SEQ ID NO: 1769

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 361 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 29011

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769

TAAGAACTCT TATCTGGATT ATGCGATGTC GGTCATTGTT GGCCGTGCGC 50
 TGCCGGATGT CCGAGATGGC CTGAAGCCGG TACACCGTCG CGTACTTTAC 100
 35 GCCATGAACG TATTGGGCAA TGAATGGAAC AAAGCCTATA AAAAATCAGC 150
 CCGTGTCTGT GGTGACGTAA TCGGTAAATA CCACCCGCAC GGCGACTCCG 200
 CGGTATACGA CACCATCGTG CGTATGGCGC AGCCGTTCTC GCTGCGTTAC 250
 ATGCTGGTGG ACGGCCAGGG TAACTTTGGT TCCATCGACG GCGACTCCGC 300
 CGCGGCGATG CGTTATACCG AAATTCGTCT GGCGAAAATC GCTCATGAGC 350
 40 TGATGGCCGA T 361

2) INFORMATION FOR SEQ ID NO: 1770

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

(B) STRAIN: ATCC 13824

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770

	TAAGAACTCT	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	50
	TGCCGGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	100
10	GCCATGAACG	TATTGGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCAGC	150
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCACCCGCAC	GGCGACTCCG	200
	CGGTATACGA	CACCATCGTG	CGTATGGCGC	AGCCGTTCTC	GCTGCGTTAC	250
	ATGCTGGTGG	ACGGCCAGGG	TAACTTTGGT	TCCATCGACG	GCGATTCCGC	300
	CGCGGCGATG	CGTTATACCG	AAATTCGTCT	GGCGAAAATC	GCTCATGAGC	350
15	TGATGGCCGA	TCTTG				365

2) INFORMATION FOR SEQ ID NO: 1771

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Klebsiella terrigena*

(B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771

35	TCGTATCTGG	ATTATGCGAT	GTCGGTCATT	GTTGGCCGTG	CGCTGCCGGA	50
	TGTCCGAGAT	GGGTTGAAAC	CGGTACACCG	TCGCGTACTT	TACGCCATGA	100
	ACGTATTGGG	CAATGACTGG	AACAAAGCCT	ATAAAAAATC	CGCCCGTGTC	150
	GTTGGTGACG	TAATCGGTAA	ATATCACCTT	CACGGTGATA	CCGCCGTTTA	200
	TGACACCATT	GTACGTATGG	CGCAGCCATT	CTCCTTGCGT	TATATGCTGG	250
40	TCGATGGCCA	GGGTAAGTTC	GGTTCTGTCT	ATGGCGACTC	CGCCGCAGCG	300
	ATGCGTTATA	CGGAAATCCG	TATGTCGAAA	ATCGCCACAG	AGCTGATGGC	350
	CGACCTC					357

45

2) INFORMATION FOR SEQ ID NO: 1772

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 968 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 5 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772

```

10 CAGTACACAG GCGAGTTCTT TTTGCGATGA GTGAGTTAAG TAATGATTGG      50
   AATAAGCCGT ATAAAAAATC TGCTCGTGTA GTAGGGGATG TCATTGGTAA      100
   ATATCATCCT CATGGGGATA CAGCTGTTTA TGACACTATT GTTCGTATGG      150
   CTCAGCCCTT TTCCATGCGT TATATGCTGA TTGATGGGCA GGGTAATTTT      200
   GGCTCTGTAG ATGGAGATGC TCCAGCTGCC ATGCGTTACA CTGAAGTAAG      250
   AATGTCCAAA GTGGCGCATG CTTTACTGGC TGATTGGGAT AAGGAAACCG      300
15 TTGATTTTAG TCCTAACTAT GATGAAACAG AATTGCTCC AGTGGTATTG      350
   CCATCGAGAA TTCCCAATTT ACTAGTTAAT GGCTCTTCCG GTATTGCGGT      400
   AGGGATGGCT ACTAATATTC CACCACATAA TCTTACCGAA GTAATCAATG      450
   CATGTATTGC TTTAGTGGAT GAACCTGACA CGAGTCTTGA AGATTTAATG      500
   GAAATTATTC CTGGCCCTGA TTTTCTTACA GCCGCAATTA TTAATGGTCG      550
20 TGCTGGAATT ATTGAAGGTT ATCGTACTGG AAAAGGGCGG GTTGTTATCA      600
   GGGCACGCAC AGAAATTGAA ACGGATGAAA GTTCAGGCCG TCAGTCAATT      650
   ATTATTCAGG AATTACCCTA TCAGGTGAAT AAAGCGCGTT TGATCGAGCG      700
   TATTGCTGAA TTGGTAAGGG ACAAGAAAAT CGAAGGAATT TCCGGCTTGA      750
   GAGATGAGTC AGACAAGCAA GGAATGAGAG TAGTCATTGA ATTAAAACGC      800
25 AATGAAGTAG CAGATGTGGT ATTGAATAAC CTGTTCGCTC ATACTCAAAT      850
   GCAAATGTA TTCGGAATTA ATATGGTTGC TCTGGTGGAT GGCCAACCGC      900
   GTACTTTGAA TTTGAAGCAA ATACTGGAAT ATTTTATAAA ACATCGAAGA      950
   GAGGTTGTGA CCAGACGC                                     968

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30

2) INFORMATION FOR SEQ ID NO: 1773

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 967 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
 45 (B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773

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50 CACCGCCGAG TGCTATTTGC GATGAATGTA CTGGGAAACG ATTGGAATAA      50
   ACCTTATAAA AAATCAGCCC GTGTTGTTGG GGATGTAATC GGTAAATATC      100
   ACCCGCACGG TGACAGTGCT GTCTATGAAA CGATTGTTTCG TTTAGCACAG      150
   CCTTTTCTA TGCGCTACAT GTTGGTTGAC GGTCAGGGTA ACTTCGGGTC      200
   AGTTGATGGT GACTCCGCGG CGGCTATGCG TTATACCGAA GTTCGTATGG      250
   CGAAGATCGC CCATGAACGT CTGGCGGATT TGGAAAAAGA GACGGTCGAC      300

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TTTGTTCCCTA ACTATGATGG AACAGAAAAT ATACCGGCTG TTATGCCAAC 350
 CCGTATTCCA AACTTGTTAG TTAATGGCTC TTCAGGTATT GCCGTGTTGGGA 400
 TGGCAACGAA TATCCCTCCG CATAACCTCG GTGAAGTTAT CGACGGTTGT 450
 CTTGCCTATG TTGATAATGA AGACATCACC ATAGAAGAAT TAATGGAATA 500
 5 TATTACCGGG CCTGATTTTC CGACTGCTGC GATTATTAAT GGTCGCAGAG 550
 GAATATTAGA TGCTTATCGT ACAGGGCGTG GAAAGATTTA TATCCGTGCT 600
 CAGGCTGATA TTGAAACTGA TGAGAAAACA GGTCGCGAAA CCATTATCGT 650
 GACAGAAATT CCTTATCAGG TGAATAAAGC CCGTTTAATT GAAAAAATTG 700
 CGGAGCTTGT AAAAGATAAA CGTATTGAAG GTATCAGCGG ATTACGTGAC 750
 10 GAGTCTGATA AAGACGGTAT GCGTATTGTT GTTGAGATCA AACGTGATGC 800
 AGTCGGTGAA GTAGTATTAA ATCACCTCTT TTCACAACT CAAATGCAAG 850
 TCTCTTTTGG TATTAATATG GTTGCCTTC ATCAAGGCCA ACCAAAATTA 900
 TTGAACCTAA AAGAAATTAT CGCAGCCTTT ATTCCGCCATC GTCGTGAAGT 950
 GGTGACTCGC CGTACCA 967
 15

2) INFORMATION FOR SEQ ID NO: 1774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 30 (B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774

CCAGTACACC GCAGAGTATT GTATGCGATG AATGTATTGG GAAATGATTG 50
 35 GAATAAACCC TATAAAAAAT CTGCCCCGAT TGTTGGGGAC GTCATCGGTA 100
 AATACCATCC ACATGGTGAT AGCGCTGTTT ACGAGACAAT CGTTCGTCTT 150
 GCTCAGCCTT TCTCAATGCG TTACATGCTG GTTGATGGTC AGGGAACTT 200
 CGGTTCTGTT GACGGAGACT CCGCAGCGGC AATGCGTTAT ACGGAAATCC 250
 GTATGGCGAA AATTGCCCAT GAACTACTTG CTGACCTTGA AAAAGAAACC 300
 40 GTTGATTTTCG TTCCTAACTA TGACGGAACA GAGCACATTC CTGAAGTTAT 350
 GCCAACGAAA ATCCCAAACC TTTTGGTTAA TGGGTCGTCA GGTATTGCTG 400
 TTGGGATGGC AACCAATATC CCACCTCACA ATTTAGGGGA GGTGATTAAT 450
 GGTTGTCTTG CCTATATAGA AGACGAAGAC ATCAGCATTC ATGGTTTAAT 500
 GGAACACATT CCAGGGCCTG ATTTCCCAAC CGCAGCTATT ATTAATGGCC 550
 45 GTCGTGGGAT TATTGATGCG TATCGCACAG GGCGTGGCAA GGTCTATATC 600
 CGTGCAAGCG CTGAAGTGGA AGTCGATGAG AAAAATGGTC GCGAAACCAT 650
 TATTGTCAGC GAAATTCCTT ATCAAGTGAA TAAAGCTCGC TTGATTGAAA 700
 AAATTGCTGA GTTAGTTAAA GACAAGCGTG TTGAAGGTAT CAGTGCACTG 750
 CGTGACGAGT CTGATAAAGA CGGTATGCGT ATTGTTATTG AAATCAAACG 800
 50 CGATGCGGTG GGTGAAGTTG TACTGAACAA CTTATATTCC CTGACCCAAT 850
 TGCAAGTTTC TTTTGGTATC AATATGGTAG CTCTACACCA AGGGCAGCCG 900
 AAAATACTGA ATTTAAAAGA TATCATTGCT GCTTTTGTGC GTCACCGCCG 950
 TGAAGTCGTC ACTCGTCGTA CGATTTTC 978

2) INFORMATION FOR SEQ ID NO: 1775

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775

	CCAGTACACC	GTCGCGTTCT	TTTCGCGATG	AATGTATTAG	GAAACGATTG	50
	GAATAAACCT	TATAAAAAAT	CAGCCCGTGT	TGTTGGGGAT	GTTATCGGTA	100
	AATATCACCC	GCACGGTGAC	AGTGCTGTTT	ATGAAACGAT	AGTTCGTTTA	150
20	GCACAGCCTT	TTTCTATGCG	TTACATGTTG	GTTGACGGGC	AGGGTAACTT	200
	CGGGTCAGTT	GATGGTGACT	CGGCGGCTGC	AATGCGTTAT	ACCGAAGTTC	250
	GTATGGCGAA	AATCGCCCAT	GAACGTGCTG	CGGATTTGGA	AAAAGAAACG	300
	GTTGATTTTG	TTCCTAACTA	TGATGGAACA	GAGCATATCC	CGGCAGTCAT	350
	GCCAACCCGT	ATTCCAAACT	TATTAGTCAA	TGGTTCTTCA	GGTATCGCAG	400
25	TCGGGATGGC	AACAAACATT	CCTCCGCATA	ACCTAGGTGA	AGTTATCGAC	450
	GGCTGTCTTG	CTTATGTTGA	TAACGAAGAC	ATCACTATTG	AAGAGTTGAT	500
	GGAGCATATC	ACGGGGCCTG	ATTTCCCAAC	TGCCGCTATT	ATTAATGGCC	550
	GCAGAGGAAT	TTTAGATGCT	TACCGTACTG	GGCGCGGAAA	AATTTATATT	600
	CGTGACACAAG	CTGATGTAGA	AACCGATGAG	AAAAGTGGTC	GCGAAACAAT	650
30	TATCGTGACG	GAAATTCCTT	ATCAGGTGAA	CAAAGCTCGC	TTAATTGAAA	700
	AAATTGCAGA	GCTTGTTAAA	GATAAACGTA	TTGAAGGCAT	TAGCGGATTA	750
	CGTGATGAGT	CAGATAAAGA	TGGTATGCGC	ATTGTTGTTG	AAATTAAGCG	800
	TGATGCTGTT	GGTGAAGTTG	TACTAAATCA	CTTATTTTCT	CAGACTCAGA	850
	TGCAGGTTTC	TTTTGGTATT	AACATGGTTG	CACTGCATCA	AGGTCAACCG	900
35	AAAGTGTTAA	ACCTGAAAGA	AATTATTTCA	GCCTTTATTC	GTCACCGTCG	950
	TGAAGTGGTG	ACTCGTCGTA	CTATTTTTT			978

40 2) INFORMATION FOR SEQ ID NO: 1776

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 940 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776

	TGGGTAATGA	CTGGAATAAG	CCATACAAAA	AATCGGCCCCG	TGTAGTCGGG	50
	GACGTTATCG	GTAAATATCA	CCCGCATGGT	GACAGCGCGG	TCTACGACAC	100
5	AATTGTGCGT	ATGGCCCAGC	CGTTCTCACT	GCGCTATATG	CTGGTGGATG	150
	GGCAGGGCAA	CTTCGGTTCC	GTTGATGGCG	ACTCCGCCGC	AGCGATGCGT	200
	TATACCGAAA	TCCGTATGTC	TAAAATTGCT	CACGAATTGT	TGGCGGACTT	250
	AGAAAAAGAT	ACCGTCGACT	TCGTGCCGAA	CTATGACGGT	ACGGAGCAAA	300
	TTCCTGCCGT	AATGCCAACC	CGAATCCCTA	ACTTGCTGGT	TAACGGCTCG	350
10	TCAGGTATTG	CTGTCCGTAT	GGCAACCAAT	ATTCCGCCGC	ATAACCTTTC	400
	TGAGGTTATT	GATGGCTGTC	TGGCCTATAT	CGAAGATGAA	AACATCACCA	450
	TTGAAGGGTT	GATGGAGTAC	ATCCCGGGGC	CAGATTTCCT	AACTGCTGCG	500
	ATTATCAATG	GTCGCCGTGG	TATTGAAGAA	GCTTATCGTA	CTGGCCGTGG	550
	CAAGGTGTAT	ATCCGTGCCC	GTGCTGAAGT	TGAGGCTGAC	GCTTAAACCG	600
15	GTCGCGAAAC	CATTATTGTT	CACGAGATCC	CGTATCAGGT	GAACAAGGCG	650
	CGGTTGATTG	AAAAAATCGC	CGAGCTGGTT	AAAGAAAAAC	GCGTAGAAGG	700
	CATCAGTGCG	TTGCGTGATG	AGTCTGATAA	AGACGGCATG	CGTATCGTGA	750
	TTGAAATCAA	ACGTGATGCT	GTCGGGGAAG	TGGTTCTGAA	CAACCTCTAT	800
	TCTCTGACGC	AATTGCAGGT	GACTTTCGGT	ATCAATATGG	TGGCTCTGTC	850
20	TCAAGGGCAG	CCTAAGTTGC	TTAACCTGAA	AGACATTTTG	GTTGCTTTTC	900
	TGCGCCACCG	CCGTGAAGTG	GTGACTCGCC	GTACCATTTT		940

25 2) INFORMATION FOR SEQ ID NO: 1777

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777

40	CCGTTTATTG	GCGATGGCCT	GAAGCCGGTC	CAGCGTCGCA	TCGTCTATGC	50
	GATGTCTGAA	CTGGGTCTGA	ACGCCAGCGC	GAAGTTCAA	AAGTCCGCC	100
	GCACCGTCGG	TGACGTGCTG	GGTAAATACC	ATCCCCACGG	CGACAGCGCG	150
	TGCTATGAAG	CCATGGTGCT	GATGGCTCAG	CCCTTCTCCT	ACCGCTATCC	200
45	GCTGGTTGAC	GGTCAGGGAA	ACTGGGGGGC	GCCGGACGAT	CCTAAATCCT	250
	TCGCCGCAAT	GCGTTATACC	GAATCCCGTT	TGTCGAAGTA	TGCTGAACTG	300
	CTGCTGAGCG	AACTGGGGCA	AGGCACCGTT	GACTGGGTAC	CAAACCTCGA	350
	CGGCACTTTG	CAGGAGCCGA	AGATGCTGCC	TGCGCGCCTG	CCCAATATTC	400
	TGCTAAACGG	TACTACCGGC	ATTGCCGTTG	GGATGGCGAC	GGACATTCCG	450
50	CCGCACAACC	TGCGTGAAGT	GGCCCGGGCG	GCCATTACCC	TGATTGAAAA	500
	GCCGCAAACT	TCGCTGGATG	ACCTGCTGGA	TATCGTGACG	GGGCCGGATT	550
	ATCCTACCGA	AGCGGAAATC	ATTACCCCCC	GTGCCGAAAT	CCGCAAAATC	600
	TACCAGAATG	GCCGCGGTTT	GGTGCGGATG	CGCGCGGTAT	GGGCCAAAGA	650

AGACGGCGCG GTGGTGAT

668

5 2) INFORMATION FOR SEQ ID NO: 1778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778

20 GTTTATTGGC GATGGCCTGA AGCCGGTCCA GCGTCGCATC GTCTATGCGA 50
 TGTCTGAACT GGGTCTGAAC GCCAGCGCGA AGTTCAAAAA GTCCGCCCCG 100
 ACCGTCGGTG ACGTGCTGGG TAAATACCAT CCCCACGGCG ACAGCGCGTG 150
 CTATGAAGCC ATGGTGCTGA TGGCTCAGCC CTTCTCCTAC CGCTATCCGC 200
 25 TGGTTGACGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC TAAATCCTTC 250
 GCCGCAATGC GTTATACCGA ATCCCGTTTG TCGAAGTATG CTGAACTGCT 300
 GCTGAGCGAA CTGGGGCAAG GCACCGTTGA CTGGGTACCA AACTTCGACG 350
 GCACTTTGCA GGAGCCGAAG ATGCTGCCTG CGCGCCTGCC CAATATTCTG 400
 CTAAACGGTA CTACCGGCAT TGCCGTTGGG ATGGCGACGG ACATTCCGCC 450
 30 GCACAACCTG CGTGAAGTGG CCCGGGCGGC CATTACCCTG ATTGAAAAGC 500
 CGCAAACCTC GCTGGATGAC CTGCTGGATA TCGTGCAGGG GCCGGATTAT 550
 CCTACCGAAG CGGAAATCAT TACCCCCCGT GCCGAAATCC GCAAAATCTA 600
 CCAGAATGGC CGCGGTTCGG TGCGGATGCG CGCGGTATGG GCCAAAGAAG 650
 ACGGCGCGGT GGTGATTAGC GCGCTGCCGC ATCAGGTTC CGGCGCCCCG 700
 35 GTGCTTGAGC AGAT 714

2) INFORMATION FOR SEQ ID NO: 1779

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779

	TTGGCGATGG	CTTAAAACCG	GTCCAGCGTC	GCATCGTCTA	TGCGATGTCC	50
	GAGCTGGGGC	TGAACGCCAG	CGCGAAATTC	AAAAAGTCCG	CCCGCACCGT	100
	CGGCGACGTG	TTGGGTAAAT	ATCACCCGCA	CGGCGACAGC	GCCTGCTATG	150
5	AAGCGATGGT	GCTGATGGCG	CAGCCGTTCT	CTTACCGCTA	TCCGCTGGTG	200
	GATGGTCAGG	GAAACTGGGG	GGCGCCGGAC	GATCCCAAAT	CTTTCGCCGC	250
	CATGCGTTAC	ACCGAATCCC	GCCTGTGCGAA	GTATGCCGAG	CTGCTGCTCA	300
	GCGAGCTGGG	GCAGGGGACG	GTCGACTGGG	TGCCAAACTT	TGACGGTACG	350
	CTGCAGGAGC	CGAAAATGCT	GCCAGCGCGT	TTGCCGAACA	TCCTGCTGAA	400
10	CGGCACCACC	GGCATCGCGG	TAGGTATGGC	GACCGATATT	CCTCCGCACA	450
	ACCTGCGGGA	AGTGGCCAAA	GCGGCGATTA	CGCTGATTGA	GCAGCCGAAA	500
	ACCACCCTCG	ACGAAGTCT	GGATATCGTA	CAGGGGCCGG	ATTTCCCGAC	550
	CGAGGCGGAG	ATCATCACCT	CGCGGGCGGA	AATTCGAAAA	ATCTACCAGA	600
	ACGGGCGCGG	CTCAGTGC GC	ATGCGCGCGG	TGTGGAGTAA	AGAGGACGGC	650
15	GCGGTGGTGA	TCAGCGCGCT	GCCGCATCAG	GTCTCCGGCG	CCAAAGTGCT	700
	GGAGCAGATT	GCGGCGCAGA	TG			722

20 2) INFORMATION FOR SEQ ID NO: 1780

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 692 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Klebsiella planticola*
 - (B) STRAIN: ATCC 33531
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780

35	GTCCAGCGTC	GCATCGTTTA	TGCGATGTCT	GAGCTGGGGC	TGAACGCCAG	50
	CGCGAAGTTC	AAAAAGTCCG	CCCGCACCGT	GGGTGATGTG	CTGGGTAAAT	100
	ATCACCCGCA	CGGCGATAGC	GCATGCTATG	AAGCTATGGT	GCTGATGGCG	150
	CAGCCATTCT	CCTACCGCTA	CCCGCTGGTG	GATGGGCAGG	GGAAGTGGGG	200
40	GGCACC GGAC	GATCCTAAAT	CCTTCGCCGC	GATGCGTTAT	ACCGAATCCC	250
	GTTTGTGCGAA	GTATGCGGAA	CTGCTGCTGG	GCGAACTGGG	GCAGGGAACC	300
	GTCGACTGGG	TGCCGAACTT	CGACGGGACG	ATGCAGGAGC	CGAAAATGCT	350
	GCCTGCGCGT	CTGCCGAATA	TTCTGCTGAA	CGGCACTACC	GGCATCGCCG	400
	TCGGTATGGC	AACCGATATT	CCTCCGCACA	ACCTGCGTGA	AGTGGCGCAG	450
45	GCGGCGATTA	CCCTGATCGA	AAAACCGCAG	ACCTCGCTCG	ACGAACTGCT	500
	GGATATCGTT	CACGGACCCG	ACTACCCGAC	CGAAGCCGAA	ATCATTACTC	550
	CACGCGCGGA	GATCCGCAAA	ATCTACCAGA	ACGGCCGCGG	TTCGGTGC GG	600
	ATGCGCGCGG	TATGGAAAAA	AGAGGACGGC	GCGGTCTGTA	TTACGGCGTT	650
	GCCGCATCAG	GTTTCCGGCG	CCCGCGTGCT	GGAGCAAATT	GC	692
50						

2) INFORMATION FOR SEQ ID NO: 1781

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781

15 GTTTATTGGC GATGGCTTAA AACCGGTCCA GCGTCGCATC GTCTATGCGA 50
 TGTCCGAGCT GGGGCTGAAC GCCAGCGCGA AATTCAAAAA GTCCGCCCCG 100
 ACCGTCGGCG ACGTGTTGGG TAAATATCAC CCGCACGGCG ACAGCGCCTG 150
 CTATGAAGCG ATGGTGCTGA TGGCGCAGCC GTTCTCTTAC CGCTATCCGC 200
 20 TGGTGGATGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC CAAATCTTTC 250
 GCCGCCATGC GTTACACCGA ATCCCGCCTG TCGAAGTATG CCGAGCTGCT 300
 GCTCAGCGAG CTGGGGCAGG GGACGGTCGA CTGGGTGCCA AACTTTGACG 350
 GCACGCTGCA GGAGCCGAAA ATGCTGCCAG CGCGTTTGCC GAACATCCTG 400
 CTGAACGGCA CCACCGGCAT CGCGGTAGGC ATGGCGACCG ATATTCCTCC 450
 25 GCACAACCTG CGGGAAGTGG CCAAAGCGGC GATTACGCTG ATTGAGCAGC 500
 CGAAAACCA CCTCGACGAA CTGCTGGATA TCGTACAGGG GCCGGATTTT 550
 CCGACCGAGG CGGAGATCAT CACCTCGCGG GCGGAAATTC GCAAAATCTA 600
 CCAAAACGGG CGCGGCTCAG TGCGCATGCG CGCGGTGTGG AGTAAAGAGG 650
 ACGGCGCGGT GGTGATCAGC GCGCTGCCGC ATCAGGTCTC CGGCGCCAAA 700
 30

2) INFORMATION FOR SEQ ID NO: 1782

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782

ATTGGCGATG GCTTAAAACC GGTCCAGCGT CGCATCGTCT ATGCGATGTC 50
 50 CGAGCTGGGG CTGAACGCCA GCGCGAAATT CAAAAGTCC GCCCGCACCG 100
 TCGGCGACGT GTTGGGTAAA TATCACCCGC ACGGCGACAG CGCCTGCTAT 150
 GAAGCGATGG TGCTGATGGC GCAGCCGTTC TCTTACCGCT ATCCGCTGGT 200
 GGATGGTCAG GGAAACTGGG GGGCGCCGGA CGATCCCAA TCTTTCGCCG 250

	CCATGCGTTA	CACCGAATCC	CGCCTGTCGA	AGTATGCCGA	GCTGCTGCTC	300
	AGCGAGCTGG	GGCAGGGGAC	GGTCGACTGG	GTGCCAAACT	TTGACGGCAC	350
	GCTGCAGGAG	CCGAAAATGC	TGCCAGCGCG	TCTGCCGAAC	ATCCTGCTGA	400
	ACGGCACCAC	CGGCATCGCG	GTAGGCATGG	CGACCGATAT	TCCTCCGCAC	450
5	AACCTGCGGG	AAGTGGCCAA	AGCGGCGATT	ACGCTGATTG	AGCAGCCGAA	500
	AACCACCCTC	GACGAACTGC	TGGATATCGT	ACAGGGGCCG	GATTTCCTGA	550
	CCGAGGCGGA	GATCATCACC	TCGCGGGCGG	AAATTTCGAA	AATCTACCAG	600
	AACGGGCGCG	GCTCAGTGCG	CATGCGCGCG	GTGTGGAGTA	AAGAGGACGG	650
	CGCGGTGGTG	ATCAGTGCGC	TGCCGCATCA	GGTCTCTGGC	GCCAAAGTGC	700
10	TGGAGCAGAT	TGCGGCGCAG	ATGCGC			726

2) INFORMATION FOR SEQ ID NO: 1783

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 29011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783

30	GGCTTAAAC	CGGTCCAGCG	TCGCATCGTC	TATGCGATGT	CCGAGCTGGG	50
	GCTGAACGCC	AGCGCGAAAT	TCAAAAAGTC	CGCCCGCACC	GTCGGCGACG	100
	TGTTGGGTAA	ATATCACCCG	CACGGCGACA	GCGCCTGCTA	TGAAGCGATG	150
	GTGCTGATGG	CGCAGCCGTT	CTCTTACCGC	TATCCGCTGG	TGGATGGTCA	200
	GGGAAACTGG	GGGGCGCCGG	ACGATCCCAA	ATCTTTTGCC	GCCATGCGTT	250
35	ACACCGAATC	CCGCCTGTCG	AAGTATGCCG	AGCTGCTGCT	CAGCGAGCTG	300
	GGGCAGGGGA	CGGTCGACTG	GGTGCCAAAC	TTTGACGGCA	CGCTGCAGGA	350
	GCCGAAAATG	CTGCCAGCGC	GTCTGCCGAA	CATCCTGCTG	AACGGCACCA	400
	CCGGCATCGC	GGTAGGCATG	GCGACCGATA	TTCCTCCGCA	CAACCTGCGG	450
	GAAGTGGCCA	AAGCGGCGAT	TACGCTGATT	GAGCAGCCGA	AAACCACCCT	500
40	CGACGAACTG	CTGGATATCG	TACAGGGGCC	GGATTTCCCG	ACCGAGGCGG	550
	AGATCATCAC	CTCGCGGGCG	GAAATTCGCA	AAATCTACCA	GAACGGGCGC	600
	GGCTCAGTGC	GCATGCGCGC	GGTGTGGAGT	AAAGAGGACG	GCGCGGTGGT	650
	GATCAGTGCG	CTGCCGCATC	AGGTCTCCGG	CGCCAAAGTG	CTGGAGCAGA	700
	TTGCGG					706

45

2) INFORMATION FOR SEQ ID NO: 1784

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

(B) STRAIN: ATCC 13884

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784

```

TTGGCGATGG CTTAAAACCG GTCCAGCGTC GCATCGTCTA TGCATGTCC      50
GAGCTGGGGC TGAACGCCAG CGCGAAATTC AAAAAGTCCG CCCGCACCGT    100
CGGCGACGTG TTGGGTAAAT ATCACCCGCA CGGCGACAGC GCCTGCTATG    150
15 AAGCGATGGT GCTGATGGCG CAGCCGTTCT CTTACCGCTA TCCGCTGGTG    200
GATGGTCAGG GAAACTGGGG GGCGCCGAC GATCCCAAAT CTTTCGCCGC    250
CATGCGTTAC ACCGAATCCC GCCTGTCGAA GTATGCCGAG CTGCTGCTCA    300
GCGAGCTGGG GCAGGGGACG GTCGACTGGG TGCCAAACTT TGACGGCACG    350
CTGCAGGAGC CGAAAATGCT GCCAGCGCGT CTGCCGAACA TCCTGCTGAA    400
20 CGGCACCACC GGCATCGCGG TAGGCATGGC GACCGATATT CCTCCGCACA    450
ACCTGCGGGA AGTGGCCAAA GCGGCGATTA CGCTGATTGA GCAGCCGAAA    500
ACCACCCTCG ACGAACTGCT GGATATCGTA CAGGGGCCGG ATTTCCCGAC    550
CGAGGCGGAG ATCATCACCT CGCGGGCGGA AATTCGCAA ATCTACCAGA    600
ACGGGCGCGG CTCA                                     614

```

25

2) INFORMATION FOR SEQ ID NO: 1785

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella terrigena*

40 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785

```

GCCTGAAACC GGTCCAGCGG CGCATCGTTT ATGCGATGTC CGAACTGGGT      50
45 CTGAACGCCA CCGCTAAATT CAAAAAATCC GCGCGCACC GTCGGCGACGT    100
GCTGGGTAAA TATCACCCGC ACGGCGATAG CGCCTGCTAT GAGGCGATGG    150
TGCTGATGGC GCAGCCGTTT TCTTACCGCT ACCCGCTGGT GGACGGTCAG    200
GGCAACTGGG GCGCCCCGGA CGATCCCAA TCCTTCGCCG CGATGCGTTA    250
TACCGAATCC CGCCTGTCAA AGTATGCGGA GCTGCTGCTG GGCGAGCTGG    300
50 GTCAGGGAAC CGTTGACTGG GTACCTAACT TTGACGGTAC GATGCAGGAG    350
CCGAAAATGC TGCCTGCGCG TTTGCCGAAT ATTCTGCTCA ACGGCACCAC    400
CGGTATCGCC GTGGGGATGG CCACCGATAT TCCGCCGCAC AACCTGCGCG    450
AAGTGGCCAA AGCGGCCATC ACCCTGATTG AAAAGCCGCA GACCTCGCTC    500

```

GACGAACTGC TGGATATCGT TCACGGGCCG GACTACCCCA CCGAAGCTGA 550
 AATCATCACC CCGCGCGCCG AGATCCGCAA AATCTATCAG AACGGTCGCG 600
 GCTCGGTTCG CATGCGTGCG GTGTGGAAAA AAGAGGACGG CGCGGTGGTG 650
 ATTAGCGCCC TGCCGCAT 668

5

2) INFORMATION FOR SEQ ID NO: 1786

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 7064

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786

CATTACGTTC TAACACTCAA GGACGCGGAA CATTCTCTAT GGTGTTTGAC 50
 25 CACTATGAAG AAGTACCAA GTCTGTTTCT GAAGAAATTA TCAAAAAAAA 100
 TAAAGGTGAA TAA 113

30 2) INFORMATION FOR SEQ ID NO: 1787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787

45 AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT 50
 TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAAA 100
 AAAAATAAAG GTGAATAA 118

50

2) INFORMATION FOR SEQ ID NO: 1788

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788

15 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
 GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
 AAAAAATAA AGGTGAATAA 120

20 2) INFORMATION FOR SEQ ID NO: 1789

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789

 AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT 50
 TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAAA 100
 AAAAATAAAG GTGAATAA 118

40

2) INFORMATION FOR SEQ ID NO: 1790

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790

5

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1791

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 120 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus pseudomycoides*

(B) STRAIN: NRRL B-617

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791

GCAACGTCAT TACGTTCTAA CACGCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATCA 100
30 AAAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1792

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792

50 CGTCATTACG TTCTAACACT CAAGGACGCG GAACATTCTC TATGGTGTTT 50
GACCACTATG AAGAAGTACC AAAGTCTGTT TCTGAAGAAA TTATCAAAAA 100
AAATAAAGGT GAATAA 116

2) INFORMATION FOR SEQ ID NO: 1793

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

20

2) INFORMATION FOR SEQ ID NO: 1794

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
35 (B) STRAIN: ATCC 15816
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794

CACTCAAGGA CGCGGAACAT TCTCTATGGT GTTTGATCAC TATGAAGAAG 50
40 TACCAAAGTC TGTTTCTGAA GAAATTATCA AAAAAATAA AGGTGAATAA 100

2) INFORMATION FOR SEQ ID NO: 1795

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795

GCAACGGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCTGAA GAAATTATTA 100
AAAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1796

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
25 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796

GCGACAGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
30 ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATTA 100
AAAAAAATAA AGGCGAATAA 120

35 2) INFORMATION FOR SEQ ID NO: 1797

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797

50

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1798

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798

TTGATTTTTA TCGATTGTTT AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCCATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1799

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799

TTGATTTTTA TCGATTGTTT AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

45 2) INFORMATION FOR SEQ ID NO: 1800

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
10 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1801

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

(A) ORGANISM: *Bacillus pseudomycoides*

(B) STRAIN: NRRL B-617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACTTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
30 CTAAGGAGGA ATTTAGA 117

35

2) INFORMATION FOR SEQ ID NO: 1802

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 bases

40

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: CIP 9444

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100

CTAAGGAGGA ATTTAGA

117

5 2) INFORMATION FOR SEQ ID NO: 1803

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803

20 TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCGCTTT CTAGCCTAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

25

2) INFORMATION FOR SEQ ID NO: 1804

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
30 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM *Bacillus cereus*
(B) STRAIN: ATCC 49064

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCACCTT CTAGCCTAA TATAAAATAA CCTATATAAA 100
45 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1805

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814

10	ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC	50
	AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA	100
	CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC	150
	GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA	200
	CGTTGAGTAC GAAACTGAAA CTCGTCCTA TGCACACGTT GACTGCCCAG	250
15	GTCACGCTGA CTATGT	266

2) INFORMATION FOR SEQ ID NO: 1815

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815

35	ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC	50
	AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA	100
	CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC	150
	GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA	200
	CGTTGAGTAC GAAACTGAAA CTCGTCCTA TGCACACGTT GACTGCCCAG	250
40	GTCACGCTGA CTATGTTAA	269

2) INFORMATION FOR SEQ ID NO: 1816

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
- (B) STRAIN: ATCC 6462

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805

TTGATTTT	TCAATTG	TTC	GAGTATA	ACT	ACTTATG	TAA	GCTTAGAA	AAG	50
TGGGACG	TAA	GTTTCG	CTTT	CTAGTCT	AAA	TATAAA	AATAA	CCTATATA	100
AA									117

15

2) INFORMATION FOR SEQ ID NO: 1806

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806

TTGATTTT	TTC	TCGATTG	TTC	AAGTATA	ACT	ACTTATG	TAA	GCTTAGAA	AAG	50
TGGGACG	TAA	GTTTCA	CTTT	CTAGTCT	AAA	TATAAA	AATAA	CCTATATA	AA	100
AA										117

35

40 2) INFORMATION FOR SEQ ID NO: 1807

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807

TTGATTTTTC TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
5 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1808

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808

25 TTGATTTTTC TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

30

2) INFORMATION FOR SEQ ID NO: 1809

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- 35 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 9440

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809

TTGATTTTTC TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
50 CTAAGGAGGA ATTTAG 117

2) INFORMATION FOR SEQ ID NO: 1810

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus mycoides*
 - (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810

```

15  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
    AATCGGCCAC GTTGACCATG GTAAACTAC  ATTAAGTCTGCT GCGATCACTA      100
    CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
    GACGCTGCTC CAGAAGAAAG AGAGCGCGGA ATCACAATCT CAACTGCACA      200
20  CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG      250
    GTCACGCTGA CTATGTTAAA AACATGAT                                278

```

25 2) INFORMATION FOR SEQ ID NO: 1811

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus thuringiensis*
 - (B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811

```

40  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
    AATCGGCCAC GTTGACCATG GTAAACTAC  ATTAAGTCTGCT GCGATCACTA      100
    CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
    GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
45  CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG      250
    GTCACGCTGA CTATGTTAAA AACATGAT                                278

```

50 2) INFORMATION FOR SEQ ID NO: 1812

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
15 CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GAATGCCCAG	250
GTCACGCTGA	CTATGTTAAA				270

20

2) INFORMATION FOR SEQ ID NO: 1813

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10204

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
40 CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GACGCTGCTC	CAGAAGAAAG	AGAGCGCGGA	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GAATGCCCAG	250
GTCATGCTGA	CTATGTTAAA	AACATGAT			278

45

2) INFORMATION FOR SEQ ID NO: 1814

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 266 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816

```
ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAACTAC  ATTAAGTCT  GCGATCACTA      100
CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
10 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTATGTTA                                268
```

15

2) INFORMATION FOR SEQ ID NO: 1817

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817

```
ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAACTAC  ATTAAGTCT  GCGATCACTA      100
CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
35 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTATGTTAAA AACATGAT                                278
```

40

2) INFORMATION FOR SEQ ID NO: 1818

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818

5 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTGA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTGA 268

2) INFORMATION FOR SEQ ID NO: 1819

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819

30 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTGA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTAAA AACATGAT 278

35

2) INFORMATION FOR SEQ ID NO: 1820

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycolides*
 (B) STRAIN: NRRL B-617

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGACCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 5 CGTTGAGTAC GAAACTGAAA CTCGTCAC TA GCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

10 2) INFORMATION FOR SEQ ID NO: 1821

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821

25 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 30 CGTTGAGTAC GAAACTGAAA CTCGTCAC TA GCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTA 263

35 2) INFORMATION FOR SEQ ID NO: 1822

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822

50 CAATCGAAGT ACAACGTTCT CTTCGWGTAT TGGACGGTGC GGTTACTGTT 50
 CTTGACTCAC AATCAGGTGT TGAGCCTCAA ACTGAAACAG TTTGGCGTCA 100
 AGCAACTGAG TACGGAGTTC CACGTATCGT ATTTGCTAAC AAAATGGACA 150

	AAATCGGTGC	TGACTTCCTT	TACTCAGTAA	GCACACTTCA	CGACCGTCTT	200
	CAAGCAAACG	CACACCCAAT	CCAATTGCCA	ATCGGTGCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGATA	TTCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGGTT	GAAGCAGTCG	CTGAAACTGA	400
	TGAAGACTTG	ATGATGAAAT	ACCTTGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGCTATCCGT	AAAGCAACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GTTCTGCCTT	CAAGAACAAG	GGTGTTCAAT	TGATGCTTGA	550
	TGCGGTTATC	GACTACCTTC	CAAGCCCACT	TGATATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGACGAA	650
	GAGCCATTTC	CAGCTCTTGC	CTTCAAGATC	ATGACGGACC	CATTTGTAGG	700
	TCGTTTGACA	TTCTTCCGTG	TATACTCARG	TGTTCTCCAA	TCARGKTCTT	750
	ACGTATTGAA	CACATCTAAA	GGTAAACGTG	AACGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CTAACAGCCG	TCAAGAAATT	GACACTGTTT	ACTCAGGTGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TYCAACTGGT	GACTCATTGM	900
	CAGATGAAAA	AGCTAAAATC	ATCCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGATAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCAGGTAT	GGGTGAGCTT	1100
20	CACTTGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTGAAGC	1150
	GAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGTTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTCGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	TCTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	CGCGGCTTCA	CTTGCCCTTA	1500
	AAGAAGCTGC	TAAGTCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACCATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTC	TGCTTACG				1668

35 2) INFORMATION FOR SEQ ID NO: 1823

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823

50	AGACCTGCGT	TCACAAACAC	AGGGTCGTGC	TTCTTACTCT	ATGGAGTTCT	50
	TGAAGTACAA	CGAAGCGCCA	AACAACGTTG	CTACAGCAAT	CATTGAAGCT	100
	CGTAAGGCTA	GATAA				115

2) INFORMATION FOR SEQ ID NO: 1824

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Buttiauxella agrestis*
(B) STRAIN: ATCC 33320
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824

CTGCGTTCAC TGACCAAGGT CGTGCATCTT ACTCCATGGA ATTCCTGAAG 50
TATGATGACG CGCCAAACAA CGTAGCTCAG GCCGTAATCG AAGCTCGCGG 100
TAAATAA 107

2) INFORMATION FOR SEQ ID NO: 1825

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825

TTACTCCATG GAGTTCCTGA AGTATGATGA TGCGCCGAAC AACGTTGCTC 50
AGGCCGTAAT CGAAGCCCGT GGTAAATAA 79

2) INFORMATION FOR SEQ ID NO: 1826

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
(B) STRAIN: ATCC 14029

5. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826

CAGCTGCGTT CTCTGACCAA AGGTCGTGCA TCATACACTA TGGAAATTCCT 50
GAAGTATGAT GATGCGCCAA ACAACGTTGC TCAGGCCGTT ATTGAAGCCC 100
GTGGTAAGTA A 111

10

2) INFORMATION FOR SEQ ID NO: 1827

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
25 (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827

GATTTGCGCT CTGCAACTCA TGGGCGTGCT TCGTACTCCA TGGAGTTCTT 50
30 GAAGTACTCT GATGCACCGC AAAACATTGC GAAAGCGATT ATTGAATCTC 100
GTAGCTAA 108

35 2) INFORMATION FOR SEQ ID NO: 1828

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
(B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828

50 CTCAGCTGCG TTCTCTGACC AAAGGTCGTG CATCTTACTC CATGGAATTC 50
CTGAAGTATG ATGATGCGCC TAACAACGTT GCTCAGGCCG TTATTGAAGC 100
TCGTGGCAAA TAA 113

2) INFORMATION FOR SEQ ID NO: 1829

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829

GCCGCAGGGT TAAAACCAAA GTCCCGTGCT CTCTCCTGAA GGGGAGAGCA 50
CTATAGTAAG GAATATAGCC 70

20

2) INFORMATION FOR SEQ ID NO: 1830

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 66 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Budvicia aquatica*
(B) STRAIN: ATCC 35567
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830

GCCTCGGGTA AAATTATAT CCCAGTCCCC CTCGTATAGA GGGGGATAGA 50
GTAAAGGAAG ATAATC 66

40

2) INFORMATION FOR SEQ ID NO: 1831

- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 81 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
(B) STRAIN: ATCC 14029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831

5

TCCACAGGAT TAAAACCCAG GTTTAAACCT AAGTCCCGTG CTCTCTCCTC 50
AGGGGAGAGC ACAATAGTAA GGAATATAGC C 81

10

2) INFORMATION FOR SEQ ID NO: 1832

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
(B) STRAIN: ATCC 12841

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832

GCTACTAGTT TAAAACATTG ATCCCGTGCT CTCTCTATGA AGGGAGAGCA 50
CAAGAGTAAG GAATAAAGCC 70

30

2) INFORMATION FOR SEQ ID NO: 1833

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 72 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
(B) STRAIN: ATCC 8071

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833

TTTCCAGTTA CGACATAAAT GTTATTATGG TCCAGCTTTG ACTGGACTAT 50
TCTGAAAAGA AAGGAATATA TC 72

50

2) INFORMATION FOR SEQ ID NO: 1834

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Buttiauxella agrestis*
 (B) STRAIN: ATCC 33320
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834

15 GCCCCGGGTT TTAAAAACA TTGATCCCGT GCTCTCTCCA GAAGGGGAGA 50
 GCGCAACAGT AAGGAATATA GCC 73

20 2) INFORMATION FOR SEQ ID NO: 1835

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 795 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter coli*
 (B) STRAIN: ATCC 43479
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835

CTGCAGCTGA TGGTCCTATG CCACAAACTA GAGAGCACAT CCTTCTATCA 50
 CGCCAAGTAG GTGTTCCATA TATCGTTGTA TTTATGAATA AAGCAGATAT 100
 GGTGATGAT GCTGAACTTT TAGAATTGGT TGAAATGGAA ATTAGAGAAT 150
 40 TATTAAGCTC TTATGATTTC CCAGGTGATG ACACACCTAT TATTTTCAGGT 200
 TCTGCTTTAA AAGCTCTTGA AGAAGCAAAA GCTGGACAAG ATGGCGAATG 250
 GTCAGCGAAA ATTATGGATC TTATGGCTGC TGTTGATAGC TATATTCCAA 300
 CTCCAACCTCG TGACACTGAA AAAGATTTCT TAATGCCAAT TGAAGATGTT 350
 TTCTCAATTT CAGGTCGTGG TACTGTTGTT ACAGGTAGAA TTGAAAAAGG 400
 45 TATTGTAAAA GTTGGTGATA CTATAGAAAT CGTTGGTATT AAAGATACTC 450
 AAACAACAAC TGTAAC TGGC GTTGAAATGT TTAGAAAAGA AATGGACCAA 500
 GGTGAAGCAG GGGATAATGT TGGTGTCTT CTTCGTGCTA CAAAAAAGA 550
 AGAAGTTATC CGCGGTATGG TTCTTGCTAA ACCAAAATCA ATTACTCCAC 600
 ATACTGATTT CGAAGCTGAA GTTTATATCC TAAATAAAGA TGAGGGTGGT 650
 50 AGACATACTC CATTCTTTAA TAACTATAGA CCGCAATTCT ATGTAAGAAC 700
 AACAGATGTA ACAGGTTCTA TTAAATTAGC TGATGGCGTT GAAATGGTTA 750
 TGCCTGGTGA AAATGTAAGA ATTACTGTAA GCTTGATTGC ACCAG 795

2) INFORMATION FOR SEQ ID NO: 1836

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836

GCCATACTAG TTGTTTCTGC AGCTGATGGC CCAATGCCAC AAAC TAGAGA 50
 GCACATTTTG CTATCTCGTC AAGTTGGTGT TCCATATATA GTTGTTTTTA 100
 TGAACAAAGC TGATATGGTA GATGACGCAG AGTTGCTAGA ATTAGTTGAA 150
 20 ATGGAGATCA GAGAGTTATT AAGCGAATAT GACTTCCCTG GTGATGATAC 200
 TCCTATTATA AGCGGATCAG CACTTCAAGC TCTTGAAGAA GCTAAAGCTG 250
 GTAATGATGG CGAATGGTCA GCTAAGATTA TGGATCTTAT GGCTGCTGTT 300
 GATAGCTACA TACCAACTCC AGTTCGTGCT ACTGATAAAG ATTTCTTAAT 350
 GCCGATTGAA GACGTATTCT CAATTTCTGG CCGTGGTACT GTTGTTACTG 400
 25 GTAGAATTGA AAAAGGTATA GTTAAAGTTG GTGATACTAT CGAAATCGTA 450
 GGTATTAGAG ATACACAAAC TACAACAGTT ACCGGCGTTG AAATGTTTAG 500
 AAAAGAAATG GATCAAGGCG AGGCTGGTGA TAACGTTGGT GTTCTTTTAC 550
 GCGGTACAAA GAAAGAAGAC GTTGAAAGAG GTATGGTTCT TTGTAAGCCA 600
 AAATCAATTA CTCCTCATAC TAAATTTGAG GGAGAAGTTT ATATCTTGAC 650
 30 TAAGGAAGAG GCGGTTAGAC ATACTCCATT CTTCAACAAC TATAGACCAC 700
 AATTTTATGT AAGAACAACA GATGTTACTG GATCAATCAC TCTTCCAGAG 750
 GGTACTGAGA TGGTTATGCC TGGTGATAAC TTAAAAATCA CTGTTGAGTT 800
 AATCAACCCA GTTGCTC 817

35

2) INFORMATION FOR SEQ ID NO: 1837

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837

CCATACTAGT TGTTTCTGCA GCTGATGGCC CAATGCCACA AACTAGAGAG 50

	CACATTTTGC	TATCTCGTCA	AGTTGGTGTT	CCATATATAG	TTGTTTTTAT	100
	GAACAAAGCT	GATATGGTAG	ATGACGCAGA	GTTGCTAGAA	TTAGTTGAAA	150
	TGGAGATCAG	AGAGTTATTA	AGCGAATATG	ACTTCCCTGG	TGATGATACT	200
	CCTATTATAA	GCGGATCAGC	ACTTCAAGCT	CTTGAAGAAG	CTAAAGCTGG	250
5	TAATGATGGC	GAATGGTCAG	CTAAGATTAT	GGATCTTATG	GCTGCTGTTG	300
	ATAGCTACAT	ACCAACTCCA	GTTTCGTGCTA	CTGATAAAGA	TTTCTTAATG	350
	CCGATTGAAG	ACGTATTCTC	GATTTCTGGC	CGTGGTACTG	TTGTTACTGG	400
	TAGAATTGAA	AAAGGTATAG	TTAAAGTTGG	TGATACTATC	GAAATCGTAG	450
	GTATTAGAGA	TACACAAACT	ACAACAGTTA	CCGGCGTTGA	AATGTTTAGA	500
10	AAAGAAATGG	ATCAAGGCGA	GGCTGGTGAT	AACGTTGGTG	TTCTTTTACG	550
	CGGTACAAAG	AAAGAAGACG	TTGAAAGAGG	TATGGTTCTT	TGTAAGCCAA	600
	AATCAATTAC	TCCTCATACT	AAATTTGAGG	GAGAAGTTTA	TATCTTGACT	650
	AAGGAAGAGG	GCGGTAGACA	TACTCCATTC	TTCAACAACT	ATAGACCACA	700
	ATTTTATGTA	AGAACAACAG	ATGTTACTGG	ATCAATCACT	CTTCCAGAGG	750
15	GTA CTGAGAT	GGTTATGCCT	GGTGATAACT	TAAAAATCAC	TGTTAGTT	798

2) INFORMATION FOR SEQ ID NO: 1838

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Buttiauxella agrestis*
 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838

35	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
	TATCGGCCAC	GTTGACCATG	GTA AA ACTAC	TCTGACTGCA	GCAATCACTA	100
	CCGTTCTGGC	TAAAACCTAC	GGCGGTTCTG	CACGCGCATT	CGACCAGATC	150
	GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
	CGTTGAATAT	GACACCCCGA	CTCGTCACTA	CGCGCACGTT	GACTGCCCAG	250
40	GGCACGCCGA	CTACGTTAAA	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCGATGC	CACAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATTC	ATGATCGTGT	400
	TCATGAACAA	ATGTGACATG	GTTGATGACG	AAGAGCTGCT	GGA ACTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGATTTC	CGGGCGACGA	500
45	CATCCCAGTG	GTTTCGTGGT	CAGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	GTCACCTGGA	TAACTACATC	600
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCC	ATCTCCGGCC	GTGGTACTGT	TGTTACTGGT	CGTG TAGAGC	700
	GTGGTATCAT	TAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAT	750
50	ACCGTGAAAT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATTAAAC	850
	GTGAAGATAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCTATCAAG	900
	CCGCACACTC	AGTTCGAATC	AGAAGTTTAT	ATCCTGTCCA	AAGATGAAGG	950

CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	1050
GTAATGCCGG	GCGACAACAT	TCAAATGGTT	GTTACCCTGA	TCCACCCAAT	1100
CGCAATGGAC	GACGGT				1116

5

2) INFORMATION FOR SEQ ID NO: 1839

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 13182

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
25 TATCGGCCAC	GTTGACCATG	GTAAACTAC	TCTGACCGCT	GCAATCACTA	100
CCGTTCTGGC	TAAACCTAC	GGTGGTGCTG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GACTGCCCCG	250
GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
30 GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	350
TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	400
TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	450
GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	500
CACTCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCTCTGGAA	GGCGACGCTG	550
35 AGTGGGAATC	TAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	600
CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	650
CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	700
GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	750
ACTGCTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
40 CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	850
GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	900
CCGCACACCA	AGTTCGAATC	TGAAGTTTAT	ATCCTGTCCA	AAGACGAAGG	950
CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	1050
45 GTTATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	1100
CGCGATGGA					1109

50 2) INFORMATION FOR SEQ ID NO: 1840

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
- (B) STRAIN: ATCC 14029

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840

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      GTGTCTAAAG AAAAATTTGA ACGTACTAAA CCGCACGTTA ACGTTGGTAC      50
      TATCGGCCAC GTTGACCACG GTAAAACTAC CCTGACTGCA GCTATCACTA      100
15    CCGTACTGTC TAAAGTATAC GGTGGTCAGG CTCGTGCATT CGATCAGATC      150
      GATAACGCGC CAGAAGAAAA AGCTCGTGGT ATCACCATCA ACACTTCTCA      200
      CGTAGAGTAC GACACCCCAA CTCGTCACTA CGCGCACGTT GACTGCCCAG      250
      GTCACGCCGA CTACGTGAAG AACATGATCA CTGGTGCTGC TCAGATGGAC      300
      GGCCTATATCC TGGTAGTAGC TGCCTACTGAC GGCCCAATGC CTCAGACTCG      350
20    TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTAC ATCATCGTGT      400
      TCCTGAACAA GTGTGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      450
      GAAATGGAAG TACGTGAGCT GCTGTCTCAG TACGACTTCC CAGGCGACGA      500
      TACTCCAGTT GTTCGCGGTT CTGCACTGAA AGCGCTGGAA GGCGATGCTC      550
      AGTGGGAAGA GAAGATTGTT GAACTGGCAG GCTACCTGGA CAGCTACATC      600
25    CCTGAGCCAG AGCGTGCTAT CGACAAGCCA TTCCTGCTGC CAATCGAAGA      650
      CGTATTCTCT ATCTCCGGCC GTGGTACTGT AGTAACTGGT CGTGTAAGAGC      700
      GCGGTATCAT CAAAGTTGGT GAAGAAGTAG AAATCGTTGG TATCAAAGAG      750
      ACTACCAAGA CTACTTGTAC TGGCGTTGAA ATGTTCCGTA AGCTGCTGGA      800
      CGAAGGTCGT GCGGGCGAGA ACGTAGGTGT TCTGCTGCGT GGTACCAAGC      850
30    GTGATGACGT AGAGCGTGGT CAGGTTCTGG CTAAGCCAGG CTCAATCAAC      900
      CCACACACCA ACTTTGTAGC AGAAGTTTAT ATTCTGTCCA AAGATGAAGG      950
      TGGTCGTAC ACTCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      1000
      GTACAACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG      1050
      GTAATGCCAG GTGACAACAT TCAAATGGTT GTTACCCTGA TTGCACCAAT      1100
35    CGCGATGG                                     1108

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2) INFORMATION FOR SEQ ID NO: 1841

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841

	TGGCAAAAGC	TAAATTTGAA	CGTATTAAGC	CTCACGTAAA	CGTGGGCACC	50
	ATTGGTCACG	TTGACCATGG	TAAAACCACT	CTGACTGCAG	CTATCTCTCA	100
	CGTACTGGCT	AAGACCTACG	GTGGCGAAGC	TAAAGACTTC	TCTCAAATCG	150
5	ATAACGCTCC	AGAAGAGCGT	GAGCGCGGTA	TTACCATCAA	TACCTCTCAC	200
	ATCGAATATG	ACACGCCATC	ACGCCACTAC	GCCCACGTAG	ACTGCCCAGG	250
	CCACGCTGAC	TATGTTAAAA	ACATGATCAC	TGGTGCTGCA	CAGATGGACG	300
	GCGCGATTCT	GGTAGTCGCT	TCAACAGACG	GTCCAATGCC	ACAGACTCGT	350
	GAGCACATCC	TGCTTTCTCG	TCAGGTTGGC	GTACCATTCA	TCATCGTATT	400
10	CATGAACAAA	TGTGACATGG	TAGATGACGA	AGAGCTGTTA	GAGCTAGTTG	450
	AGATGGAAGT	GCGTGAACTG	TTATCAGAAT	ACGATTTCCT	AGGTGATGAC	500
	TTACCGGTAA	TCCAAGGTTT	AGCTCTGAAA	GCGCTAGAAG	GCGAGCCAGA	550
	GTGGGAAGCA	AAAATCCTTG	AATTAGCAGC	GGCGCTGGAT	TCTTACATTC	600
	CAGAACCACA	ACGTGACATC	GATAAGCCGT	TCCTACTGCC	AATCGAAGAC	650
15	GTATTCTCAA	TTTCAGGCCG	TGGTACAGTA	GTAACAGGTC	GTGTTGAGCG	700
	TGGTATTGTA	CGCGTAGGCG	ACGAAGTTGA	AATCGTTGGT	GTACGTGCGA	750
	CAACTAAGAC	AACGTGTACT	GGTGTAGAAA	TGTTCCGTAA	ACTGCTTGAC	800
	GAAGGTCGTG	CAGGTGAGAA	CTGTGGTATT	TTGTTACGTG	GTACTAAGCG	850
	TGATGACGTA	GAACGTGGTC	AAGTATTAGC	GAAGCCAGGT	TCAATCAACC	900
20	CACACACTAC	TTTTGAATCA	GAAGTTTACG	TACTGTCAA	AGAAGAAGGT	950
	GGTCGTCACA	CGCCATTCTT	CAAAGGCTAC	CGTCCACAGT	TCTACTTCCG	1000
	TACAACTGAC	GTAACCGGTA	CTATCGAACT	GCCAGAAGGC	GTAAGATGG	1050
	TAATGCCAGG	CGATAACATC	AAGATGGTAG	TGACACTGAT	TTGCCCAATC	1100
	GCGATGG					1107
25						

2) INFORMATION FOR SEQ ID NO: 1842

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1116 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Obesumbacterium proteus*
 - 40 (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1842

	GTGTCTAAAG	AAAAATTGTA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
45	AATCGGCCAC	GTTGACCACG	GTAAACTAC	CCTGACTGCT	GCAATCACTA	100
	CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CACGTGCATT	CGACCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GA CTGCCCAG	250
	GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
50	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAGCTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CAGGCAATGA	500

	TACTCCAATC	ATCCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCGTA	GAAGTGGCTG	AAACTCTGGA	TTCTTACATC	600
	CCAGAACCAG	AACGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTTACCGGT	CGTGTAGAGC	700
5	GCGGTATCGT	TAAAGTTGGT	GAAGAAGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTTAAAT	CAACTTGTTAC	CGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	800
	CGAAGGTCGT	GCAGGCGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	850
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAA	900
	CCACACACCA	AGTTCGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
10	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTGGAAATG	1050
	GTAATGCCAG	GCGATAACAT	CAAAATGATC	GTTACCCTGA	TCCACCCAAT	1100
	CGCAATGGAC	GATGGT				1116

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2) INFORMATION FOR SEQ ID NO: 1843

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1129 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAACAAC	TCTGACTGCT	GCTATCACCA	100
35	GCGTTTTAGC	TAAAACTTAT	GGCGGTAACG	CTCGTGCAAT	CGATCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCACGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAGTAT	GATACTCCTG	CTCGCCACTA	CGCACACGTA	GACTGCCCCAG	250
	GACACGCCGA	CTATGTGAAA	AACATGATCA	CCGGTGCTGC	TCAAATGGAC	300
	GGCGCGATCT	TAGTTGTTGC	GGCAACTGAT	GGTCCTATGC	CACAGACTCG	350
40	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAACTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAGCT	TCTTTCTGCT	TATGATTTCC	CTGGTGACGA	500
	TACTCCAGTT	GTTGTTGGTT	CTGCGCTGAA	AGCGTTAGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCATT	GAATTAGCCG	GATATCTGGA	TAGCTACATC	600
45	CCAGAGCCAG	AGCGTGCGAT	TGACCGTCCG	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATTTACAGCC	GTGGTACAGT	TGTTACCGGT	CGTGTAGAGC	700
	GCGGAATCGT	TAAAGTCGGT	GAAGCCGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTACAAA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGTTACTTGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	850
50	GTGAAGAAAT	CGAACGCGGT	CAAGTACTGG	CTAAGCCAGG	TTCAATCAAC	900
	CCGCACACCA	ACTTTGTATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050

GTGATGCCTG GTGACAACAT TCAGATGACT GTAACCTCTGA TTGCACCAAT 1100
 CGCGATGGAC GAAGGTTTAC GCTTCGCTA 1129

5

2) INFORMATION FOR SEQ ID NO: 1844

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844

ATATTCATAA TGCATTACAA GTTGTGAAAA CAACAAGTGA CGGAAGTGAA 50
 AAGACTGTTA CATTGGAAAC TGCTGTAGAA TTAGGGGATG GTGCAGTTTCG 100
 TACGATTGCC ATGGAATCTA CAGATGGTTT GCAACGTGGC ATGAAAGTAG 150
 25 TGGACTTAGG ACGCACAATT AGCGTTCCTG TGGGACCTGA AACATTAGGT 200
 CGTGTATTCA ACGTTTTAGG AGATACAATC GACTTGAAAG AACCATTCCC 250
 AGAAGACTTT ACAAGACATG AAATCCATAA ACCAGCACCA AAATTTGAAG 300
 AATTAAACAG TCAATATGAA ATTCTACAA CAGGGATTAA AGTTATTGAC 350
 CTTTTAGCAC CTTATCTTAA AGGTGGTAAA ATCGGTTTAT TCGGTGGTGC 400
 30 CGGTGTAGGG AAAACCGTAT TAATTCAAGA ATTAATTCAT AATATCGCTG 450
 AAGAACTTGG TGGTATTTC AATTATACAG GGGTAGGGGA ACGTACTCGT 500
 GAAGGGAATG ACCTTTACCA TGAAATGCAA GAATCAGGCG TATCTGCTAA 550
 AACAGCGATG GTGTTTGGGC AAATGAACGA ACCACCAGGA GCTCGTATGC 600
 GTGTAGCACT AACAGGGTTA ACTATTGCGG AATACTTCCG TGATATGGAA 650
 35 AAACAAGACG TGCTTTTATT CATCGATAAC ATTTATCGTT TCACGCAAGC 700
 AGGTTTCAGAA GTGTCAGCGT TACTTGGTGC TATGCCTTCT GCCGTAGGGT 750
 ATCAACCAAC ATTAGCGACA GAAATGGGTC AATTACAAGA ACGTATCAGT 800
 TCAACTAAAG 810

40

2) INFORMATION FOR SEQ ID NO: 1845

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*

(B) STRAIN: ATCC 9345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845

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5  TGCTCTGCCA GAAATTAACA ACGCCCTCCT CACCGAAGTA GACCTCTCCG      50
   GCCAAGGCGA AGGCGAAAGC GTTCTCAAGA TGA CTCTTGA GGTGCTCAG      100
   CACCTCGGCG ATAACATCGT CCGTACCATC GCCATGAAGC CAACCGACGG      150
   TCTGGTTTCG GCGGCCACCG TTATCGATAC CGGCGCCCCA ATCACCCTGC      200
   CAGTTGGCGA CGCAACTAAA GGTCATGTTT TCAACGTGAC CGGTGATGTC      250
10  CTAAACTTGG GCGAAGGCGA AACCTTGAC GTCAAGGAAC GGTGGCCAAT      300
   CCACCGCAAG GCTCCACAGT TCGACGAACT CGAACC GGAA ACCAAGATGT      350
   TCGAAACAGG CATCAAGGTG ATCGATCTCC TCACCCCATATA CGTACAGGGC      400
   GGCAAGATCG GTCTGTTTGG CGGTGCTGGT GTTGTAAGA CCGTTCCTTAT      450
   CCAGGAAATG ATCCAGCGTG TTGCACAGGA TCATGGCGGT GTGTCCGTGT      500
15  TCGCGGGTGT GGGTGAACGT ACCCGTGAAG GTAACGATCT TATCCACGAA      550
   ATGGAAGATG CGGGCGTTCT TGATAAGACC GCGCTTGTGT TCGGCCAGAT      600
   GGATGAACCG CCAGGGGTTC GTTTGCGTAT TGCACCTTCC GGCCTGACCA      650
   TGGCGGAATA CTTCCGTGAC GTGCAAAACC AGGACGTGCT TTTGTTTCATC      700
   GATAACATCT TCCGCTTCAC CCAGGCAGGT TCGGAAGTGT CCACGTTGCT      750
20  TGGCCGTATG CCATCAGCAG TGGGCTACCA GCCGACCTTG GCAGATKAAA      800
   TGGGCGCATT GCAGG                                     815

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25 2) INFORMATION FOR SEQ ID NO: 1846

(i) SEQUENCE CHARACTERISTICS:

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30  (A) LENGTH: 1073 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Basidiobolus ranarum
      (B) STRAIN: ATCC 24670

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846

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40  ACCTTCCTCC TATCTTGA AH GCCCTGGAGG TCCAAAACCA CAGCTCTCGY      50
   TTAGTTTTAG AGGTGTCCCA GCATTTGGGT GAAAACACCG TTCGTACTAT      100
   TGCTATGGAC GGTACTGAAG GATTGGTTCG TGGTCAAAAT GTCGTAGATA      150
   CCGGATATCC TATTAGAGTT CCTGTCGGTC CTGAATGTTT GGGTCGTATC      200
45  ATGAACGTTA TTGGCGAGCC TGTTGATGAG CGCGGYCCTA TCAAGACCAA      250
   GAAGCTTGCA CCCATCCACG CTTCTCCCCC CGAGTTCGTY GACCAATCCA      300
   CCACCCCGA AATCTTGAG ACTGGTATTA AGGTGTGCGA TTTGTTGGCC      350
   CCTTACGCTC GTGGTGGTAA GATCGGTCTT TTCGGTGGTG CCGGTGTCGG      400
   TAAGACTGTG TTTATCCAGG AGTTGATYAA CAACGTTGCC AAGGCCACG      450
50  GTGGTTACTC CGTGTTGCT GGTGTTGGTG AGCGTACTCG TGAGGGTAAC      500
   GATTTGTACC ACGAGATGAT TCAAACGGT GTCATCAAGC TTGATGGCCA      550
   ATCCAAGGCT GCCCTTGTCT ACGGMC AAAT GAACGAGCCC CCAGGTGCTC      600
   GTGCCCGMGT CGCTTTGACC GGTCTTACCG TTGCTGAATA CTTCCGTGAT      650

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GAGGAAGGHC AAGATGTGTT GCTCTTCATT GACAACATTT TCCGTTTCAC 700
 CCAAGCTGGT TCTGAAGTGT CYGCCTTGTT GGGTCGTATC CCCTCCGCTG 750
 TCGGTTACCA ACCCACCTTG GCCACCGATA TGGGTGTCAT GCAAGAGCGT 800
 ATTACCACCA CCAAGAAGGG TTCCATTACC TCTGTCCAGG CCATTTACGT 850
 5 CCCTGCTGAT GATTTGACCG ATCCCGCTCC TGCCACTACT TTTGCCCATC 900
 TTGACGCCAC CACCGTGTTG TCTCGTTCCA TCTCTGAGTT GGGTATTTAC 950
 CCCGCTGTGC ATCCCTCGA CTCCAAGTCT CGTATGTTGG ATCCYCGTAT 1000
 TGTCGGTGAA GAGCACTACG ACATCGCCAC TGGTGTTCAG AAGATTCTCC 1050
 ARTCTTACAA GTCTCTCCAG GAT 1073
 10

2) INFORMATION FOR SEQ ID NO: 1847

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Blastomyces dermatitidis*
 25 (B) STRAIN: ATCC 56220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847

TGTCTTTATC CAGGAGTTGA TTGTACGTCT TGCCTCACCC TTTGGGTATT 50
 30 TTGCGAATAC TAATTATAGT AGAACAACAT TGCCAAGGCT CACGGTGTT 100
 ACTCTGTCTT CACTGGTGTC GGTGAACGTA CTCGTGAGGG TAACGATTTG 150
 TACCACGAAA TGCAGGAAAC TGGTGTCAAT CAGCTCGAGG GTGAATCCAA 200
 GGTGCGCCCTC GTGTTGCGTC AGATGAACGA GCCCCCTGGT GCCCGTGCCC 250
 GTGTCGCTCT TACTGGTTTG ACCATTGCCG AGTACTCCG TGACGAGGAG 300
 35 GGTCAAGATG TGCTTCTCTT CATTGACAAC ATTTTCCGTT TCACTCAGGC 350
 CGGTTCTGAG GTGTCTGCCC TTTTGGGTCG TATCCCCTCT GCCGTCGGTT 400
 ACCAGCCCAC TCTCGCCGTC GACATGGGTG TCATGCAGGA GCGTATTACC 450
 ACCACCACCA AGGGTTCCAT CACCTCCGTC 480

40

2) INFORMATION FOR SEQ ID NO: 1848

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 566 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 50
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848

5	TGTCTTCATT	CAGGAGTTGA	TTGTACGTCC	CTTCCTCTCT	ACAAATGACG	50
	GGCGAGGAAA	ATTTTGGCT	TTTTCTAATA	GCTCGTTATA	GAACAACATT	100
	GCCAAAGCCC	ACGGTGGTTA	CTCCGTTTTT	ACTGGTGTGCG	GCGAGCGGAC	150
	CCGTGAAGGA	AACGATTTGT	ACCACGAGAT	GCAGGAAACC	CGTGTTATCC	200
	AGCTCGATGG	CGAGTCTAAG	GTCGCACTCG	TCTTCGGTCA	GATGAACGAG	250
10	CCCCCGGAG	CCCGTGCCCG	TGTTGCCCTC	ACTGGCCTGA	CCATTGCTGA	300
	ATATTTCCGT	GACGAGGAAG	GTCAAGACGG	TATGTATTCA	TATAAATTAC	350
	TCCGGGCAAA	TTGACTCAGA	ACCGCACTCA	CTCACACATA	TATTAGTGCT	400
	TCTCTTTATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	TCCGAAGTGT	450
	CCGCCCTGCT	TGGTCGTATT	CCCTCCGCCG	TCGGTTACCA	ACCCACTCTC	500
15	GCCGTCGACA	TGGGTGGTAT	GCAGGAACGT	ATCACAACCA	CCACCAAGGG	550
	CTCCATTACC	TYCGTG				566

20 2) INFORMATION FOR SEQ ID NO: 1849

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 817 bases
	(B) TYPE: Nucleic acid
25	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Campylobacter coli</i>
	(B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849

35	AATGAAGCCA	TTGTTGTAAA	TTTTGAAAGT	GAAGGCAAAA	AACAAAAACT	50
	TGTTTTAGAA	GTAGCAGCAC	ACTTGGGCGA	TAATAGAGTT	AGAACTATTG	100
	CTATGGATAT	GACAGATGGC	TTGGTAAGAG	GACTTAAAGC	AGAAGCTTTG	150
	GGTGCTCCTA	TTAGCGTTCC	TGTGGGTGAA	AAAGTTTTAG	GAAGAATTTT	200
40	TAATGTTACG	GGAGATTGTA	TCGATGAAGG	TGAAGAAATT	TCTTTTGATA	250
	AAAAATGGGC	AATTCATAGA	GATCCACCAG	CTTTTGAAGA	TCAAAGCACA	300
	AAAAGTGAGA	TTTTTGAAAC	AGGGATTAAA	GTTGTGGATT	TACTTGCTCC	350
	TTATGCAAAA	GGTGGTAAAG	TAGGTCTTTT	TGGTGGTGCA	GGTGTTGGTA	400
	AAACTGTTAT	TATTATGGAG	CTTATTCACA	ATGTTGCATT	TAAACATAGC	450
45	GGCTATTCTG	TATTTGCAGG	TGTAGGTGAG	AGAACTCGTG	AAGGAAATGA	500
	CCTTTATAAT	GAAATGAAAG	AAAGTAATGT	TTTAGACAAA	GTTGCTCTAT	550
	GTTATGGACA	AATGAATGAA	CCACCAGGGG	CAAGAAATCG	TATTGCTTTA	600
	ACAGGTTTAA	CAATGGCTGA	GTATTTTAGA	GATGAAATGG	GTCTTGATGT	650
	GCTTATGTTT	ATTGATAATA	TCTTTAGATT	TTCACAATCA	GGTCTGAAA	700
50	TGTCAGCACT	TTTAGGAAGA	ATTCCATCAG	CTGTGGGTTA	TCAACCAACC	750
	CTAGCAAGTG	AAATGGGTAA	ATTCCAAGAA	AGAATTACTT	CAACTAAAAA	800
	AGGATCAATT	ACTTCAG				817

2) INFORMATION FOR SEQ ID NO: 1850

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850

AAGGCAACAC GCATAAACTT ATTTTAGAGA CTGCTGCACA CCTTGGAGAT 50
 AATCGTGTA GAACATATCGC TATGGATATG AGCGAAGGAC TTACAAGAGG 100
 GTTAGATGCT ATAGCGCTTG GGTCGCCTAT CAGTGTTCCT GTTGGAGAAA 150
 20 AAGTTTTAGG AAGAATATTC AACGTAATTG GTGATCTTAT AGACGAAGGC 200
 GAAGAAGAAA AATTTGATAA AAAATGGTCG ATTCATAGAG ATCCGCCGGC 250
 ATTTGAAGAT CAAAGCACAA AAAGTGAAAT TTTTGAAACA GGTATAAAAG 300
 TCGTAGATCT TTTGGCTCCT TATGCAAAAG GCGGTAAAGT TGGACTATTT 350
 GGC GGTGCCG GCGTTGGTAA AACAGTTATC ATTATGGAAC TTATCCACAA 400
 25 CGTTGCATTC AAACACAGCG GCTATTCGGT ATTTGCCGGT GTCGGTGAAA 450
 GAACAAGAGA GGGTAACGAT CTTTATAATG AAATGAAAGA ATCCGGCGTT 500
 TTGGATAAAG TTGCCTTATG TTATGGACAA ATGAATGAAC CGCCGGGTGC 550
 AAGAAACCGT ATAGCGCTTA CTGGTCTTAC AATGGCTGAG TATTTTCGTG 600
 ACGAGATGGG ACTAGATGTT CTTATGTTTA TCGATAACAT CTTCCGTTTC 650
 30 TCACAATCAG GCTCAGAGAT GTCGGCTCTT CTTGGACGTA TCCCAAGTGC 700
 GGTGGTTAT CAACCAACGT TAGCTAGCGA AATGGGAAGA CTTCAAGAAA 750
 GAATCACATC AACTAAAAA GGTTC 775

35

2) INFORMATION FOR SEQ ID NO: 1851

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851

CGAAGCTATT GAAGTAAATT TTACAGTAGA AGGCAACACG CATAAACTTA 50
 TTTTAGAGAC TGCTGCACAC CTTGGAGATA ATCGTGTAAG AACTATCGCT 100

ATGGATATGA GCGAAGGACT TACAAGAGGG TTAGATGCTA TAGCGCTTGG 150
 GTCGCCTATC AGTGTTCCCTG TTGGAGAAAA AGTTTTAGGA AGAATATTCA 200
 ACGTAATTGG TGATCTTATA GACGAAGGCG AAGAAGAAAA ATTTGATAAA 250
 AAATGGTCGA TTCATAGAGA TCCGCCGGCA TTTGAAGATC AAAGCACAAA 300
 5 AAGTGAAATT TTTGAAACAG GTATAAAAGT CGTAGATCCTT TTGGCTCCTT 350
 ATGCAAAGG CGGTAAAGTT GGAATATTG GCGGTGCCGG CGTTGGTAAA 400
 ACAGTTATCA TTATGGAAC TATCCACAAC GTTGCAATCA AACACAGCGG 450
 CTATTCGGTA TTTGCCGGTG TCGGTGAAAG AACAAGAGAG GGTAAACGATC 500
 TTTATAATGA AATGAAAGAA TCCGGCGTTT TGGATAAAGT TGCCTTATGT 550
 10 TATGGACAAA TGAATGAACC GCCGGGTGCA AGAAACCGTA TAGCGCTTAC 600
 TGGTCTTACA ATGGCTGAGT ATTTTCGTGA CGAGATGGGA CTAGATGTTC 650
 TTATGTTTAT CGATAACATC TTCCGTTTCT CACAATCAGG CTCAGAGATG 700
 TCGGCTCTTC TTGGACGTAT CCAAGTGCG GTTGGTTATC AACCAACGTT 750
 AGCTAGCGAA ATGGGAAGAC TTCAAGAAAG AATCACATCA ACT 793
 15

2) INFORMATION FOR SEQ ID NO: 1852

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter gracilis*
 30 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852
 GGAATATTTA CCGAAGATTA ACGAAGCTAT CGAGGTAAAA TTTGACGTCG 50
 35 AGGGCGCTCA TCGCAGGCTG ATCCTAGAGG TAGCCGCGCA CCTTGGAGAC 100
 AATCGCGTCC GCACGATCGC TATGGATATG AGCGATGGAC TTAGGCGAGG 150
 GCTTGAGGCC GTCGCTTTGG GCGCGCCTAT TACGGTGCCT GTGGGCGAGA 200
 AAGTTTTGGG TAGAATTTT AATGTTACGG GCGATCTGAT CGACGAAGGC 250
 GAGGATGAAA AATTTGAAAC CCGCTGGTCG ATCCACAGAG ATCCGCCTAG 300
 40 CTTTGAAAAT CAAAGCACGA AGAGTGAAAT TTTTGAAACC GGCATTAAGG 350
 TAGTCGATCT GCTCGCCCT TATGCAAAGG GCGGTAAGGT AGGACTATTC 400
 GCGGGTGCTG GCGTCGGTAA GACCGTCATC ATCATGGAAC TGATTCACAA 450
 CGTCGCTTTC AAACACAGCG GCTACTCCGT ATTTGCGGGT GTCGGCGAGC 500
 GAACGAGAGA GGGAAACGAC CTTTATAACG AGATGAAAGA ATCGGGCGTT 550
 45 TTGGATAAAG TCGCCTTGAC CTATGGTCAG ATGAACGAAC CGCCGGGAGC 600
 GAGAAACCGT ATCGCGCTAA CCGGTCTTAC GATGGCCGAG TATTTCCGCG 650
 ACGAGCTAGG GCTTGACGTT TTGATGTTA TTGATAATAT CTTCCGCTTC 700
 TCGCAGTCGG GTTCGGAGAT GTCCGCGCTT TTAGGACGAA TTCCGTCCGC 750
 GGTGCGTTAT CAGCCTACGC TTGCCAGCGA AATGGGTAAA TTACAGGAGC 800
 50 GCATTACTTC TACTAAGAAG GGCTC 825

2) INFORMATION FOR SEQ ID NO: 1853

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
(B) STRAIN: ATCC 33560

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853

TTTACCTCAA ATTAATGAAG CAATTGTTGT AAATTTTGAA AGCGAAGGAA 50
AAAAACATAA ACTTGTTTAA GAAGTAGCAG CTCATTTAGG AGATAATAGA 100
GTTAGAACTA TTGCTATGGA TATGACAGAT GGT TTGGTAA GGGGCTTAAA 150
20 AGCTGAGGCT TTAGGTGCTC CTATTAGTGT TCCTGTTGGT GAGAAAGTTT 200
TAGGAAGAAT TTTCAATGTT ACTGGAGATT TGATCGATGA AGGTGAAGAA 250
ATTTCTTTTG ATAAAAAATG GGCAATTCAT AGAGATCCGC CAGCTTTTGA 300
AGATCAAAGC ACAAAAAGTG AGATTTTGA AACAGGGATT AAAGTTGTAG 350
ATTTGCTTGC TCCTTATGCA AAAGGTGGTA AAGTAGGTCT TTTTGGTGGT 400
25 GCAGGTGTTG GTAAACTGT TATTATTATG GAGCTTATTC ACAATGTTGC 450
ATTTAAGCAT AGCGGCTATT CTGTATTTGC AGGTGTGGGT GAGAGAAGTC 500
GTGAAGGAAA TGACCTTTAT AATGAAATGA AAGAAAGTAA TGT TTTAGAC 550
AAAGTTGCTC TATGTTATGG ACAAATGAAT GAACCACCAG GAGCAAGAAA 600
TCGTATTGCT TTAACAGGTT TAACAATGGC TGAGTATTTT AGAGATGAAA 650
30 TGGGTCTTGA TGTGCTTATG TTTATTGATA ATATCTTTAG ATTTTCACAA 700
TCAGGTTCG AAATGTCAGC ACTTTTAGGA AGAATTCCAT CAGCTGTGGG 750
TTATCAACCA ACCCTAGCAA GTGAAATGGG TAAATTCCAA GAAAGAATTA 800
CTTCAACTAA AAAAGGCT 818

35

2) INFORMATION FOR SEQ ID NO: 1854

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
(B) STRAIN: ATCC 43198

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854

ATTACCTGAT ATCAACAACG CCTTATTGGT CTATAAAAAT GATGAACAAA 50

	AAAGTAAAAT	TGTGCTAGAA	GCTGCCCTTAG	AATTAGGTGA	TGGCATCATT	100
	CGTACAATTG	CCATGGAATC	AACGGATGGT	TTACAACGTG	GGATGGAAGT	150
	TGTCGATACT	GGTAAACCAA	TTTCAGTTCC	AGTTGGTAAA	GAAACGCTAG	200
	GACGTGTCTT	TAACGTTTTA	GGGGATACGA	TTGATATGCA	AGAACCATTT	250
5	GCACAAGATG	CAGATCGTTC	TGCAATTCAT	AAAGCTGCAC	CAAAATTTGA	300
	AGACTTAAGT	ACAAGTACTG	AAATTTTAGA	AACAGGGATT	AAAGTTATCG	350
	ACTTATTAGC	ACCATATTTA	AAAGGTGGTA	AAGTCGGTCT	ATTCGGGGGT	400
	GCCGGAGTAG	GTAAAACCGT	TTTAATCCAA	GAATTAATCC	ATAATATTGC	450
	ACAAGAACAT	GGTGGGATTT	CTGTATTTAC	CGGTGTTGGT	GAACGTACAC	500
10	GTGAAGGAAA	TGACTTGTAT	CATGAAATGC	GTGATTCAGG	AGTTATTGAA	550
	AAAAC TGCCA	TGGTGT TTGG	TCAAATGAAC	GAACCACCTG	GAGCTCGTAT	600
	GCGTGTTGCT	TTAACTGGGT	TAACGATTGC	TGAATATTTT	CGTGATGTAG	650
	AAGGACAAGA	TGTGTTGCTA	TTTATTGATA	ACATCTTCCG	TTTCACTCAA	700
	GCGGGTTCTG	AAGTATCAGC	CTTGCTTGGT	CGTATGCCAT	CTGCCGTGGG	750
15	TTATCAACCT	ACATTGGCTA	CAGAAATGGG	TCAATTACAA	GAACGTATCA	800
	CTTCAACTAA	GAAGGGCTCT	ATCACTTCTA			830

20 2) INFORMATION FOR SEQ ID NO: 1855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855

35	TCTTTACCAG	ATATCAATAA	TGCGCTTATT	GTCTATAAAA	ATGATGAACA	50
	AAAAAGTAAA	ATCGTGCTTG	AAGCTGCTTT	AGAGCTAGGA	GATGGCATT	100
	TTCGTACGAT	TGCAATGGAA	TCAACTGATG	GATTGCAACG	TGGAATGGAA	150
	GTTTTTCGATA	CAGGTAAGCC	AATTTTCAGTA	CCAGTAGGTC	GTGAAACATT	200
40	AGGTCGTGTA	TTTAATGTTT	TAGGTGATAC	CATTGATACG	CAAGAAGCTT	250
	TTCCTGCTGA	TGCGAATCGT	GATGCGATT	ATAAATCAGC	TCCAGCTTTT	300
	GAAGAATTAA	GTACAAGTAC	TGAAATCCTA	GAAACAGGGA	TTAAAGTTAT	350
	CGACTTACTA	GCACCATACT	TAAAAGGTGG	GAAAGTTGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACC	GTATTAATTC	AAGAATTAAT	TCATAATATC	450
45	GCCCAAGAAC	ATGGGGGTAT	TTCAGTATTT	ACCGGTGTTG	GTGAACGTAC	500
	ACGTGAAGGA	AATGACTTGT	ATCACGAAAT	GCGTGATTCA	GGCGTTATCG	550
	AAAAA ACTGC	TATGGTGTTT	GGGCAAATGA	ACGAACCACC	TGGAGCACGT	600
	ATGCGTGTTG	CGCTAACTGG	ACTAACTATT	GCGGAATACT	TCCGTGATGT	650
	TGAAGGCCAA	GACGTATTGC	TATTTATTGA	TAATATCTTC	CGTTTTACTC	700
50	AAGCAGGTTC	TGAAGTTTCT	GCCTTACTTG	GTCGTATGCC	TTCTGCGGTA	750
	GGTTATCAAC	CTACTTTGGC	TACTGAAATG	GGTCAATTGC	AAGAACGGAT	800
	TACATCAACG	AAGAAAGGTT	CGA			823

2) INFORMATION FOR SEQ ID NO: 1856

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856

TTACCAGACA TTAATAATGC CTTGGTTGTC TATAAAAATG ACGAACAAAA 50
 AACCAAGATT GTATTAGAAG CTGCCTTAGA ACTAGGAGAT GGTGTGATTC 100
 GAACTATCGC CATGGAATCT ACTGATGGCT TACAACGGGG AATGGAAGTT 150
 20 GTCGATACTG GCAGTTCCAT TTCTGTACCG GTAGGAAAAG AAACATTGGG 200
 TCGTGTATTT AACGTTTTAG GAAATACAAT TGA CT TAGAA GAACCTTTTC 250
 CAGCGGATGC TAAACGTAGT GGTATCCATA AAAAAGCGCC TGATTTTGAT 300
 GAATTAAGCA CTAGTACAGA AATTTTAGAA ACAGGGATTA AAGTTATTGA 350
 CCTATTAGCC CCTTATTTAA AAGGTGGTAA AGTCGGATTA TTCGGTGGTG 400
 25 CCGGAGTTGG TAAAACCGTT TTAATTCAAG AATTAATTCA TAATATTGCC 450
 CAAGAACATG GTGGGATTTC TGTTTTTACT GGTGTTGGTG AAAGAACACG 500
 TGAAGGTAAT GACTTGATT ATGAAATGAA AGAATCTGGC GTTATCGAAA 550
 AAAGTGCAT GGTATTTGGT CAAATGAATG AGCCACCTGG TGCCCGGATG 600
 CGGGTTGCTT TAACCGGACT TACCATTGCG GAATACTTCC GGGACGTTGA 650
 30 AGGACAAGAT GTATTGCTCT TTATCGATAA TATTTTCCGT TTTACCCAAG 700
 CTGGTTCAGA AGTATCTGCC TTATTAGGAC GGATGCCCTC TGCCGTTGGT 750
 TATCAACCAA CTTTGGCTAC TGAAATGGGA CAACTTCAAG AACGGATTAC 800
 CTAACGAAA AAAGTTCTA TTACAT 826

35

2) INFORMATION FOR SEQ ID NO: 1857

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857

TCCTTACCAG ACATCAACAA TGCGTTGATT GTTTACAAA AAAATAAAAC 50

	AAAAGTTGTT	CTTGAAGCTG	CTTTGGAAC	TGGTGATGGT	GTTATCCGCA	100
	CGATCTCTAT	GGAATCAACA	GATGGCTTGC	AACGTGGAAT	GGAAGTTGTC	150
	GATACAGGCA	AACCAATCTC	AGTTCCCGTT	GGTAAAGAAA	CTTTAGGTCTG	200
	TGTGTTTAAC	GTATTAGGTG	AAACAATCGA	CAAAGAAGCG	CCTTTTCCAG	250
5	AAGATGCAGT	AAAAAGCGGT	ATTCATAAAA	AAGCGCCGGC	TTTTGAAGAA	300
	CTTAGTACCA	GTAATGAAAT	TTTAGAAACA	GGGATCAAAG	TTATCGACTT	350
	ATTAGCTCCT	TACTTAAAGG	GTGGTAAAGT	CGGACTATTT	GGTGGTGCCG	400
	GTGTTGGTAA	AACCGTCTTG	ATCCAAGAAT	TGATTTCATA	TATCGCCCAA	450
	GAACACGGTG	GTATTTTCAGT	GTTTACGGGT	GTTGGTGAAC	GTACTCGTGA	500
10	AGGGAACGAC	CTTTATTATG	AAATGAAGGA	ATCAGGCGTT	ATTGAGAAAA	550
	CTGCCATGGT	GTTTGGACAA	ATGAACGAGC	CGCCAGGTGC	GCGTATGCGT	600
	GTTGCCTTGA	CTGGTTTGAC	ATTGGCTGAA	TATTTCCGAG	ATGAAGAAGG	650
	ACAAGATGTG	CTGTTGTTTA	TCGACAACAT	CTTCCGTTTC	ACTCAAGCCG	700
	GTTCTGAAGT	TTCTGCCTTG	CTTGCCCGGA	TGCCTTCAGC	CGTTGGCTAC	750
15	CAACCAACTT	TGGCAACTGA	AATGGGTCAA	TTGCAAGAAC	GAATCACTTC	800
	AACGAAGAAG	GGCT				814

20 2) INFORMATION FOR SEQ ID NO: 1858

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858

35	CGCATTAGTT	GTTTATAAAA	ATGATGAGCA	AAAATCAAAA	GTTGTTCTTG	50
	AAGCAGCATT	AGAATTAGGT	GACGGTGTGA	TCCGTACGAT	CGCAATGGAA	100
	TCGACGGATG	GACTACAACG	TGGAATGGAA	GTCATCGACA	CAAGCAAAGC	150
	GATCTCTGTA	CCAGTTGGAA	CAGAAACATT	AGGTCGTGTG	TTCAACGTGT	200
40	TAGGTGAAAC	AATCGATTG	GAAGCACCAT	TTCCAGAGGA	TGCCCAAAGA	250
	AGCGAGATCC	ACAAGAAAGC	ACCAAATTTT	GATGAATTAA	GCACAAGTAC	300
	AGAGATTCTT	GAAACTGGGA	TCAAAGTCAT	TGACTTATTA	GCACCTTATT	350
	TAAAAGGTGG	GAAAGTTGGA	TTGTTTGGGG	GTGCCGGTGT	TGGTAAAACC	400
	GTA CTGATCC	AAGAATTGAT	CCATAATATC	GCCCAAGAAC	ATGGGGGAAT	450
45	CTCAGTGTTT	ACCGGTGTAG	GGGAACGTAC	CCGTGAAGGA	AACGATCTGT	500
	ATTACGAAAT	GAAAGATTCA	GGCGTAATCG	AAAAAACAGC	GATGGTGTTT	550
	GGACAAATGA	ATGAGCCACC	AGGTGCTCGT	ATGCGTGTCG	CACTAACTGG	600
	ATTGACGATT	GCGGAATATT	TCCGTGATGT	CGAAGGACAA	GACGTGCTCT	650
	TATTTATTGA	TAATATTTTC	CGTTTCACCC	AAGCAGGTTC	AGAAGTATCT	700
50	GCCTTACTAG	GACGTATGCC	ATCAGCGGTT	GGTTATCAAC	CAACCTTAGC	750
	GACTGAAATG	GGACAACTCC	AAGAACGGAT	CACTTCAACG	A	791

2) INFORMATION FOR SEQ ID NO: 1859

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859

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5      TCCTTACCAG ACATCAACAA TGC GTTGATT GTTTATAAAA AAGATAAAAC      50
      AAAAGTTGTT CTTGAAGCTG CTTTGGA ACT TGGTGATGGT GTTATTCGCA      100
      CAATCGCCAT GGAATCAACG GATGGATTAC AACGTGGAAT GGAAGTTGTC      150
20     GATACTGGCA AGCCTATTTT TGTTC CAGTA GGAAAAGAAA CTCTAGGTCG      200
      TGTATTTAAT GTATTAGGTG AAACAATCGA CAAGGAAGCG CCTTTTCCAG      250
      AAGATGCAGA AAAAAGTGGT ATTCACAAGA AAGCACCAAC TTTCGAAGAA      300
      CTTAGCACAA GTAATGAGAT CTTAGAAACA GGAATCAAAG TTATTGACTT      350
      GTTAGCTCCT TACTTAAAAG GTGGTAAAGT TGGATTATTT GGTGGTGCCG      400
25     GTGTTGGTAA AACAGTCTTG ATTCAAGAGC TAATTCATAA TATCGCTCAA      450
      GAACATGGTG GTATTTCTGT GTTTACTGGT GTTGGTGAAC GTACTCGTGA      500
      AGGGAACGAC CTTTATTATG AAATGAAAGA TTCTGGTGTT ATTGAGAAAA      550
      CTGCTATGGT GTTCGGTCAA ATGAACGAGC CGCCAGGTGC ACGTATGCGT      600
      GTTGCCCTTAA CTGGTTTAA CTTAGCCGAA TACTTCCGTG ATGAAGAAGG      650
30     ACAAGATGTG TTGCTATTTA TTGACAACAT TTTCCGTTTC ACTCAAGCCG      700
      GATCAGAAGT TTCTGCCTTA CTTGGCCGTA TGCCGTCAGC AGTTGGTTAC      750
      CAACCGACTT TAGCAACTGA AATGGGTCAA TTACAAGAAC GTATTACGTC      800
      GACGAAAAAA GGTTCAA      817

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2) INFORMATION FOR SEQ ID NO: 1860

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Globicatella sanguis*
 (B) STRAIN: ATCC 51173
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860

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CCTGACATTC ATAATGCATT AATTGTAACG AACGCTGATA TGGCGGATGT      50

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	AATGCAAGAA	AATATTTTCGG	ATGAAGAAAA	ATTATTAACC	TTAGAAGTTG	100
	CACTGGATTT	AGGTCATGGA	ATGGTCCGGA	CAATTGCGAT	GGAATCAACC	150
	GATGGTTTGG	AACGCGGCAT	GACAGTTGTG	GATTATTTAA	CACCGATTAA	200
	AGTGCCAGTA	GGCGAAGCCA	CTTTAGGTAG	AGTATTCAAT	GTTTTAGGTG	250
5	AGACAATTGA	TGAACTAGAA	CCGGTTGGCG	ACGATGTTGA	ACTCAAAAGT	300
	ATTCATCGTG	AAGCCCCTAA	ATATGAGGAC	TTAGATAATA	GTTTTTCATGT	350
	TTTAGAAACC	GGAATTAAGG	TCATCGATTT	ATTAGCTCCT	TATATTAAAG	400
	GGGGAAAAAT	CGGTTTATTC	GGTGGTGCCG	GAGTGGGTAA	AACGGTCTTA	450
	ATTCAAGAAT	TAATTCATAA	TATTGCAGAA	CAATTAGGAG	GTATCTCAGT	500
10	TTTCACTGGG	GTTGGAGAAC	GTACCCGTGA	AGGGAATGAC	CTCGTTTTTG	550
	AAATGCGAGA	GTCAGGTGTA	AGCAAGAAGA	CGGCCATGGT	TTTCGGTCAA	600
	ATGAATGAAC	CACCTGGAGC	ACGTATGCGT	GTTGTCTTAA	CAGGACTTAC	650
	AATGGCGGAA	TATTTCCGTG	ACGAATTGAA	ACAAGACGTC	TTATTATTTA	700
	TTGATAATAT	TTATCGTTTT	ACTCAAGCAG	GTTCCGAAGT	GTCAGCCTTA	750
15	TTAGGTCGTA	TGCCTTCAGC	AGTAGGGTAT	CAACCAACTT	TAGCAAGTGA	800
	AATGGGACAA	ATGCAAGAAC	GTATTACGTC	WACGAAGCRC	GGTTCCATTA	850
	CA					852

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2) INFORMATION FOR SEQ ID NO: 1861

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Lactococcus garvieae*
- (B) STRAIN: ATCC 49156
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861

	GCGCGACTCT	TCCTGAGATT	AATAACGCAC	TCATCGTTTA	CAAAGATGTA	50
	GACGGCGTTA	AAACTAAAAT	CGTCCTTGAA	GTGGCGTTGG	AACTTGGTGA	100
	TGGTGCCGTA	CGTACCATCG	CTATGGAATC	AACTGATGGC	TTGACACGTG	150
40	GAATTGAAGT	TCTCGATACA	GGTAAAGCAA	TCAGCGTACC	TGTTGGTCAA	200
	GAAACACTTG	GACGTGTCTT	CAATGTACTT	GGAGATGCTA	TTGATGGAGG	250
	GGAAGCATTT	GCTGAAAATG	CAGAACGCAG	CCCTATCCAT	AAAAAAGCCC	300
	CATCTTTTGA	TGAACTTTCA	ACAGCAAATG	AAATTCTGGT	GACAGGGATT	350
	AAAGTTATTG	ACTTGCTTGC	CCCATACCTT	AAAGGTGGTA	AGATTGGGTT	400
45	GTTCCGTGGT	GCCGGAGTTG	GTAAACCGT	CCTTATCCAA	GAGTTGATTC	450
	ACAATATTGC	CCAAGAACAC	GGTGGTATTT	CCGTATTTAC	TGGTGTGGG	500
	GAACGTACAC	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AAGAATCAGG	550
	CGTTATCGAA	AAAACAGCCA	TGGTCTTCGG	TCAAATGAAT	GAACCACCTG	600
	GAGCACGTAT	GCGTGTTGCT	CTTACTGGTT	TGACAATTGC	TGAATATTTT	650
50	CGTGATGTAG	AAAAACAAGA	CGTTTTGCTT	TTCATTGATA	ATATCTTCCG	700
	TTTCACCCAA	GCCGGTTCAG	AAGTATCTGC	CCTCTTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	TTACCAACCT	ACGCTTGCAA	CTGAAATGGG	TCAACTTCAA	800
	GAACGTATCA	CTTCAACAAA	ACAAGGTT			828

2) INFORMATION FOR SEQ ID NO: 1862

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis*
 (B) STRAIN: ATCC 11454

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862

AATTGCCTGA RATTAACAAT GCCTTGATTG TCTACAAAGA TGTCATGGC 50
 CTA AAAACAA AAATTACTCT TGAAGTTGCT TTGGA ACTTG GTGATGGTGC 100
 AGTTCGTACA ATCGCTATGG AATCTACTGA TGGCTTGACT CGTGGACTTG 150
 20 AAGTCCTTGA TACAGGTAAA GCAGTCAGCG TTCCTGTTGG GGAAGCCACT 200
 CTTGGTCGTG TTTTAAACGT TCTTGGTGAT GTTATTGACG GTGGGGAAGA 250
 ATTTGCTGCT GATGCAGAAC GTAATCCTAT CCATAAAAAA GCTCCAACAT 300
 TTGACGAATT GTCAACTGCA AACGAAGTTC TCGTAACTGG GATTAAAGTT 350
 GTCGATTTGC TTGCACCTTA CCTTAAAGGT GGTAAAGTTG GACTTTTCGG 400
 25 TGGTGCCGGA GTTGGTAAAA CCGTCCTTAT TCAAGAATTG ATTCACAACA 450
 TCGCCCAAGA ACACGGAGGT ATTTCTGTGT TTACCGGTGT TGGGGAACGT 500
 ACTCGTGAAG GGAATGACCT TTA CTGGGAA ATGAAAGAAT CAGGCGTTAT 550
 TGAAAAAACT GCCATGGTCT TTGGTCAAAT GAATGAACCA CCAGGAGCAC 600
 GTATGCGTGT TGCCCTTACT GGT TTGACAA TTGCTGAATA TTTCCGTGAT 650
 30 GTTCAAGGTC AAGACGTACT GCTTTTCATT GACAACATCT TCCGTTTCAC 700
 ACAAGCTGGT TCAGAAGTTT CTGCCCTTTT GGGACGTATG CCTTCTGCCG 750
 TTGGTTACCA ACCAACACTT GCTACTGAAA TGGGGCAATT GCAAGAACGT 800
 ATCACTTCTA CTAAGAAGGG TTCTGTTA 828

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2) INFORMATION FOR SEQ ID NO: 1863

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863

CTTACCTGAA ATCTACAACG CCCTAGTTAT TGAATATAAA TCTGATGCAG 50

	AAGAAGCACC	AACTAGCCAA	CTTACTTTAG	AAGTAGCCAT	TCAATTAGGT	100
	GATGACGTTG	TTCGTACAAT	TGCAATGGCA	TCAACTGATG	GTGTTCAAAG	150
	AGGTATGGAA	GTTATTGATA	CTGGGAGCCC	AATCACAGTT	CCAGTTGGTA	200
	CAGTAACACT	TGGTCGTGTA	TTTAACGTAT	TAGGAAACAC	TATCGATTTG	250
5	GATGAGCCAC	TTCCAAGCGA	TATCAAGCGT	AATAAAATTC	ACCGTGAAGC	300
	ACCAACATTT	GACCAATTAG	CAACAACACT	TGAAATTCTT	GAAACAGGAA	350
	TAAAAGTTGT	AGACTTGCTA	GCCCCATATT	TAAAAGGTGG	TAAAATTGGT	400
	TTGTTTCGGCG	GAGCGGGTGT	TGGTAAAACC	GTTTTAATCC	AAGAACTTAT	450
	TCATAATATC	GCTCAAGAAC	ATGGTGGTAT	TTCTGTGTTC	GCTGGTGTTC	500
10	GAGAACGTAC	TCGTGAAGGG	AACGATCTTT	ACTTTGAAAT	GAAAGACTCT	550
	GGTGTAAATTG	AAAAAACTGC	CATGGTATTC	GGTCAAATGA	ACGAACCACC	600
	AGGTGCTCGT	ATGCGTGTAG	CTTTAACAGG	TCTTACAATC	GCTGAATATT	650
	TCCGTGATGA	AGAACACCAA	GATGTACTTC	TATTCATTGA	TAATATTTTC	700
	CGCTTTACTC	AAGCTGGTTC	AGAGGTTTTCG	GCTTTACTAG	GTCGTATGCC	750
15	ATCTGCAGTA	GGTTATCAAC	CAACTCTAGC	TACCGAAATG	GGACAATTAC	800
	AAGAACGTAT	TACTTCTACT	AATGT			825

20 2) INFORMATION FOR SEQ ID NO: 1864

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864

35	GTCATATTCC	AGAGCTTTAT	GACGCTCTGG	AGGTTAAGGG	CGATGGTAAG	50
	CATCGTTTCA	ACCTAGTTCT	TGAGGTTCAA	CAGCAGATTG	GCGGTGGTGT	100
	GGTACGCTGC	ATTGCCATGG	GTTCTTCTGA	CGGTTTGAGC	AGAGGAATTG	150
	AGGCTGTAAA	TACTGGTGCC	GGTGTTAAGG	TTCCAGTTGG	TCGTGAGACC	200
40	CTAGGACGTA	TTATGAACGT	TTTAGGTCAG	CCTGTAGATG	AGAGAGGTCC	250
	TATCGGACAG	AAAGAGGATT	GGGAAATTCA	CCGTCCAGCT	CCTACCTATG	300
	CTGAGCAGTC	ATCAACTACA	GAAATTCTAG	AAACCGGTAT	TAAGGTTATG	350
	GACCTTATCT	GCCCATTTCG	TAAGGGTGGT	AAAGTTGGTC	TGTTTCGGTGG	400
	TGCCGGTGTG	GGTAAGACAG	TTAACATGAT	GGAGCTTATC	AATAACATTG	450
45	CTAAGGCTCA	CTCAGGTCTA	TCTGTATTTA	CCGGTGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	CAGGAATCAA	AGGTTATCGA	550
	TAAGGTATCA	ATGATTTACG	GTCAGATGAA	CGAGCCTCCA	GGGAACCGTC	600
	TACGTGTTGC	TCTGACAGGT	CTGACTGTTG	CTGAGAAGTT	CCGTGACGAA	650
	GGTCTGGATG	TGCTTCTGTT	CATCGATAAC	ATCTATCGTT	ATACACTGGC	700
50	TGGTACAGAG	GTATCTGCTC	TGTTAGGCCG	TATGCCCTCA	GCTGTGGGTT	750
	ACCAGCCTAC	ACTGGCTGAG	GAAATGGGTG	TATTACAGGA	GCGTATTGCT	800
	TCAACTAAGA	AAGGTTCTAT	T			821

2) INFORMATION FOR SEQ ID NO: 1865

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865

	TGATACTTTA	CCAGATATCA	ATAATGCATT	AGCCGTATAT	AAAAATGATG	50
	AGAACAAGAC	GCGTGTTGTA	TTGGAAGCTA	CTTTAGAACT	TGGAGATGGG	100
	GTAATTCGTG	CCATTTCTAT	GGGGTCTACT	GACGGCTTGC	AACGTGGCAT	150
20	GGAAGTTGTG	GATACACAAG	AACCTATTTC	TGTTCCGGTA	GGAAATGATA	200
	CTTTAGGTCG	TGTATTTAAT	GTGTTAGGAG	AAACAATAGA	TAATCAGGAG	250
	CCATTTCTCTG	AAGATGCTGA	AAAAAGTGGT	ATTACACAAA	AAGCCCCTAG	300
	TTTTTGATGAA	TTAAGTACTA	GTTTCGGAAAT	ATTAGAAACA	GGGATCAAAG	350
	TGATTGATTT	ATTAGAACCT	TATCTAAGAG	GCGGTAAAGT	CGGATTGTTT	400
25	GGAGGCGCCG	GTGTTGGAAA	AACGGTGCTA	ATTCAAGAAT	TGATCAATAA	450
	TGTTGCCCAA	GAACACGGGG	GTATTTCCGT	GTTTAATGGT	GTAGGTGAAC	500
	GTACTIONGTA	AGGTAATGAC	TTGTATTATG	AAATGCAGGA	TTCAGGCGTT	550
	ATCGAAAAAA	CAGCCATGGT	GTTTGGTCAA	ATGAACGAAC	CACCAGGTGC	600
	TCGTATGCGT	GTTGCTTTAA	CTGGCCTAAC	ACTGGCAGAA	TATTTTCGAG	650
30	ATGTTGAAGG	TCAAGACGTA	TTATTATTTA	TTGATAATAT	TTTCCGTTTT	700
	ACACAAGCAG	GTACCGAAGT	TTCCGCTTTA	CTTGGTAGAA	TGCCATCTGC	750
	TGTTGGCTAT	CAACCCACAC	TAGCAACTGA	AATGGGGCAA	CTGCAAGAAC	800
	GGATTACGTC	AACGGATAAG	GG			822

35

2) INFORMATION FOR SEQ ID NO: 1866

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866

ATCTCCTCAG	GATCKATAGG	ACTTGATATA	GCTCTTG GTA	TAGGCGGCGT	50
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	ACCAAAAGGA	AGAATAGTCG	AAATTTATGG	GCCAGAAAGC	TCTGGTAAAA	100
	CAACTCTTAC	TTTGCATTTA	ATAGCAGAAT	CTCAAAAAGT	CGGCGGAGTT	150
	TGCGCGTTTG	TAGATGCAGA	GCATGCACTT	GATGTAAAT	ATGCTAAAAA	200
	TTTAGGCGTT	GATACGGATA	ACTTATATAT	TTCTCAACCG	GACTTCGGAG	250
5	AGCAAGCTCT	TGATATAGTA	GAAACTCTAG	CTAGAAGCGG	CGCCGTTGAT	300
	CTTATAGTAA	TAGATAGCGT	AGCAGCTYTA	ACACCAAAAA	GCGAAATAGA	350
	AGGCGATATG	GGAGATCAGC	ACGTAGGGCT	GCAAGCAAGA	CTCATGAGTC	400
	AAGCACTTAG	AAAATTAACC	GGAGTTGTCC	ATAAAATGGG	AACTACAGTT	450
	GTATTTATAA	ACCAAATTCG	TATGAAAATC	GGCGCTATGG	GCTATGGCAC	500
10	TCCTGAAACT	ACTACTGGCG	GAAATGCGCT	TAAATTTTAC	GCTTCAGTTA	550
	GACTTGACGT	ACGTAAAATA	GCTACTTTAA	AACAGAGCGA	TGAGCCAATC	600
	GGAAACCGCG	TAAAAGTAAA	AGTAGTAAAA	AACAAAGTCG	CTCCTCCTTT	650
	TAGACAAGCC	GAATTTGATA	TCATGTTTGG	AGAAGGTATC	AGCAAAGAAG	700
	GAGAGATAAT	AGATTACGGC	GTAAAACCTG	ATATTATCGA	TAAAAGCGGC	750
15	GCTTGGTTTA	GCTATGATAA	TTCAAAATTA	GGTCAAGGCA	GAGAAAATCT	800
	AAAAGCGTTT	TTAAAAGA				818

20 2) INFORMATION FOR SEQ ID NO: 1867

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867

35	TCTCCTCAGG	ATCKATAGGA	CTTGATATAG	CTCTTGGTAT	AGGCGGCGTA	50
	CCAAAAGGAA	GAATAGTCGA	AATTTATGGG	CCAGAAAGCT	CTGGTAAAC	100
	AACTCTTACT	TTGCATTTAA	TAGCAGAATC	TCAAAAAGTC	GGCGGAGTTT	150
	GCGCGTTTGT	AGATGCAGAG	CATGCACTTG	ATGTTAAATA	TGCTAAAAAT	200
40	TTAGGCGTTG	ATACGGATAA	CTTATATATT	TCTCAACCGG	ACTTCGGAGA	250
	GCAAGCTCTT	GATATAGTAG	AAACTCTAGC	TAGAAGCGGC	GCCGTTGATC	300
	TTATAGTAAT	AGATAGCGTA	GCAGCTYTAA	CACCAAAAAG	CGAAATAGAA	350
	GGCGATATGG	GAGATCAGCA	CGTAGGGCTG	CAAGCAAGAC	TCATGAGTCA	400
	AGCACTTAGA	AAATTAACCG	GAGTTGTCCA	TAAAATGGGA	ACTACAGTTG	450
45	TATTTATAAA	CCAAATTCGT	ATGAAAATCG	GCGCTATGGG	CTATGGCACT	500
	CCTGAAACTA	CTACTGGCGG	AAATGCGCTT	AAATTTTACG	CTTCAGTTAG	550
	ACTTGACGTA	CGTAAAATAG	CTACTTTAAA	ACAGAGCGAT	GAGCCAATCG	600
	GAAACCGCGT	AAAAGTAAAA	GTAGTAAAAA	ACAAAGTCGC	TCCTCCTTTT	650
	AGACAAGCCG	AATTTGATAT	CATGTTTGGG	GAAGGTATCA	GCAAAGAAGG	700
50	AGAGATAATA	GATTACGGCG	TAAAACCTGA	TATTATCGAT	AAAAGCGGCG	750
	CTTGGTTTAT	CTATGATAAT	TCAAAATTAG	GTCAAGGCAG	AGAAAATCTA	800
	AAAGCGTTTT	TAAA				814

2) INFORMATION FOR SEQ ID NO: 1868

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33560

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868

GATAGCATAG GCWCAGGTTC AGTTGGACTT GATCTTGCTT TAGGTATAGG 50
 CGGTGTTCCA AAAGGAAGAA TTATAGAAAT TTATGGGCCT GAAAGTTCAG 100
 GTAAACTAC TCTAACTCTA CACATTATCG CAGAATGCCA AAAAGCAGGT 150
 20 GGGGTTTGTG CTTTATCGA TGCAGAACAT GCACTTGATG TGAAATATGC 200
 TAAAAATTTA GGTGTAAATA CAGATGATTT GTATGTTTCT CAACCTGATT 250
 TTGGAGAGCA AGCCTTAGAA ATTGTAGAAA CTATAGCWAG AAGTGGTGCA 300
 GTAGATCTTA TWGTAGTAGA TAGCGTTGCA GCWCTTACCC CAAAAGCAGA 350
 AATTGAAGGC GATATGGGCG ATCARCATGT AGGACTTCAA GCAAGACTTA 400
 25 TGTCTCAAGC TCTAAGAAAA CTTACAGGTA TAGTTCATAA AATGAATACC 450
 ACAGTAATTT TCATCAACCA AATTCGTATG AAAATCGGTG CTATGGGTTA 500
 TGGTACTCCT GAAACCACAA CAGGTGGAAG TGCATTAAAA TTTTATGCTT 550
 CTGTGCGTTT AGATGTTAGA AAAGTAGCAA CCTTAAAMCA AAACGWAGAM 600
 CCTATAGGAA ACCGCGTTAA AGTAAAAGTA GTTAAAAATA AAGTTGCTCC 650
 30 TCCATTCAGM CAAGCTGAAT TTGATGTGAT GTTTGGAGAG GGTTTAAGCC 700
 GTGAAGGTGA ATTGATCGAT TATGGTGTA AACTTGATAT CGTAGATAAA 750
 AGTGGTGCCT GGTTCCTTA TAAAGATAAA AACTTGGAC AAGGTAGAGA 800
 AAATTCAAAA GCTTCTTAA AAGA 824

35

2) INFORMATION FOR SEQ ID NO: 1869

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869

AGAAAGTTCT GGTAACAA CGGTTGCACT GCATGCGATT GCAGAAAGTTC 50

AAAAACATGG CGGGACGGCA GCCTTTATTG ATGCCGAGCA CGCGTTGGAC 100
 CCTCAATACG CACAACGTCT AGGTGTAAAC ATTGATGAAT TGCTGCTATC 150
 ACAACCAGAT ACTGGGGAAC AAGGCTTAGA AATTGCAGAT GCTTTAGTTT 200
 CAAGTGGCGC AGTCGATATT ATCGTTATTG ACTCGGTGGC CGCGCTAGTC 250
 5 CCCCCTGCTG AAATCGATGG CGAGATGGGT GATGCGCACG TTGGTCTGCA 300
 GGCTCGTTTG ATGTCACAAG CATTGCGCAA GCTGTCAGGC TCTATCAACA 350
 AAACAAAGAC TATCGCCGTC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1870

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870

TGAAAGTTCA GGTAAAACAA CAGTTGCACT ACACGCTATT GCAGAAGTAC 50
 AAAAAAATGG CGGAACGGCC GCTTTCATTG ATGCTGAGCA TGCGTTAGAT 100
 CCGCAATATG CACAAAAATT AGGTGTGAAT ATCGATGAAC TACTTCTTTC 150
 30 ACAGCCTGAC ACAGGAGAAC AAGGTCTAGA GATCGCTGAT GCTTTAGTAT 200
 CAAGTGGGGC TGTAGATATC GTAGTAGTCG ATTCAGTTGC TGCTTTAGTT 250
 CCACGAGCAG AAATCGACGG CGAAATGGGT GACTCACATG TCGGGTTACA 300
 AGCACGTTTG ATGTCTCAAG CATTGCGTAA ACTCTCTGGT TCGATCAACA 350
 AAACAAAAC AATCGCTATT TTCATCAACC AAATCCGT 388

35

2) INFORMATION FOR SEQ ID NO: 1871

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 50 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871

AGAGAGTTCC GGTAAAACAA CTGTTGCGCT TCATGCAATT GCGGAAGTAC 50
 AAGCACAAGG CGGAACAGCA GCATTTATCG ATGCTGAGCA TCGGTTGGAT 100
 CCGGCTTATG CTA AAAACCT AGGTGTAAAT ATTGATGAAT TATTACTATC 150
 TCAACCAGAT ACAGGAGAAC AAGCTTTAGA GATTGCTGAA GCTTTAGTTA 200
 5 GAAGTGGTGC AGTTGATATG TTAGTAATTG ACTCCGTTGC AGCACTTGTA 250
 CCACGTGCTG AAATCGAAGG CGAGATGGGC GATGCTCATG TTGGATTACA 300
 AGCACGTTTA ATGTCCAAG CATTGCGTAA ACTTTCTGGT GTTATTAATA 350
 AATCAAAAAC CATTGCTATT TTCATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1872

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872

AGAGTCATCT GGTAAGACAA CGGTTGCCCT TCATGCAGTT GCGCAAGCAC 50
 AAAAAGAAGG TGGTATTGCT GCCTTTATCG ATGCGGAACA TGCCCTTGAT 100
 30 CCAGCTTATG CTGCGGCCCT TGGTGTCAAC ATTGACGAAT TGCTCTTGTC 150
 ACAACCAGAC TCAGGAGAGC AAGGTCTTGA GATTGCAGGA AAATTGATTG 200
 ACTCAGGAGC CGTGGATCTT GTCGTAGTCG ACTCAGTTGC GGCCCTTGTC 250
 CCTCGTGCGG AAATTGATGG AGATATCGGT GATAGCCACG TTGGTTTGCA 300
 GGCTCGTATG ATGAGCCAGG CTATGCGTAA ACTTGGTGCT TCTATCAATA 350
 35 AAACCAAAAC AATTGCCATC TTTATCAACC AATTGCGT 388

40

2) INFORMATION FOR SEQ ID NO: 1873

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873

	GAACATGACG	CCGACTTTTT	CACGCAATTG	GTTGATAAAG	ATGGCAATTG	50
	TTTTGGTTTT	ATTGATAGAA	GCTCCGAGTT	TACGCATGGC	CTGGCTCATC	100
	ATTTCGAGCCT	GCAAACCAAC	GTGACTGTCT	CCAATATCCC	CATCAATTTT	150
5	CGCACGAGGT	ACAAGGGCCG	CAACTGAGTC	GATAACGACA	AGGTCAACTG	200
	CACCTGAGTC	AATCAATTTT	CCAGCAATTT	CAAGACCTTG	TTCACCTGAG	250
	TCTGGTTGTG	ACAAGAGCAA	TTCGTCAATA	TTCACACCAA	GGGCTGCAGC	300
	ATAGGCTGGG	TCAAGAGCAT	GTTCCGCATC	GATAAAGGCT	GCAATACCAC	350
	CTTCTTTCTG	TGCTTGCGCA	ACAGCGTGAA	GGGCAACCGT	TGTCTTACCA	400
10	GATGATTCTG	GCGCRTACAY	TTCGATGATA			430

2) INFORMATION FOR SEQ ID NO: 1874

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 64746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874

30	TTGTCGTTGT	TGCTGCCTCC	GACGGTCAGA	TGTAGGTGGA	ACATCTTGGG	50
	AAATACGTCG	TAAAACACGT	CGCTTACGTT	TTCGCGAATA	GGCCCCAGAC	100
	TCGTGAGCAT	TTGCTGCTCG	CCCGCCAGGT	TGGTGTCCAG	AAGATCGTTG	150
	TCTTCGTCAA	CAAAATCGAT	GCTATTGATG	ATCCGGAGAT	GCTGGAAGTG	200
	GTCGAACTCG	AGATGCGTGA	GCTGCTGAAC	AGCTACGGTT	TCGAGGGTGA	250
35	AGAGACTCCG	ATCATTTTCG	GTTCCGCTCT	CTGTGCTCTC	GAAGGACGCC	300
	GTGACGACAT	CGGTAAAGAC	AGAATTGAGC	AGCTTATGAA	CGCTGTCGAC	350
	ACCTGGATCC	CCACTCCTCA	GCGTGACCTC	GACAAACCTT	TCTTGATGTC	400
	TGTCGAGGAA	GTGTTCTCTA	TCGCCGGCCG	TGGTACCGTG	GCTTCTGGTC	450
	GTGTCGAGCG	TGGTATCTTG	AAGAAGGACT	CTGAGGTTGA	GATTGTTGGA	500
10	GGCTCCTTCG	AACCCAAGAA	GACCAAAGTC	ACCGACATTG	AAACCTTCAA	550
	GAAGAGCTGT	GATGAATCGC	GTGCTGGTGA	CAACTCTGGT	CTCCTCCTGC	600
	GTGGTATCCG	ACGTGAAGAC	GTCAAGCGTG	GTATGGTCAT	TGCTGTTCCC	650
	GGCAGCACCA	AGGCTCACGA	CAAGTTCCTC	GTCTCCATGT	ACGTCTTGAC	700
	CGAGGCGGAG	GGTGGTCGTC	GTAAGGCTT	CGGTGCCAAC	TACCGTCCCC	750
15	AAGTCTTCAT	CCGTACTGCA	GGTAAGTTCC	CGCACACCGT	GTCCAGATCT	800
	TCCGAGAGAT	TAGCGATATA	TGCTAATGAT	TCATCAGACG	AGGCTGCTGA	850
	CCTCAGCTTC	CCTGACGGCG	ACCAATCTCG	CAGAGTTATG	CCTGGTGACA	900
	ACGTCGAGAT	GATCCTGAAG	ACCCACCACC	CTGTTGCTGC	TGAGGCT	947

50

2) INFORMATION FOR SEQ ID NO: 1875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus versicolor*
 (B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875

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15 GCTGCTTCCG ATGGTCAAAT GTACGTCAAC CTTATATACA CCCTCTGATA      50
   TGACAGAATG TCGCCTAACA GCACGCGTGA ACTAGGCCCC AAACCCGTGA      100
   GCACTTGCTG CTTGCCCCGCC AGGTCGGTGT CCAGAAGATT GTTGTGTTTCG      150
   TCAACAAGGT TGATGCCGTC GATGACCCCTG AGATGTTGGA ACTTGTTGAG      200
   CTGGAAATGC GTGAGCTTCT CAGCACTTAC GGCTTCGAAG GCGAGGAGAC      250
20 CCCTATCATC TTCGGTTCCG CCCTATGCGC CCTCGAGGGT CGCCGCCCCCG      300
   ATATCGGTAC TGAGCGAATT GACAGCCTTC TTGAGGCCGT TGACACCTGG      350
   ATCCCTACCC CTCAGCGTGA CCTGGACAAG CCTTTCCTGA TGTCTGTCTGA      400
   GGAGGTCTTC TCCATTGCCG GTCGTGGTAC CGTTGCCTCT GGCCGTGTTG      450
   AGCGTGGTCT CCTTAAGAAG GACAGCGAGG TCGAGATTCT CGGAGGTGGT      500
25 CAGGTCATGA AGACCAAGGT CACTGACATT GAGACATTCA AGAAGCACTG      550
   TGACGAATCC CGTGCTGGTG ACAACTCCGG TCTTCTTCTC CGTGGTATCC      600
   GCCGTGAGGA TGTCAAGCGC GGTATGGTTA TTGCTGCTCC CGCCTCTATC      650
   AAGGCCCAACA AGAAGTTCAT GGTCTCCATG TACGTCCTCA CTGAGGCAGA      700
   AGGTGGCCGT CGCAGTGGCT TCGGTGTCAA CTATCGTCCC CAGGCTTACA      750
30 TTCGCACTGC TGGTAAGTTT TCAAAACATT CGACCTCTCG CCTTAGAAGA      800
   AGAATACCTC TAACTTGTAT TTAGACGAGG CTTGCGACCT TTCTTTCCCC      850
   GATGGCGACA TGAGCCGCCG TGTCATGCCT GGTGACAACG TGGAAATGAT      900
   CCTCAACCTC AACAACCCTG TCG                                923

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2) INFORMATION FOR SEQ ID NO: 1876

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Basidiobolus ranarum*
 (B) STRAIN: ATCC 24670

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876

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CATCATTGTT GTGTCCGCCA CTGATGGTCA AATGCCTCAA ACTCGTGAGC      50

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	ATTTGTTGTT	GGCTCGCCAA	GTTGGTGTCC	AACACTTGGT	TGTCTTCATC	100
	AACAAGGTTG	ATGCCGTTGA	TGATCCTGAA	ATGTTGGAGT	TGGTCGAGAT	150
	GGAAATGCGT	GATTTGCTTT	CCCAATACGG	TTTCCCCGGA	GACAACGTCC	200
	CCATTATCCA	GGGTTCCGCT	CTCTGCGCTC	TTGAGGACCG	CAACCCCGAG	250
5	ATCGGCCGTA	ACGCCATCAT	GAAGTTGATG	GAGGCTGTTG	ATAGCAGCAT	300
	CCCCACCCCT	GCCCGTGATT	TGGACAAACC	TTTCCTCATG	CCCGTTGAAG	350
	ATGTGTTCTC	CATCTCTGGC	CGTGGTACTG	TTGCCACTGG	ACGTGTTGAG	400
	CGTGGTATGG	TCACCAAGGG	TACTGAAGTT	GAAATCGTCG	GTATGGGCGA	450
	GCACTTCAAG	ACCACCTTGA	CCGGTATTGA	AATGTTCCAC	AAGGAATTGG	500
10	ACAAGGGTAT	GGCTGGTGAC	AACATGGGTT	GCTTGCTTCG	TGGTGTCAAG	550
	CGTGAGCAAG	TCCGTCGTGG	TATGGTTATC	TGTGCCCCCG	GATCCGTCAA	600
	GCCACATAAG	AAGTTCATGG	CTCAGCTCTA	CATTCTCACC	AAGGATGAGG	650
	GAGGCCGCCA	CACTCCCTTC	GTCAACAAC	ACCGCCAC	AATGTTCTTC	700
	AGAACTGTTG	ATGTTACCGC	CATCCTTAAG	CACCCCCCTG	GTACCCCGCA	750
15	TGCTGATGAG	AAGATGGTCA	TGCCCCGAGA	CAACGTTCAA	CTCGAGTGCG	800
	AGCTCTT					807

20 2) INFORMATION FOR SEQ ID NO: 1877

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 806 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter gracilis*
 - (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877

35	AGTTGTTTCT	GCTGCGGATG	GTCCTATGCC	TCAAACTCGC	GAGCATATCT	50
	TGCTTTCTCG	TCAAGTAGGC	GTTCCATACA	TCGTAGTTTT	CCTAAACAAA	100
	ACCGATATGG	TCGATGATCC	GGATCTTTTA	GAGTTAGTTG	AAGAGGAAGT	150
	TAGAGATCTT	TTAAAGAGT	ATAAATTCCC	TGGCGACGAA	ACCCAATCA	200
10	TTAAGGGTTC	TGCTCTTAAG	GCTCTTGAGG	AAGCTAAGGC	CGGACAAGAC	250
	GGCGAATGGT	CTGCAAAGAT	TATGGAGCTT	ATGGACGCGG	TTGATAGCTA	300
	TATTCCAAC	CCTGTTCGCG	ATACTGATAA	AGATTTCTCT	CTTCCGATCG	350
	AAGATATTTT	CTCGATTTCC	GGTCGCGGTA	CCGTTGTAAC	CGGTAGAATC	400
	GAAAAAGGTA	TCGTAAAGT	TGGTGATACT	ATCGAGATCG	TAGGTATTAA	450
15	ACCTACTCAG	ACTACTACCG	TCACTGGCGT	TGAGATGTTT	AGAAAAGAGA	500
	TGGATCAAGG	TGAAGCCGGC	GATAATGTAG	GTGTTTTATT	GCGCGGTACT	550
	AAGAAAGAGG	AAGTAGAGCG	CGGTATGGTT	TTATGCAAAC	CAAAATCGAT	600
	CACTCCTCAT	ACTAAATTTG	AGGGCGAGGT	TTATATCCTA	ACTAAAGAAG	650
	AAGGCGGACG	CCATACTCCA	TTCTTTAATA	ATTATAGACC	GCAGTTTAC	700
30	GTTTCGTACG	CAGATGTTAC	CGGTTTCGAT	ACTCTTCCTG	AAGGAACCGA	750
	GATGGTTATG	CCGGGCGACA	ACGTTAAAAT	CACCGTTGAG	CTAATCGCTC	800
	CGATCG					806

2) INFORMATION FOR SEQ ID NO: 1878

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33292
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878

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GCTGCAGATG GCCCTATGCC ACAAACTAGA GAGCACATTC TTCTTTCTCG      50
TCAAGTAGGC GTTCCATATA TTGTTGTTTT TATGAATAAA GCAGATATGG      100
TTGATGATGC TGAACTTTTA GAGTTAGTTG AAATGGAAAT TAGAGAATTA      150
20 TTAAGCTCTT ATGATTTCCC AGGCGATGAT ACACCTATTA TTTCTGGTTC      200
TGCTTTAAAA GCTCTTGAAG AAGCTAAAGC TGGACAAGAT GGTGAATGGT      250
CAGCAAAAAT TATGGATCTT ATGGCTGCAG TTGATAGCTA TATTCCAACT      300
CCAACTCGTG AACTGAAAA AGACTTCTTG ATGCCAATTG AAGATGTTTT      350
CTCAATTTCA GGTCTGGTA CTGTTGTAC AGGTAGAATT GAAAAAGGTG      400
25 TTGTAAAGT AGGTGATACT ATCGAAATCG TTGGTATTAA AGATACTCAA      450
ACAACAACG TAACAGGTGT TGAAATGTTC AGAAAAGAAA TGGATCAAGG      500
CGAAGCAGGA GATAACGTAG GTGTTCTTCT TCGTGGTACT AAAAAAGAAG      550
AAGTTATCCG TGGTATGGTT CTTGCTAAAC CAAAATCAAT TACTCCACAC      600
ACTGACTTCG AAGCTGAAGT TTATATCTTA AATAAAGATG AAGGTGGTAG      650
30 ACATACTCCA TTCTTTAACA ACTATAGACC ACAGTTTAT GTAAGAACAA      700
CTGATGTTAC AGGTTTCGATT AAATTAGCTG ATGGTGTTGA AATGGTTATG      750
CCAGGTGAAA ATGTGAGAAT TACTGTAAGC TTGATCGCTC CAGTAGCACT      800
TGAAGA                                                    806

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35

2) INFORMATION FOR SEQ ID NO: 1879

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879

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ATGTATGCAA CCGAGAGCAC TCCCGGATCT TGGTTTAAAT GGCACATAA      50

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	TAAGACAGGC	CTCAAAC TCG	AGAGCATTTA	CTTCTCGCCC	GTCAGATCGG	100
	TATCCAAAAA	ATCGTCGTCT	TCGTGAACAA	GGTTGATGCC	ATCGAGGACA	150
	AAGAGATGTT	GGAGCTTGTT	GAATTGGAGA	TGCGTGAAC T	CCTAACCAGC	200
	TACGGTTTCS	AGGGTGAAGA	AACTCCCATC	ATTTT TGGCT	CTGCTCTCTG	250
5	TGCCCTCSAA	GGAAGACAAC	CCGAGATCGG	TGTTACCAAG	ATTGATGAGC	300
	TCTTGCAGGC	CGTCGACACC	TGGATTCCCA	CTCCTCAGCG	TGAGACTGAC	350
	AAGCCCTTCT	TGATGTCCAT	TGAGGAAGTG	TTCTCTATTT	CCGGACGAGG	400
	AACCGTTGTC	TCCGGCCGTG	TGGAGCGTGG	TATCCTCAAG	AAGGACTCCG	450
	AAGTTGAAAT	TGTCGGCGGT	TCGCCCCGAGC	CAATCAAAAAC	CAAGGTTACC	500
10	GATATCGAAA	CCTTTAAGAA	GTCTTGCGAC	GAGTCTCGCG	CTGGTGATAA	550
	CTCCGGCTTG	CTCCTACGAG	GCGTTAAGCG	TGAAGATATT	AGCCGTGGCA	600
	TGGTCGTCGC	TGTACCAGGA	AGTGTC AAG	CCCATACTGA	ATTCTTAGTT	650
	TCGCTTTACG	TCCTCACCGA	AGCTGAGGGT	GGGCGCAAAT	CTGGATTCAG	700
	CAGCAAGTAC	CGCCACAG A	TGTTCAATCG	CACTGCCGGT	ATGTAATACT	750
15	GTGATAATTT	CGTTGACATG	GTACTGATTG	AATTCTATAG	ACGAAGCGGC	800
	TCAGCTCAGC	TGGCCCGGAG	AAGATCAAGA	CAAGATGGCT	ATGCCAGGAG	850
	ACAATATCGA	AATGATT TGC	ACCACCTTGC	ACCCAGTTGC	CGCCGA	896

20

2) INFORMATION FOR SEQ ID NO: 1880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880

	CTGGTAGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACYC	GTGAGCACAT	50
	CCTGCTGGGT	CGCCAGGTTG	GCGTGCCATA	CATCATCGTG	TTCCTGAACA	100
	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAGCTGGT	TGAAATGGAA	150
10	GTMCGTGACC	TGCTGTCACA	GTACGACTTC	CCAGGCGACG	ACACGCCAAT	200
	CGTGCRYGGT	TCTGCGCTGA	AAGCGCTGGA	RGGCGAAGCA	GAGTGGGAAG	250
	CGAAGATCAT	CGAACTGGCT	GGCCATCTGG	ATAACTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAACC	GTTCTGCTG	CCAATTGAAG	ACGTGTTCTC	350
	CATCTCTGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	CGCGGTRTSG	400
15	TTAAAGTGGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	TACCGTGAAA	450
	TCAACCTGTA	CCGGCGTTGA	GATGTTCCGT	AAGCTGCTGG	ACGAAGGCCG	500
	TGCGGGTGAG	AACTGTGGTA	TCCTGCTGCG	CGGTATCAAG	CGCGAAGATA	550
	TCCAGCGTGG	TCAGGTTCTG	GCGAAGCCAG	GCACCATCAA	GCCACACACC	600
	AAGTTCGAGT	CAGAAGTTTA	TATTCTGTCT	AAAGACGAAG	GCGGCCGTCA	650
50	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACCGG	GACTATCGAA	CTGCCAGAAG	GCGTTGAGAT	GGTGATGCCA	750
	GGCGACAACA	TTCAGATGGT	TGTGACCCTG	ATCCACCCGA	TCGCCATG	798

2) INFORMATION FOR SEQ ID NO: 1881

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881

20 ATCCTGGTTG TTGCTGCGAC TGACGGYCCG ATGCCGCAGA CCCGTGAGCA 50
 CATCCTGCTG GGTCTGCAGG TAGGCGTTCC GTACATCATC GTGTTCTCTGA 100
 ACAAATGCGA CATGGTTGAT GACGAAGAGC TGCTGGAAC TGGTTGAAATG 150
 GAAGTTCGYG AACTGCTGTC TCAGTACGAC TTCCCGGGCG ACGACACTCC 200
 GATCGTTCGT GGTTCCTGCTC TGAAAGCGCT GGAAGGCGAC GCAGAGTGGG 250
 AAGCGAAAAT CATCGAACTG GCTGGCTTCC TGGATTCTTA CATYCCGGAA 300
 CCAGAGCGTG CGATTGACAA GCCGTTCTCTG CTGCCGATCG AAGACGTATT 350
 25 CTCCATCTCC GGTCTGTTGTA CCGTTGTTAC CCGTCGTGTA GARCGCGGTA 400
 TCATCAAAGT GGGCGAAGAA GTTGAAATCG TTGGTATCAA AGAGACTCAG 450
 AAGTCTACCT GTACTGGCGT TGAAATGTTT CGCAAAC TGC TGGACGAAGG 500
 CCGTGCCGGT GAGAACGTAG GTGTTCTGCT GCGTGGTATC AAACGTGAAG 550
 AAATCGAACG TGGTCAGGTA CTGGCTAAGC CGGGCACCAT CAAGCEGCAC 600
 30 ACCAAGTTCG AATCTGAAGT GTACATTCTG TCCAAAGATG AAGGCGGCCG 650
 TCATACTCCG TTCTTCAAAG GCTACCGTCC GCAGTTCTAC TTCCGTACTA 700
 CTGACGTGAC TGGCACCATC GAACTGCCGG AAGGCGTAGA GATGGTAATG 750
 CCGGGCGACA ACATCAAAT GGTGTGTTACC CTGATCCACC CGATCGCGAT 800
 GGACGACGGT 810

35

2) INFORMATION FOR SEQ ID NO: 1882

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: BM10711
 (C) ACCESSION NUMBER : AF015628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882

	ATGAATTTT	ATTTAGAGGA	GTTTAACTTG	TCTATTCCCG	ATTCAGGTCC	50
	ATACGGTATA	ACTTCATCAG	AAGACGGAAA	GGTATGGTTC	ACACAACATA	100
	AGGCAAACAA	AATCAGCAGT	CTAGATCAGA	GTGGTAGGAT	AAAAGAATTC	150
5	GAAGTTCCTA	CCCCTGATGC	TAAAGTGATG	TGTTTAATTG	TATCTTCACT	200
	TGGAGACATA	TGGTTTACAG	AGAATGGTGC	AAATAAAATC	GGAAAGCTCT	250
	CAAAAAAAGG	TGGCTTTACA	GAATATCCAT	TGCCACAGCC	GGATTCTGGT	300
	CCTTACGGAA	TAACGGAAGG	TCTAAATGGC	GATATATGGT	TTACCCAATT	350
	GAATGGAGAT	CGTATAGGAA	AGTTGACAGC	TGATGGGACT	ATTTATGAAT	400
10	ATGATTTGCC	AAATAAGGGA	TCTTATCCTG	CTTTTATTAC	TTTAGGTTTCG	450
	GATAACGCAC	TTTGGTTCAC	GGAGAACCAA	AATAATTCTA	TTGGAAGGAT	500
	TACAAATACA	GGGAAATTAG	AAGAATATCC	TCTACCAACA	AATGCAGCGG	550
	CTCCAGTGGG	TATCACTAGT	GGTAACGATG	GTGCACTCTG	GTTTGTGCGAA	600
	ATTATGGGCA	ACAAAATAGG	TCGAATCACT	ACAACGGTG	AGATTAGCGA	650
15	ATATGATATT	CCAACTCCAA	ACGCACGTCC	ACACGCTATA	ACCGCGGGGA	700
	AAAATAGCGA	AATATGGTTT	ACTGAATGGG	GGGCAAATCA	AATCGGCAGA	750
	ATTACAAACG	ACAAAACAAT	TCAAGAATAT	CAACTTCAA	CAGAAAATGC	800
	GGAACCTCAT	GGTATTACCT	TTGGAAAAGA	TGGATCCGTA	TGGTTTGCAT	850
	TAAAATGTAA	AATTGGGAAG	CTGAATTTGA	ACGAATGA		888
20						

2) INFORMATION FOR SEQ ID NO: 1883

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883

35 AGCCGCTTGA GCAAATTAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1884

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884

50

GTATCCCGCA GATAAATCAC CAC

23

2) INFORMATION FOR SEQ ID NO: 1885

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885

AGCGAAAAAC ACCTTGCCGA C

21

15

2) INFORMATION FOR SEQ ID NO: 1886

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886

GACGCCCCGCG CCACCACT

18

30

2) INFORMATION FOR SEQ ID NO: 1887

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887

45 GACGCCCCGCG ACACCACTA

19

2) INFORMATION FOR SEQ ID NO: 1888

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888

GACGCCCCGCA ACACCACTA

19

10

2) INFORMATION FOR SEQ ID NO: 1889

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889

GTTCGCAACT GCAGCTGCTG

20

25

2) INFORMATION FOR SEQ ID NO: 1890

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890

40

TTCGCAACGG CAGCTGCTG

19

2) INFORMATION FOR SEQ ID NO: 1891

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891

CCGGAGCTGC CGAICGGG

18

5

2) INFORMATION FOR SEQ ID NO: 1892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892

CGGAGCTGCC AARCGGGG

18

20

2) INFORMATION FOR SEQ ID NO: 1893

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893

35 GGAGCTGGCG ARCGGGGT

18

2) INFORMATION FOR SEQ ID NO: 1894

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894

50

GACCGGAGCT AGCGARCG

18

2) INFORMATION FOR SEQ ID NO: 1895

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895

15 CGGAGCTAGC AARCGGGGT

19

2) INFORMATION FOR SEQ ID NO: 1896

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896

30 GAAACGGAAC TGAATGAGGC G

21

2) INFORMATION FOR SEQ ID NO: 1897

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897

45 CATTACCATG GGCGATAACA G

21

50 2) INFORMATION FOR SEQ ID NO: 1898

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898

CCATTACCAT GAGCGATAAC AG

22

10

2) INFORMATION FOR SEQ ID NO: 1899

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: 15571
- (C) ACCESSION NUMBER: AF124984

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899

30	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
35	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
40	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
45	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
	GGCAACGCTA	A				861

50

2) INFORMATION FOR SEQ ID NO: 1900

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: SLK-47
- (C) ACCESSION NUMBER: Y11069

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900

15	CTGTTAGCCA	CCCTGCCGCT	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	50
	GCAAATTAAA	CTAAGCGAAA	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	100
	AAATGGATCT	GGCCAGCGGC	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	150
	CGCTTTCCCA	TGATGAGCAC	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	200
	GGCGCGGGTG	GATGCCGGTG	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	250
20	GCCAGCAGGA	TCTGGTGGAC	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	300
	GACGGCATGA	CGGTCGGCGA	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	350
	TAACAGCGCC	GCCAATCTGC	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	400
	TGACTGCCTT	TTTGCGCCAG	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	450
	TGGGAAACGG	AACTGAATGA	GGCGCTTCCC	GGCGACGCCC	GCGCCACCAC	500
25	TACCCCGGCC	AGCATGGCCG	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	550
	GTCTGAGCGC	CCGTTTCGCA	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	600
	CGGGTCGCCG	GACCGTTGAT	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	650
	CGCCGATAAG	ACCGGAGCTG	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	700
	TGCTTGCCCC	GAATAACAAA	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	750
30	GATACCCCGG	CGAGCATGGC	CGAGCGAAAT			780

2) INFORMATION FOR SEQ ID NO: 1901

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: U92041

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901

50	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200

CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
 ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
 TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA 350
 ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
 5 TACTGGCCAC CGTCGGCGGC CCCGCGAGGAT TGA CTGCCTT TTTGCGCCAG 450
 ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
 GGCGCTTCCC GGCGACGCC GCAACACCAC TACCCCGGCC AGCATGGCCG 550
 CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA 600
 CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT 650
 10 CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG 700
 GCGAGCGGGG TGCGCGCGGG ATTGTGCGCC TGCTTGGCCC GAATAACAAA 750
 GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACCCCGG CGAGCATGGC 800
 CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
 GGCAACGCTA A 861
 15

2) INFORMATION FOR SEQ ID NO: 1902

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 30 (B) STRAIN: 803
 (C) ACCESSION NUMBER: AF164577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902

35 ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT 50
 GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CAAAGCGAAA 100
 GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC 150
 CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC 200
 CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
 40 ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
 TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA 350
 ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
 TGCTGGCCAC CGTCGGCGGC CCCGCGAGGAT TGA CTGCCTT TTTGCGCCAG 450
 ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
 45 GGCGCTTCCC GGCGACGCC GCGACACCAC TACCCCGGCC AGCATGGCCG 550
 CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA 600
 CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT 650
 CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG 700
 CCGAGCGGGG TGCGCGCGGG ATTGTGCGCC TGCTTGGCCC GAATAACAAA 750
 50 GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACGCGG CGAGCATGGC 800
 CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
 GGCAACGCTA A 861

2) INFORMATION FOR SEQ ID NO: 1903

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 700603
 (C) ACCESSION NUMBER: AF132290

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903

	ATGCGTTATT	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
20	GCCAGCTGTC	GGGCAGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
25	ACTCTGTGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TGCTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
30	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	CCAAACGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
	GCAGAGCGGA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
35	GGCAACGCTA	ACCCGGCGGT	GGCCGCGCGC	GTTATCCGGC	TCGTAG	896

2) INFORMATION FOR SEQ ID NO: 1904

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: JC2926
 (C) ACCESSION NUMBER: AF148851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904

	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
5	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
10	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
15	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGCCCC	GAATAACAAA	750
	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
20	GGCAACGCTA	A				861

2) INFORMATION FOR SEQ ID NO: 1905

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (C) ACCESSION NUMBER: AF096930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905

40	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
45	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTAC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
50	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700

GCAAACGGGG TGC GCGCGGG ATTGTCGCCC TGCTTGGCCC GAATAACAAA 750
 GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACGCCGG CGAGCATGGC 800
 CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
 GGCAACGCTA A 861

5

2) INFORMATION FOR SEQ ID NO: 1906

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906

20 CCTTATTCCC TTTTTTGCGG

20

2) INFORMATION FOR SEQ ID NO: 1907

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907

35

CACCTATCTC AGCGATCTGT CT

22

40 2) INFORMATION FOR SEQ ID NO: 1908

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908

AACAGCGGTA AGATCCTTGA GAG

23

2) INFORMATION FOR SEQ ID NO: 1909

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909

ATGACTTGGT TAAGTACTCA CC

22

15

2) INFORMATION FOR SEQ ID NO: 1910

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910

ATGACTTGGT TGAGTACTCA CC

22

30

2) INFORMATION FOR SEQ ID NO: 1911

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911

45 CCATAACCAT GGGTGATAAC AC

22

50

2) INFORMATION FOR SEQ ID NO: 1912

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid

1000